



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 168695

TO: Patricia Duffy  
Location: rem/3B05/3C18  
Art Unit: 1645  
Wednesday, July 13, 2005  
Case Serial Number: 10/063546

From: Toby Port  
Location: Biotech-Chem Library  
REM-1A59  
Phone: 571-272-2523  
[toby.port@uspto.gov](mailto:toby.port@uspto.gov)

### Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port  
X22523

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## Duffy, Patricia

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**From:** Duffy, Patricia  
**Sent:** Sunday, July 10, 2005 10:27 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** SPDI search

10/063,546

SEQ ID NO:38 and oligomers thereof.  
standard spdi output.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

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STIC-Biotech/ChemLib

158696

mg

From: Duffy, Patricia  
Sent: Sunday, July 10, 2005 10:27 AM  
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Subject: SPDI search

10/063,546

SEQ ID NO:38 and oligomers thereof.  
standard spdi output.

Patricia A. Duffy, Ph.D.  
Art Unit 1645  
Remsen 3B05; Mailbox 3C18  
571-272-0855

RECEIVED  
JUL 11 2005  
STIC

*Needs Nirap.spdi*

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: July 12, 2005, 17:08:52 / Search time 168 Seconds  
(without alignments)  
1657,544 Million cell updates/sec

Title: US-10-063-546-38  
Perfect score: 3945  
Sequence: 1 MEGACYTQGLTFLLQLLS.....LSTAFKVLPEKDMIRNMK 720  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database: A\_Geneseq\_16Dec04:\*  
1: geneseqp1960s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66695	standard;	protein;	720	AA.	
DE	Membrane-bound protein					PRO1344.
PN	W09963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 3;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					sequence #85.
PN	W0200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	W0200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 4						
ID	AA86518	standard;	protein;	720	AA.	
DE	Human PRO1344 (UN0659)					protein sequence SEQ ID NO:231.
PN	W020073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 4;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 5						
ID	AA695869	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane					protein PRO1344.
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 5;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 6						
ID	ABU58484	standard;	protein;	720	AA.	

DE	Human PRO polypeptide					#85.
PN	US2003027272-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 7						
ID	ABU86032	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane					protein PRO1344.
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane					protein (PRO) #85.
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 9						
ID	ABR66221	standard;	protein;	720	AA.	
DE	Human secreted polypeptide					PRO1344, SEQ ID NO:170.
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	
DE	Human secreted polypeptide					PRO1344, SEQ ID NO:170.
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 11						
ID	ABU95551	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane					protein (PRO) #85.
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					#65.
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	
DE	Novel human secreted or transmembrane					protein PRO1344.
PN	US2002113252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane					protein PRO1344.
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	
DE	Human PRO polypeptide					#85.
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 3945;	DB 6;	Length 720;		
Best Local Similarity	100.0%;	Pred. No. 1.5e-204;				
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane					protein PRO1344.
PN	US2003036147-A1.					

PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 17  
ID ABR68160 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 18  
ID ABU60542 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
FN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 19  
ID ABU96213 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 20  
ID ABU92644 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 21  
ID ABO08721 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 22  
ID ABO02773 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 23  
ID ABR74927 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 24  
ID ABR94689 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
FN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 25  
ID ABU13924 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
FN US2002103125-A1.  
PD 01-NOV-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 26  
ID ABU85662 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 27  
ID ABU98822 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 28  
ID ABU98037 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 29  
ID ABU91743 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US200302277-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 30  
ID ABU89436 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
FN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 31  
ID ABU86277 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 32  
ID ABU67490 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
FN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 33  
ID ABU80518 standard; protein; 720 AA.  
DE Human PRO protein #85.  
FN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 34  
ID ABU72509 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 35  
ID ABU90894 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
FN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 36  
ID ABO33953 standard; protein; 720 AA.

DE Human secreted/transmembrane protein PRO1344.  
PN US200309013-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 37  
ID ABR99436 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 38  
ID ABR99826 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 39  
ID ABO16349 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 40  
ID ABR9249 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 41  
ID ABO1890 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 42  
ID ABR7811 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 43  
ID ABO71970 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003018183-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 44  
ID ABO85047 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 45  
ID ABO00186 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 46  
ID ABO1518 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040060-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 47  
ID ABO02163 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 48  
ID ABO8737 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 49  
ID ABO83432 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 50  
ID ABO0623 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 51  
ID ABR5269 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 52  
ID ABO09331 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 53  
ID ABO19195 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 54  
ID ABO1213 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 55  
ID ABR6631 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 56  
ID ABO16044 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040060-A1.

PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 57  
ID AB013750 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US200304916-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 58  
ID AB071524 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US200301385-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 59  
ID AB056553 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, SEQ ID 170.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 60  
ID AB007501 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 61  
ID AB003688 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 62  
ID AB067136 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 63  
ID AB015739 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 64  
ID AB056020 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 65  
ID AB072305 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 66  
ID AB055348 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032102-A1.

PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 67  
ID AB095293 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 68  
ID AB071196 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 69  
ID AB007806 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 70  
ID AB070047 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 71  
ID AB069380 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 72  
ID AB001521 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 73  
ID AB081323 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 74  
ID AB060120 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 75  
ID AB090978 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 76  
ID AB067855 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027269-A1.

PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 77  
ID ABR65243 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 78  
ID ABR6465 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 79  
ID ABR71877 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 80  
ID ABUS9258 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 81  
ID ABUS5357 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 82  
ID ABUS9047 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 83  
ID ABUS3127 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 84  
ID ABUS9493 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 85  
ID ABUS9531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 86  
ID ABUS84042 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 87  
ID ABUS9693 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 88  
ID ABO25955 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 89  
ID ABR64938 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 90  
ID ABO27299 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 91  
ID ABR68770 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 92  
ID ABO06586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 93  
ID ABR99131 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 94  
ID ABUS7015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 95  
ID ABUS5967 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 96  
ID ABUS8254 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 97  
ID ABU87265 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 98  
ID ABU83737 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 99  
ID ABO08111 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 100  
ID ABU92494 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003045684-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 101  
ID ABO81822 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 102  
ID ABU65986 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 103  
ID ABU81164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US2003027212-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 104  
ID ABR59815 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 105  
ID ABU94003 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036155-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 106  
ID ABU99856 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022396-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 107  
ID ABR66526 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 108  
ID ABR90944 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 109  
ID ABO5379 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003027986-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 110  
ID ABU58964 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2002142961-A1.  
PD 03-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 111  
ID ABU94371 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 112  
ID ABU79253 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 113  
ID ABR6582 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 114  
ID ABR8687 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 115  
ID ABU94676 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 116  
ID ABO04603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;



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RESULT 117
ID ABR70352 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 118
ID ABU92342 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003023187-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 119
ID ABU98517 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 120
ID ABR65916 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 121
ID ABR64633 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 122
ID ABU59407 standard; protein; 720 AA.
DE Novel human secreted or transmembrane protein PRO1109.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 123
ID ABU79558 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 124
ID ABU92949 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 125
ID ABU95908 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 126
ID ABU91128 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 127
ID ABU90221 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 128
ID ABO09636 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 129
ID ABO10908 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 130
ID ABR70962 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 131
ID ABU98281 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 132
ID ABU87570 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 133
ID ABU91438 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 134
ID ABU89286 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 135
ID ABU84652 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 136
ID ABR69742 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;
Pred. No. 1.5e-204;
RESULT 137
ID ABU80119 standard; protein; 720 AA.
DE Human PRO protein #85.
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PN US2003036139-A1.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 138  
ID AB082493 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 139  
ID AB092173 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 140  
ID AB093388 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 141  
ID AB009941 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 142  
ID AB009026 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 143  
ID AB096457 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 144  
ID AB010879 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 145  
ID AB010594 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 146  
ID AB061631 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 147

ID AB072127 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003023042-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 148  
ID AB095603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 149  
ID AB096812 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 150  
ID AB070657 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 151  
ID AB005008 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 152  
ID AB008416 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 153  
ID AB088570 standard; protein; 720 AA.  
DE Human secreted and transmembrane polypeptide PRO1344.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 154  
ID AB034084 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 155  
ID AB005623 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 156  
ID AB074012 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 157  
ID ABR95604 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 158  
ID ABR80901 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 159  
ID ABR81206 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 160  
ID ABM00902 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 161  
ID ABR88504 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 162  
ID ABM77325 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 163  
ID ABO28809 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 164  
ID ABO31554 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 165  
ID ABM07971 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 166

ID ABO40451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068682-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 167  
ID ABO35876 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 168  
ID ABO44015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 169  
ID ADA77922 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 170  
ID ABM24810 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003106539-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 171  
ID ABO03078 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 172  
ID ABR90334 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 173  
ID ABM17248 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 174  
ID ABR94994 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 175  
ID ABR95299 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 176
ID ADB17095 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38)
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 177
ID ABO21537 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 178
ID ABR97801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 179
ID ABR97589 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 180
ID ABM7630 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 181
ID ABM27860 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 182
ID ABM06141 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 183
ID ABM03647 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 184
ID ABM35098 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 185
ID ABM26335 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 186
ID ABO48117 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 187
ID ABR92859 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 188
ID ABO24620 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 189
ID ADA37742 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003068297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 190
ID ABM11631 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 191
ID ABM02732 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 192
ID ABM16028 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 193
ID ABO27589 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 194
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ID ABM29080 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068721-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 195  
ID ABM07056 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 196  
ID ABM21150 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 197  
ID ABM09496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 198  
ID ABO41366 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 199  
ID ABO36181 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 200  
ID ABO43710 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 201  
ID ABM76410 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 202  
ID ABM76106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 203  
ID ABM25725 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104542-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 204  
ID ABM26030 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 205  
ID ADA21428 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 206  
ID ABO03383 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 207  
ID ABO02468 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 208  
ID ABO44257 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 209  
ID ABR90639 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 210  
ID ABR73707 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 211  
ID ABO16959 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 212  
ID ABR94384 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044917-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 213  
ID ABR75891 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003044829-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 214  
ID ABR71267 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 215  
ID ABR93164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 216  
ID ABR93469 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 217  
ID ADA10215 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 218  
ID ABR7894 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 219  
ID ABO27894 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 220  
ID ABO30029 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 221  
ID ABO33238 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 222  
ID ABM04926 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 223  
ID ABM0886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 224  
ID ABO36486 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 225  
ID ABO35571 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 226  
ID ABO39536 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 227  
ID ABM10411 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 228  
ID ABM1936 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 229  
ID ABO52082 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 230  
ID ABO52387 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 231  
ID ADA19900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 232  
ID ABO23705 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003032134-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 233  
ID ADB17283 standard; protein; 720 AA.  
DE Human transmembrane PRO polypeptide (SegID 38).  
PN US2003050465-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 234  
ID ADH17759 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003054987-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 235  
ID ABR97191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054481-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 236  
ID ABR86979 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049778-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 237  
ID ABM11021 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049782-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 238  
ID ABM28165 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054476-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 239  
ID ABO32164 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003068733-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 240  
ID ABM15291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068692-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 241  
ID ABM06446 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068709-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 242  
ID ABM04257 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068716-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 243  
ID ABM22370 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068740-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 244  
ID ABM07666 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068751-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 245  
ID ABO40756 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003068684-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 246  
ID ABM35403 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073179-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 247  
ID ABM33166 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003087374-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 248  
ID ABO52692 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049773-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 249  
ID ABO50252 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049777-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 250  
ID AB09246 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003040055-A1.

PD 27-FEB-2003. 100.0%; Score 3945; DB 6; Length 720;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 251  
ID ABO04298 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036164-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 252  
ID ABO05928 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040074-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 253  
ID ABM18468 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054480-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 254  
ID ADA27867 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 255  
ID AB897496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059885-A1.  
PD 27-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 256  
ID ABR80596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049740-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 257  
ID ABM01207 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049770-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 258  
ID ABR88809 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073169-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 259  
ID ABM13461 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064457-A1.  
PD 03-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 260  
ID ABM20845 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068711-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 261  
ID ABO41976 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049745-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 262  
ID ABO42586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049751-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 263  
ID ABM10106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003067478-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 264  
ID ABO38621 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068773-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 265  
ID ABM32861 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073185-A1.  
PD 17-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 266  
ID ABM22675 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003087373-A1.  
PD 08-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 267  
ID ABM74886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096353-A1.  
PD 22-MAY-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 268  
ID ADA79714 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073173-A1.  
PD 17-APR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;  
RESULT 269  
ID ABR96276 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054458-A1.  
PD 20-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 3945; DB 6; Length 720;



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Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 270
ID ABM02427 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US200305986-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 271
ID ABM86369 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 272
ID ABM8674 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 273
ID ABM16638 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 274
ID ABM29690 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 275
ID ABO29114 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 276
ID ABM23895 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 277
ID ABM23285 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 278
ID ABM22065 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 279
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 280
ID ABM28470 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 281
ID ABM28775 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 282
ID ABM66419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 283
ID ABM75801 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 284
ID ABM34081 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 285
ID ABM34386 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 286
ID ABO20317 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 287
ID ABO21232 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 288
ID ABO22147 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 289  
ID ADA20072 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344.  
PN US2003055222-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 290  
ID ABO34185 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003060601-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 291  
ID ABR6581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054460-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 292  
ID ADA94447 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 293  
ID ABR85759 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049753-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 294  
ID ABR9741 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049763-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 295  
ID ABM00597 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 296  
ID ABM00292 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073172-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 297  
ID ABO29724 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068700-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 298

ID ABM23590 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068736-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 299  
ID ABM29385 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068679-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 300  
ID ABO38316 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068767-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 301  
ID ABO45616 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003073182-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 302  
ID ABM20540 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104557-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 303  
ID ADA81441 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003092121-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 304  
ID ABO16654 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003027276-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 305  
ID ABO18280 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044920-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 306  
ID ABO22707 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027265-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 307  
ID ABO23012 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054461-A1.  
PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 308  
ID ABR92554 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US200306446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 309  
ID ABR81511 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 310  
ID ABM77935 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 311  
ID ABR89724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073171-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 312  
ID ABM2640 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 313  
ID ABM13766 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 314  
ID ABO28504 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 315  
ID ABO30334 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 316  
ID ABM07361 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 317  
ID ABM03952 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 318  
ID ABO37096 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 319  
ID ABO41671 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 320  
ID ABO35266 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 321  
ID ABM25115 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 322  
ID ABO47507 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 323  
ID ABO47812 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 324  
ID ABO48422 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 325  
ID ABO51472 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049766-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 326  
ID ABO51777 standard; protein; 720 AA.

DE Human PRO polypeptide #85.  
PN US2003049767-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 327  
ID ABO50557 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 328  
ID ABR79681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 329  
ID ABM16943 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 330  
ID ABO17975 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 331  
ID ABO20927 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 332  
ID ABR96886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 333  
ID ADA38672 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 334  
ID ABM12241 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 335  
ID ABM16333 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 336  
ID ABM24200 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 337  
ID ABM14681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068696-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 338  
ID ABM04562 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 339  
ID ABM06751 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 340  
ID ABM09191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 341  
ID ABO39231 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 342  
ID ABM75496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 343  
ID ABM25420 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 344  
ID ABM19930 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 345  
ID ABO46836 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.

PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 346  
ID ABO47141 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049765-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 347  
ID ADA83239 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049752-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 348  
ID ABR71572 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032133-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 349  
ID ABR7182 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032136-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 350  
ID ABR98521 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036129-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 351  
ID ABO06891 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040053-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 352  
ID ABR64844 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040057-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 353  
ID ABR73402 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054467-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 354  
ID ABR76496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044932-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 355  
ID ABR73097 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027270-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 356  
ID ABM18163 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054469-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 357  
ID ABO20622 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032126-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 358  
ID ABO25365 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054463-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 359  
ID ABO25670 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003054466-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 360  
ID ABR94079 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059879-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 361  
ID ADA92793 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 362  
ID ABR79986 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049738-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 363  
ID ABM11326 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064469-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 364  
ID ABO32933 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003064453-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 365  
ID ABO30639 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 366  
ID ABO30944 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 367  
ID ABM27250 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 368  
ID ABM29995 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 369  
ID ABM05531 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 370  
ID ABM15596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 371  
ID ABM08581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 372  
ID ABO42281 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 373  
ID ABO38011 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 374  
ID ABO45921 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 375  
ID ABM66724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 376  
ID ADB20282 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 377  
ID ABM19625 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 378  
ID ABO49337 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 379  
ID ABO49642 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 380  
ID ADA78534 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 381  
ID ABR88199 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 382  
ID ADA00369 standard; protein; 720 AA.  
DE Human secreted/cranmembrane polypeptide PRO 1344.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 383  
ID ABM26945 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068739-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 384  
ID ABO03442 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068763-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 385  
ID ABO39841 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068689-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 386  
ID ABO49947 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049776-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 387  
ID ABO50862 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049780-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 388  
ID ABO05318 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036126-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 389  
ID ABR74622 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044924-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 390  
ID ABR77101 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044927-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 391  
ID ABR17858 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040072-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 392  
ID ABR95909 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040073-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 393  
ID ABO21842 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054475-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 394  
ID ABO20012 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032124-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 395  
ID ABO24315 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064467-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 396  
ID ABR86064 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049759-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 397  
ID ABR10716 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064455-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 398  
ID ABR76715 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054465-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 399  
ID ABR89419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073170-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 400  
ID ABR12546 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073176-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 401  
ID ABR05836 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068717-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 402  
ID ABO34961 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.

[illegible]

Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 412			
ID	ABO18585 standard; protein; 720 AA.		
DE	Human secreted/transmembrane protein (PRO) #85.		
PN	US2003044921-A1.		
PD	06-MAR-2003.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 414			
ID	ABM01512 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003059882-A1.		
PD	27-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 415			
ID	ABM02122 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003059884-A1.		
PD	27-MAR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 416			
ID	ABR87284 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003068687-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 417			
ID	ABM12851 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003073186-A1.		
PD	17-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 418			
ID	ABM30605 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003064443-A1.		
PD	03-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 419			
ID	ABM24505 standard; protein; 720 AA.		
DE	Human secreted polypeptide PRO1344, SEQ ID NO:1170.		
PN	US2003064444-A1.		
PD	03-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 420			
ID	ABO29419 standard; protein; 720 AA.		
DE	Human secreted/transmembrane protein (PRO) #85.		
PN	US2003068697-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 421			
ID	ABO29419 standard; protein; 720 AA.		
DE	Human secreted/transmembrane protein (PRO) #85.		
PN	US2003068697-A1.		
PD	10-APR-2003.		
PA	(GETH ) GENENTECH INC.		
Query Match	100.0%;	Score 3945;	DB 7; Length 720;
Best Local Similarity	100.0%;	Pred. No.1.5e-204;	
RESULT 421			



ID ABO31249 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PD US2003068710-A1.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 422  
ID ABM14376 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003068686-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 423  
ID ABM09801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 424  
ID ABO38926 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PD US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 425  
ID ABO31691 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003104538-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 426  
ID ABO51167 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PD US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 427  
ID ABO03993 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PD US2003036158-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 428  
ID ABO10463 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PD US2003036151-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 429  
ID ABO53170 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PD US2003044806-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 430  
ID ABR77706 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003040067-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 431  
ID ABR78916 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003054456-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 432  
ID ABO24010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PD US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 433  
ID ABR3774 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 434  
ID ABM01817 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 435  
ID ABM78240 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 436  
ID ABR90029 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 437  
ID ADA22354 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PD US2003040473-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 438  
ID ABM27555 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 439  
ID ABM13156 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PD US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 440  
ID ABO31859 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068731-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR14071 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068683-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR08276 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068754-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO40146 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068681-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR74581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096351-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR33776 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096358-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR20235 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104556-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO48727 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049756-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO22540 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR72792 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036122-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO15434 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036121-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR85149 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040065-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO15129 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044919-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO17264 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040077-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR17553 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044928-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ADA06520 standard; protein; 720 AA.  
DE Human secreted/transmembrane PRO polypeptide #65.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ADA39213 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR85454 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049746-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABR77020 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054464-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
ID ABO28199 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064459-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;

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Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 460
ID ABM22980 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 461
ID ABM30300 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 462
ID ABM21760 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 463
ID ABM21455 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 464
ID ABM1986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 465
ID ABO41061 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 466
ID ABO36791 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 467
ID ABO37401 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 468
ID ABM75191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 469
ID ABO33471 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 470
ID ABO46226 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 471
ID ADA82605 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 472
ID ADB85611 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 473
ID ADB96239 standard; protein; 720 AA.
DE Human PRO polypeptide #65.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 474
ID ABM31825 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 475
ID ABM31215 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 476
ID ADB85913 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 477
ID ABM32130 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 478
ID ABM32435 standard; protein; 720 AA.
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DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068713-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 479  
ID ADB68290 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 480  
ID ADB68097 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 481  
ID ABM31520 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 482  
ID ABM30910 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 483  
ID ADB90914 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 484  
ID ADC57711 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 485  
ID ADC5075 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 486  
ID ADC11942 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 487  
ID ADC06994 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 488  
ID ADC56364 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 489  
ID ADC11713 standard; protein; 720 AA.  
DE Mammalian PRO polypeptide (SeqID 38).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 490  
ID ADC07419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 491  
ID ADC11409 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 492  
ID ADC11471 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 493  
ID ADC52266 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 494  
ID ADC14531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 495  
ID ADD08063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 496  
ID ADC8188 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 497  
ID ADD07530 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193299-A1.  
PD 19-DEC-2002.

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Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 517  
ID ADH24070 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 518  
ID ADH34096 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 519  
ID ADH29929 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 520  
ID ADH23900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 521  
ID ADH08995 standard; protein; 720 AA.  
DE Human PRO polypeptide #5.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 522  
ID ADG85304 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 523  
ID ADH24580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 524  
ID ADH37746 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 525  
ID ADH02025 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 526  
ID ADH37606 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 527  
ID ADG85644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 528  
ID ADH24240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 529  
ID ADH38534 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 530  
ID ADG83655 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 531  
ID ADH29463 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 532  
ID ADH27579 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 533  
ID ADH37776 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 534  
ID ADH37953 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 535

ID ADH57373 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180920-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 536  
ID ADH53515 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 537  
ID ADH53685 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 538  
ID ADH52021 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 539  
ID ADH49876 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 540  
ID ADI25386 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 541  
ID ADH90179 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 542  
ID ADI25556 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181699-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 543  
ID ADH97730 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 544  
ID ADI35412 standard; protein; 720 AA.

DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 545  
ID ADI03578 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 546  
ID ADI11935 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 547  
ID ADH90009 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 548  
ID ADH99904 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 549  
ID ADH98410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 550  
ID ADI11085 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 551  
ID ADI11595 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 552  
ID ADH98240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 553  
ID ADH99580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181708-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 554
ID ADH98070 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 555
ID ADI05058 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 556
ID ADI03408 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 557
ID ADI04803 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 558
ID ADH78257 standard; protein: 720 AA.
DE Human PRO polypeptide #19.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 559
ID ADI19601 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 560
ID ADH90349 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 561
ID ADI03068 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 562
ID ADH77917 standard; protein: 720 AA.
DE Human PRO polypeptide #19.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 563
ID ADH97900 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 564
ID ADI01285 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 565
ID ADI01980 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 566
ID ADI03238 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 567
ID ADI11425 standard; protein: 720 AA.
DE Human PRO polypeptide #19.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 568
ID ADI02327 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 569
ID ADI11765 standard; protein: 720 AA.
DE Human PRO polypeptide #19.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 570
ID ADI05402 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.5e-204;
RESULT 571
ID ADH79474 standard; protein: 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 3945; DB 7; Length 720;
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Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 572  
ID ADH78087 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 573  
ID ADI05232 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 574  
ID ADH79644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 575  
ID ADI01470 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 576  
ID ADI01640 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 577  
ID ADI01810 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 578  
ID ADH79814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 579  
ID ADI04632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 580  
ID ADI02768 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 581  
ID ADH78087 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 582  
ID ADI25726 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 583  
ID ADI25896 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 584  
ID ADK65408 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 585  
ID ADH98750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 586  
ID ADH79991 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 587  
ID ADL32776 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 588  
ID ADM30310 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 589  
ID ADL93722 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 590

ID ADG52176 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003130483-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 591  
ID ADE74307 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 592  
ID ADE74919 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 593  
ID ADE35357 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 594  
ID ADG11607 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 595  
ID ADP96132 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 596  
ID ADG04403 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 597  
ID ADG00563 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 598  
ID ADH06608 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 599  
ID ADH06438 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 600  
ID ADG68859 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 601  
ID ADH27749 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 602  
ID ADH25090 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 603  
ID ADH33722 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 604  
ID ADG82819 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 605  
ID ADH02365 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 606  
ID ADH07972 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 607  
ID ADG69369 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 608  
ID ADH39190 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 609  
ID ADH26100 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 610  
ID ADG83930 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 611  
ID ADH19477 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 612  
ID ADG85474 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 613  
ID ADH06268 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 614  
ID ADH30098 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 615  
ID ADH24410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 616  
ID ADH33069 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 617  
ID ADG6539 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;

RESULT 618  
ID ADH07802 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 619  
ID ADG85814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 620  
ID ADH39360 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 621  
ID ADH33552 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 622  
ID ADH33892 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 623  
ID ADH01102 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 624  
ID ADG69709 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 625  
ID ADH20970 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 626  
ID ADH02195 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 627  
ID ADG69199 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180847-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 628  
ID ADH85984 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180862-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 629  
ID ADH24920 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180909-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 630  
ID ADH39537 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180915-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 631  
ID ADH20010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003219856-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 632  
ID ADH02535 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180840-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 633  
ID ADH69029 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180849-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 634  
ID ADH07632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180850-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 635  
ID ADH86154 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180863-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 636  
ID ADH24750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180908-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 637  
ID ADH25798 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180911-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 638  
ID ADH38364 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180922-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 639  
ID ADH57203 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181642-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 640  
ID ADH52191 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180921-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 641  
ID ADH49557 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180857-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 642  
ID ADH90519 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181700-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 643  
ID ADH11255 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181683-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 644  
ID ADH98920 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190698-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 645  
ID ADH012150 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190699-A1.

PD 09-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 646  
ID ADH90689 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 647  
ID ADJ54808 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 648  
ID ADJ98564 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181797-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 649  
ID ADJ98734 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 650  
ID ADH78893 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 651  
ID ADJ99127 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 652  
ID ADJ99297 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 653  
ID ADJ98915 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 654  
ID ADH79063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 655  
ID ADK00923 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 656  
ID ADK14444 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 657  
ID ADJ64579 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 658  
ID ADM31475 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 659  
ID ADM36522 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 660  
ID ADM40327 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 661  
ID ADM80893 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 662  
ID ADN37935 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 3945; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 1.5e-204;  
RESULT 663  
ID AAB70532 standard; protein; 720 AA.  
DE Human PRO2 protein sequence SEQ ID NO:4.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.

Query Match 99.8%; Score 3939; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
RESULT 664  
ID AAU00401 standard; protein; 720 AA.  
DE Human secreted protein, POLY13.  
PN WO200119856-A2.  
PD 22-MAR-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 99.8%; Score 3939; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
RESULT 665  
ID ADH89028 standard; protein; 720 AA.  
DE Human POLYX polypeptide #13.  
PN US2003198958-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R. A.  
PA (FERN/) FERNANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LITX/) LITU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLDOG F L.  
PA (SMIT/) SMITHSON G.  
PA (RAST/) RASTELLI L.  
Query Match 99.8%; Score 3939; DB 8; Length 720;  
Best Local Similarity 99.7%; Pred. No. 3.1e-204;  
RESULT 666  
ID AAV88280 standard; protein; 720 AA.  
DE Human TANGO 215 protein.  
PN WO20018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 99.8%; Score 3936; DB 3; Length 720;  
Best Local Similarity 99.7%; Pred. No. 4.5e-204;  
RESULT 667  
ID AAB85891 standard; protein; 737 AA.  
DE Human serine protease-like protein (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 99.4%; Score 3921.5; DB 4; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 668  
ID AAB93670 standard; protein; 737 AA.  
DE Human protein sequence SEQ ID NO:13202.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 99.4%; Score 3921.5; DB 4; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 669  
ID ADJ69990 standard; protein; 737 AA.  
DE Human heat mitochondrial protein as a therapeutic target SegID1796.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 99.4%; Score 3921.5; DB 7; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 670  
ID ADN04640 standard; protein; 737 AA.  
DE Antiproliferative protein sequence #505.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 671  
ID ADS85034 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SegID36.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
PA (UYJU-) UNIV JUNTENDO.

Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 672  
ID ADS85022 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SegID24.  
PN WO2004031386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 99.4%; Score 3921.5; DB 8; Length 737;  
Best Local Similarity 97.6%; Pred. No. 2.8e-203;  
RESULT 673  
ID AAB85893 standard; protein; 762 AA.  
DE Human serine protease-like protein (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 99.4%; Score 3921.5; DB 4; Length 762;  
Best Local Similarity 97.6%; Pred. No. 2.9e-203;  
RESULT 674  
ID AAB85892 standard; protein; 720 AA.  
DE Mouse serine protease-like protein (mc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 99.6%; Score 3612; DB 4; Length 720;  
Best Local Similarity 97.6%; Pred. No. 1.3e-186;  
RESULT 675  
ID AAB09927 standard; protein; 719 AA.  
DE Murine TANGO 215 protein.  
PN WO20018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 91.3%; Score 3602.5; DB 3; Length 719;  
Best Local Similarity 90.1%; Pred. No. 4.1e-186;  
RESULT 676  
ID AAB19180 standard; protein; 649 AA.  
DE Human protease, PRTS-17 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 88.7%; Score 3500.5; DB 5; Length 649;  
Best Local Similarity 90.0%; Pred. No. 1.2e-180;  
RESULT 677  
ID AAB70531 standard; protein; 567 AA.  
DE Human PRO1 protein sequence SEQ ID NO:2.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 78.3%; Score 3089.5; DB 4; Length 567;  
Best Local Similarity 99.5%; Pred. No. 1.4e-158;  
RESULT 678  
ID AAB49533 standard; protein; 570 AA.  
DE Clone HPEPY75.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 74.7%; Score 2946.5; DB 3; Length 570;  
Best Local Similarity 96.8%; Pred. No. 7.2e-151;  
RESULT 679  
ID ADK41485 standard; protein; 551 AA.  
DE Human CD-1-like molecule HSKDF41, SEQ ID NO:284.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 74.6%; Score 2944; DB 5; Length 551;  
Best Local Similarity 99.3%; Pred. No. 9.5e-151;  
RESULT 680  
ID AAM41706 standard; protein; 499 AA.  
DE Human polypeptide SEQ ID NO 6637.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 65.3%; Score 2577.5; DB 4; Length 499;  
 Best Local Similarity 96.6%; Pred. No. 4.8e-131;  
 RESULT 681  
 ID AAE20817 standard; protein; 455 AA.  
 DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:79.  
 PN WO200218435-A1.  
 PD 07-MAR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 61.2%; Score 2413; DB 5; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
 RESULT 682  
 ID ABG64652 standard; protein; 455 AA.  
 DE Human albumin fusion protein #1327.  
 PN WO200177137-A1.  
 PD 18-OCT-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 61.2%; Score 2413; DB 5; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
 RESULT 683  
 ID ADL77919 standard; protein; 455 AA.  
 DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1401.  
 PN US2004010134-A1.  
 PD 15-JUN-2004.  
 PA (ROSE/) ROSEN C A.  
 (HASE/) HASELTINE W A.  
 Query Match 61.2%; Score 2413; DB 8; Length 455;  
 Best Local Similarity 99.3%; Pred. No. 3.2e-122;  
 RESULT 684  
 ID ADL06662 standard; protein; 417 AA.  
 DE Human 3T3 cell conversion promoter FP938.  
 PN CN1403477-A.  
 PD 19-MAR-2003.  
 PA (SHAN-) SHANGHAI XINSHIJI GENE TECH DEV CO LTD.  
 Query Match 52.2%; Score 2059; DB 7; Length 417;  
 Best Local Similarity 95.6%; Pred. No. 3.4e-103;  
 RESULT 685  
 ID AAM39920 standard; protein; 359 AA.  
 DE Human polypeptide SEQ ID NO 3065.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 48.4%; Score 1909; DB 4; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-95;  
 RESULT 686  
 ID AAM39957 standard; protein; 359 AA.  
 DE Human polypeptide SEQ ID NO 3102.  
 PN WO200153312-A1.  
 PD 26-JUL-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 48.4%; Score 1909; DB 4; Length 359;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-95;  
 RESULT 687  
 ID AAE20797 standard; protein; 323 AA.  
 DE Human gene 5 encoded secreted protein HSLGUT5, SEQ ID NO:59.  
 PN WO200218435-A1.  
 PD 07-MAR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 43.3%; Score 1708.5; DB 5; Length 323;  
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
 RESULT 688  
 ID ABG64653 standard; protein; 323 AA.  
 DE Human albumin fusion protein #1328.  
 PN WO200177137-A1.  
 PD 18-OCT-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 43.3%; Score 1708.5; DB 5; Length 323;  
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
 RESULT 689  
 ID ADL77920 standard; protein; 323 AA.  
 DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1402.  
 PN US2004010134-A1.  
 PD 15-JUN-2004.  
 PA (ROSE/) ROSEN C A.

PA (HASE/) HASELTINE W A.  
 Query Match 43.3%; Score 1708.5; DB 8; Length 323;  
 Best Local Similarity 94.1%; Pred. No. 2.1e-84;  
 RESULT 690  
 ID AAM24485 standard; protein; 234 AA.  
 DE Human EST encoded protein SEQ ID NO: 2010.  
 PN WO200154477-A2.  
 PD 02-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 29.8%; Score 1175.5; DB 4; Length 234;  
 Best Local Similarity 91.4%; Pred. No. 7.8e-56;  
 RESULT 691  
 ID ABP72332 standard; protein; 1019 AA.  
 DE Horseshoe crab Factor C.  
 PN WO2003002976-A2.  
 PD 09-JAN-2003.  
 PA (WHIK ) BIOWHITTAKER INC.  
 Query Match 17.0%; Score 672; DB 6; Length 1019;  
 Best Local Similarity 25.6%; Pred. No. 4.1e-28;  
 RESULT 692  
 ID AAM43394 standard; protein; 1019 AA.  
 DE Singapore horseshoe crab factor C proenzyme (CrFC 21).  
 PN SG42456-A1.  
 PD 15-AUG-1997.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 16.9%; Score 665; DB 2; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 693  
 ID AAY05750 standard; protein; 1019 AA.  
 DE Horseshoe crab Factor C.  
 PN WO9915676-A1.  
 PD 01-APR-1999.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 16.9%; Score 665; DB 2; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 694  
 ID AAM94302 standard; protein; 1019 AA.  
 DE Horseshoe crab Factor C protein #2.  
 PN US5858706-A.  
 PD 12-JUN-1999.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 16.9%; Score 665; DB 2; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 695  
 ID AAY42490 standard; protein; 1019 AA.  
 DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.  
 PN US5985590-A.  
 PD 16-NOV-1999.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 16.9%; Score 665; DB 3; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 696  
 ID AAB60935 standard; protein; 1019 AA.  
 DE Horseshoe crab recombinant Factor C #2.  
 PN WO200127289-A2.  
 PD 19-APR-2001.  
 PA (UYSI-) UNIV SINGAPORE NAT.  
 Query Match 16.9%; Score 665; DB 4; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 697  
 ID ABP72334 standard; protein; 1019 AA.  
 DE Horseshoe crab Factor C.  
 PN WO2003002976-A2.  
 PD 09-JAN-2003.  
 PA (WHIK ) BIOWHITTAKER INC.  
 Query Match 16.9%; Score 665; DB 6; Length 1019;  
 Best Local Similarity 25.4%; Pred. No. 9.7e-28;  
 RESULT 698  
 ID AAM43393 standard; protein; 1083 AA.  
 DE Singapore horseshoe crab factor C proenzyme (CrFC 26).  
 PN SG42456-A1.  
 PD 15-AUG-1997.  
 PA (UYSI-) UNIV SINGAPORE NAT.

Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 699  
ID AAY05749 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN WO9915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 700  
ID AAM94301 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C protein #1.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 701  
ID AAY42489 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 3; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 702  
ID AAB60934 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C #1.  
PN WO200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 16.9%; Score 665; DB 4; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 703  
ID AAB7233 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN WO200302976-A2.  
PD 09-JAN-2003.  
PA (WHIK ) BIOWHITTAKER INC.  
Query Match 16.9%; Score 665; DB 6; Length 1083;  
Best Local Similarity 25.4%; Pred. No. 1e-27;  
RESULT 704  
ID AAM41743 standard; protein; 146 AA.  
DE Human polypeptide SEQ ID NO 6674.  
PN WO20015312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 16.8%; Score 662; DB 4; Length 146;  
Best Local Similarity 85.4%; Pred. No. 2.3e-28;  
RESULT 705  
ID AAV11743 standard; protein; 103 AA.  
DE Human 5' EST secreted protein SEQ ID No: 343.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GENST ) GENSET.  
Query Match 14.7%; Score 580; DB 2; Length 103;  
Best Local Similarity 97.1%; Pred. No. 4.3e-24;  
RESULT 706  
ID ADE87459 standard; protein; 699 AA.  
DE Human MB1-associated serine protease-1 protein.  
PN EP1344533-A1.  
PD 17-SEP-2003.  
PA (NATL-) NATLMUNE AS.  
Query Match 12.1%; Score 476; DB 7; Length 699;  
Best Local Similarity 24.6%; Pred. No. 1e-17;  
RESULT 707  
ID ADJ91028 standard; protein; 699 AA.  
DE Human mannos binding lectin amino acid sequence SEQ ID NO:14.  
PN WO2004024925-A2.  
PD 25-MAR-2004.  
PA (NATI-) NATIMUNE AS.  
Query Match 12.0%; Score 475; DB 8; Length 699;

Best Local Similarity 24.6%; Pred. No. 1.2e-17;  
RESULT 708  
ID AAM83722 standard; protein; 698 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:3971.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.0%; Score 474.5; DB 8; Length 698;  
Best Local Similarity 24.4%; Pred. No. 1.2e-17;  
RESULT 709  
ID AAB85060 standard; protein; 728 AA.  
DE Human serine protease MASP-3 polypeptide.  
PN WO200140451-A2.  
PD 07-JUN-2001.  
PA (JENS/) JENSENIUS J C.  
PA (THIE/) THIEL S.  
Query Match 11.9%; Score 471; DB 4; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2e-17;  
RESULT 710  
ID ADE87461 standard; protein; 728 AA.  
DE Human MB1-associated serine protease-4 protein.  
PN EP1344533-A1.  
PD 17-SEP-2003.  
PA (NATL-) NATLMUNE AS.  
Query Match 11.9%; Score 468; DB 7; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2.9e-17;  
RESULT 711  
ID ADJ91027 standard; protein; 728 AA.  
DE Human mannos binding lectin amino acid sequence SEQ ID NO:13.  
PN WO2004024925-A2.  
PD 25-MAR-2004.  
PA (NATI-) NATIMUNE AS.  
Query Match 11.9%; Score 468; DB 8; Length 728;  
Best Local Similarity 25.0%; Pred. No. 2.9e-17;  
RESULT 712  
ID AAB47559 standard; protein; 728 AA.  
DE Protease PRS-1.  
PN WO200171004-A2.  
PD 27-SEP-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 11.7%; Score 461; DB 4; Length 728;  
Best Local Similarity 24.9%; Pred. No. 6.9e-17;  
RESULT 713  
ID AAG80756 standard; protein; 707 AA.  
DE Murine C1r protein.  
PN KR2001077614-A.  
PD 20-AUG-2001.  
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.  
PA (KIMT/) KIM T Y.  
Query Match 10.9%; Score 429; DB 5; Length 707;  
Best Local Similarity 22.3%; Pred. No. 3.6e-15;  
RESULT 714  
ID ABB50288 standard; protein; 705 AA.  
DE Complement component 1 r ovarian tumour marker protein, SEQ ID NO:66.  
PN WO200175177-A2.  
PD 11-OCT-2001.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 10.2%; Score 403.5; DB 4; Length 705;  
Best Local Similarity 22.9%; Pred. No. 8.4e-14;  
RESULT 715  
ID AAG80757 standard; protein; 705 AA.  
DE Human C1r protein.  
PN KR2001077614-A.  
PD 20-AUG-2001.  
PA (BIOC-) BIO CLUE & SOLUTION CO LTD.  
PA (KIMT/) KIM T Y.  
Query Match 10.2%; Score 403.5; DB 5; Length 705;  
Best Local Similarity 22.9%; Pred. No. 8.4e-14;  
RESULT 716  
ID ADP65211 standard; protein; 705 AA.  
DE Human complement component 1, r subcomponent.  
PN WO2003072827-A1.  
PD 04-SEP-2003.



PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 10.2%; Score 403.5; DB 7; Length 705;  
 Best Local Similarity 22.6%; Pred. No. 8.4e-14;  
 RESULT 717  
 ID ABG31619 standard; protein; 686 AA.  
 DE Human mannan-binding lectin associated serine protease-2 protein.  
 PN US2002082208-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 718  
 ID AAE1564 standard; protein; 686 AA.  
 DE Human MASP-2 protein.  
 PN WO200206460-A2.  
 PD 24-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 719  
 ID ABG3115 standard; protein; 686 AA.  
 DE Mannan-binding lectin associated serine protease-2 (MASP-2).  
 PN US2002082209-A1.  
 PD 27-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 (THIE/) THIEL S.  
 Query Match 10.2%; Score 401.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 720  
 ID ADL91025 standard; protein; 686 AA.  
 DE Human mannose binding lectin amino acid sequence SEQ ID NO:11.  
 PN WO2004024925-A2.  
 PD 25-MAR-2004.  
 PA (NATL-) NATLMUNE AS.  
 Query Match 10.2%; Score 401.5; DB 8; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.1e-13;  
 RESULT 721  
 ID AAE1568 standard; protein; 686 AA.  
 DE Human MASP-2 protein, alternative version.  
 PN WO200206460-A2.  
 PD 24-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 (THIE/) THIEL S.  
 Query Match 10.2%; Score 400.5; DB 5; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;  
 RESULT 722  
 ID ADE87460 standard; protein; 686 AA.  
 DE Human MB1-associated serine protease-2 protein.  
 PN EP1344533-A1.  
 PD 17-SEP-2003.  
 PA (NATL-) NATLMUNE AS.  
 Query Match 10.2%; Score 400.5; DB 7; Length 686;  
 Best Local Similarity 22.7%; Pred. No. 1.2e-13;  
 RESULT 723  
 ID ADQ27010 standard; protein; 671 AA.  
 DE Human MASP-2 mature polypeptide.  
 PN WO2004050907-A2.  
 PD 17-JUN-2004.  
 PA (UYAA-) UNIV AARHUS.  
 (AARH) AARHUS AMT.  
 Query Match 10.1%; Score 399.5; DB 8; Length 671;  
 Best Local Similarity 22.8%; Pred. No. 1.3e-13;  
 RESULT 724  
 ID AAE14565 standard; peptide; 671 AA.  
 DE Human mature MASP-2 protein.  
 PN WO200206460-A2.  
 PD 24-JUN-2002.  
 PA (JENS/) JENSENIUS J C.  
 (THIE/) THIEL S.  
 Query Match 10.1%; Score 398.5; DB 5; Length 671;  
 Best Local Similarity 22.8%; Pred. No. 1.5e-13;

RESULT 725  
 ID ADE56422 standard; protein; 694 AA.  
 DE Rat Protein BAA25797, SEQ ID NO 2275.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 694;  
 Best Local Similarity 21.2%; Pred. No. 2e-10;  
 RESULT 726  
 ID ADE83526 standard; protein; 694 AA.  
 DE Rat Protein BAA25797, SEQ ID NO 11123.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 694;  
 Best Local Similarity 21.2%; Pred. No. 2e-10;  
 RESULT 727  
 ID ADE56418 standard; protein; 695 AA.  
 DE Rat Protein DB8250, SEQ ID NO 2271.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 695;  
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;  
 RESULT 728  
 ID ADD45338 standard; protein; 695 AA.  
 DE Rat Protein DB8250, SEQ ID NO 10771.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.6%; Score 340.5; DB 7; Length 695;  
 Best Local Similarity 21.2%; Pred. No. 2.1e-10;  
 RESULT 729  
 ID ABA43579 standard; protein; 760 AA.  
 DE Human cancer associated protein sequence SEQ ID NO:1024.  
 PN WO200055350-A1.  
 PD 21-SEP-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 8.5%; Score 336; DB 3; Length 760;  
 Best Local Similarity 21.7%; Pred. No. 3.9e-10;  
 RESULT 730  
 ID ADD45340 standard; protein; 688 AA.  
 DE Human Protein Q9UCV3, SEQ ID NO 10773.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 731  
 ID ADE56420 standard; protein; 688 AA.  
 DE Human Protein Q9UCV3, SEQ ID NO 2273.  
 PN WO2003016475-A2.  
 PD 27-FEB-2003.  
 PA (GEHO) GEN HOSPITAL CORP.  
 (FARB) BAYER AG.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 732  
 ID ADP65315 standard; protein; 688 AA.  
 DE Human complement C1s component precursor (c1 esterase).  
 PN WO2003072827-A1.  
 PD 04-SEP-2003.  
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 Query Match 8.5%; Score 334; DB 7; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 4.6e-10;  
 RESULT 733  
 ID ADJ75392 standard; protein; 688 AA.  
 DE Marker gene related amino acid sequence SEQ ID NO:644.

PN EPI394274-A2.  
 PD 03-MAR-2004.  
 PA (GENO-) GENOX RES INC.  
 Query Match  
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;  
 RESULT 734  
 ID ADU91020 standard; protein; 688 AA.  
 DE Human mannose binding lectin amino acid sequence SEQ ID NO:6.  
 PN WO2004024925-A2.  
 PD 25-MAR-2004.  
 PA (NATI-) NATIMUNE AS.  
 Query Match  
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;  
 RESULT 735  
 ID ASM81337 standard; protein; 688 AA.  
 DE Tumour-associated antigenic target (TAT) polypeptide PRO2660, SEQ:3453.  
 PN WO2004030615-A2.  
 PD 15-APR-2004.  
 PA (GETH-) GENENTECH INC.  
 Query Match  
 Best Local Similarity 8.5%; Score 334; DB 8; Length 688;  
 RESULT 736  
 ID ADI16884 standard; protein; 655 AA.  
 DE Human NOVX protein homologue SegID 420.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 8.4%; Score 332; DB 5; Length 855;  
 RESULT 737  
 ID ADI16818 standard; protein; 855 AA.  
 DE Human NOVX protein homologue SegID 354.  
 PN WO200268649-A2.  
 PD 06-SEP-2002.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 8.4%; Score 332; DB 5; Length 855;  
 RESULT 738  
 ID AAE06940 standard; protein; 1019 AA.  
 DE Human enterokinase protein.  
 PN WO200157194-A2.  
 PD 09-AUG-2001.  
 PA (CORV-) CORVAS INT INC.  
 Query Match  
 Best Local Similarity 8.4%; Score 331.5; DB 4; Length 1019;  
 RESULT 739  
 ID ADA83985 standard; protein; 1019 AA.  
 DE Human PRSS7 protein.  
 PN WO2002103028-A2.  
 PD 27-DEC-2002.  
 PA (BIOM-) BIOMEDICAL CENT.  
 Query Match  
 Best Local Similarity 8.4%; Score 331.5; DB 6; Length 1019;  
 RESULT 740  
 ID ADI10400 standard; protein; 1019 AA.  
 DE Human cell surface protease #16.  
 PN WO200295007-A2.  
 PD 28-NOV-2002.  
 PA (CORV-) CORVAS INT INC.  
 Query Match  
 Best Local Similarity 8.4%; Score 331.5; DB 7; Length 1019;  
 RESULT 741  
 ID ADU46924 standard; protein; 1019 AA.  
 DE Human transmembrane serine protease (MTSP)-related polypeptide #6.  
 PN US2004001801-A1.  
 PD 01-JAN-2004.  
 PA (CORV-) CORVAS INT INC.  
 Query Match  
 Best Local Similarity 8.4%; Score 331.5; DB 8; Length 1019;  
 RESULT 742  
 ID ADU70437 standard; protein; 1019 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SegID2243.  
 PN WO2003087768-A2.

PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match  
 Best Local Similarity 8.4%; Score 330.5; DB 7; Length 1019;  
 RESULT 743  
 ID ADU70480 standard; protein; 3389 AA.  
 DE Human heat mitochondrial protein as a therapeutic target SegID2286.  
 PN WO2003087768-A2.  
 PD 23-OCT-2003.  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 Query Match  
 Best Local Similarity 8.4%; Score 329.5; DB 7; Length 3389;  
 RESULT 744  
 ID AOH72216 standard; protein; 3567 AA.  
 DE Human protein of the invention NOV54b SEQ ID NO:1112.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match  
 Best Local Similarity 8.4%; Score 329.5; DB 8; Length 3567;  
 RESULT 745  
 ID AAR13623 standard; protein; 460 AA.  
 DE Human Protein C zymogen SC.  
 PN EP43875-A.  
 PD 28-AUG-1991.  
 PA (ELIL) LILLY & CO ELI.  
 Query Match  
 Best Local Similarity 8.3%; Score 329; DB 2; Length 460;  
 RESULT 746  
 ID ABG76507 standard; protein; 1274 AA.  
 DE DNA encoding protein modification and maintenance molecule #11.  
 PN WO200260942-A2.  
 PD 08-AUG-2002.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match  
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1274;  
 RESULT 747  
 ID AAU11815 standard; protein; 1783 AA.  
 DE Cancer and neurogenesis associated gene, variant 5G-3V3.  
 PN WO200190354-A1.  
 PD 23-NOV-2001.  
 PA (UYLE-) UNIV LEEDS.  
 Query Match  
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1783;  
 RESULT 748  
 ID AAU11813 standard; protein; 1800 AA.  
 DE Cancer and neurogenesis associated gene, variant 5G-3V1.  
 PN WO200190354-A1.  
 PD 23-NOV-2001.  
 PA (UYLE-) UNIV LEEDS.  
 Query Match  
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1800;  
 RESULT 749  
 ID AAU11812 standard; protein; 1826 AA.  
 DE Cancer and neurogenesis associated gene.  
 PN WO200190354-A1.  
 PD 23-NOV-2001.  
 PA (UYLE-) UNIV LEEDS.  
 Query Match  
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 1826;  
 RESULT 750  
 ID AAU11814 standard; protein; 2008 AA.  
 DE Cancer and neurogenesis associated gene, variant 5G-3V2.  
 PN WO200190354-A1.  
 PD 23-NOV-2001.  
 PA (UYLE-) UNIV LEEDS.  
 Query Match  
 Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2008;  
 RESULT 751  
 ID AAU11817 standard; protein; 2306 AA.  
 DE Cancer and neurogenesis associated gene, variant 5R23V2.

PN W0200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEBDS.  
Query Match  
Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2306;  
RESULT 752  
ID AAV1816 standard; protein; 2352 AA.  
DE Cancer and neurogenesis associated gene, variant 5R-3V2.  
PN W0200190354-A1.  
PD 29-NOV-2001.  
PA (UYLE-) UNIV LEBDS.  
Query Match  
Best Local Similarity 8.3%; Score 328.5; DB 5; Length 2352;  
RESULT 753  
ID AAB19551 standard; protein; 683 AA.  
DE Human matrixase (truncated form).  
PN W0200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 3; Length 683;  
RESULT 754  
ID AAY90284 standard; protein; 762 AA.  
DE Human peptidase, HPEP-1 protein sequence.  
PN W0200042201-A2.  
PD 20-JUL-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 3; Length 762;  
RESULT 755  
ID AAM25628 standard; protein; 851 AA.  
DE Human protein sequence SEQ ID NO:1143.  
PN W0200153455-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 4; Length 851;  
RESULT 756  
ID ABB11428 standard; peptide; 851 AA.  
DE Human membrane-type Ser Kinase homologue, SEQ ID NO:1798.  
PN W0200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 4; Length 851;  
RESULT 757  
ID AAO55145 standard; protein; 853 AA.  
DE Protein #47 with increased gene expression in renal cell carcinoma.  
PN W02004032842-A2.  
PD 23-APR-2004.  
PA (VAND-) VAN ANDEL INST.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 8; Length 853;  
RESULT 758  
ID AAB19552 standard; protein; 855 AA.  
DE Human matrixase.  
PN W0200053232-A1.  
PD 14-SEP-2000.  
PA (GEOU) UNIV GEORGETOWN.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 3; Length 855;  
RESULT 759  
ID AAB35465 standard; protein; 855 AA.  
DE Human membrane-type serine protease MT-SPI.  
PN W0200123524-A2.  
PD 05-APR-2001.  
PA (REGC) UNIV CALIFORNIA.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 4; Length 855;  
RESULT 760  
ID AD11617 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 353.  
PN W0200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;  
RESULT 761  
ID AD116893 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 419.  
PN W0200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;  
RESULT 762  
ID AD116876 standard; protein; 855 AA.  
DE Human NOVX protein homologue SeqID 412.  
PN W0200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 5; Length 855;  
RESULT 763  
ID ADN39867 standard; protein; 855 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C237.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 7; Length 855;  
RESULT 764  
ID ADN04754 standard; protein; 855 AA.  
DE Antipsoriatic protein sequence #558.  
PN W02004028479-A2.  
PD 08-APR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 8; Length 855;  
RESULT 765  
ID ADP23334 standard; protein; 855 AA.  
DE PRO polypeptide SEQ ID NO:428.  
PN W02004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 8; Length 855;  
RESULT 766  
ID ADR66721 standard; protein; 863 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #3.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 8; Length 863;  
RESULT 767  
ID ADR66379 standard; protein; 863 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 233 #2.  
PN W02004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match  
Best Local Similarity 8.3%; Score 328; DB 8; Length 863;  
RESULT 768  
ID AAB58274 standard; protein; 449 AA.  
DE Lung cancer associated polypeptide sequence SEQ ID:612.  
PN W0200055180-A2.  
PD 21-SEP-2000.

PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
Query Match 8.3%; Score 327.5; DB 3; Length 449;  
Best Local Similarity 23.3%; Pred. No. 6.8e-10;  
RESULT 769  
ID ADI64961 standard; protein; 688 AA.  
DE Human complement component 1 protein , CIS.  
PN US2004033582-A1.  
PD 19-FEB-2004.  
PA (EDMO/) EDMONDS M.  
PA (HUI/) HUI L.  
PA (PERR/) PERRONE M.  
PA (POWE/) POWELL J R.  
PA (RAMA/) RAMANATHAN C S.  
PA (SWAN/) SWANSON B.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (ZERB/) ZERBA K.  
Query Match 8.3%; Score 327; DB 8; Length 688;  
Best Local Similarity 21.7%; Pred. No. 1.1e-09;  
RESULT 770  
ID ADI16508 standard; protein; 757 AA.  
DE Human NOVX protein to treat human pathological conditions SegID44.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 757;  
Best Local Similarity 21.6%; Pred. No. 1.2e-09;  
RESULT 771  
ID AAY06671 standard; protein; 855 AA.  
DE Tumour antigen derived gene-15 (TADG-15) protein.  
PN WO9942120-A1.  
PD 26-AUG-1999.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 8.3%; Score 327; DB 2; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 772  
ID AAB98500 standard; protein; 855 AA.  
DE Human TADG-15.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR-) UNIV ARKANSAS.  
Query Match 8.3%; Score 327; DB 4; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 773  
ID AAE06930 standard; protein; 855 AA.  
DE Human membrane-type serine protease (MTSP) 1.  
PN WO200157194-A2.  
PD 09-AUG-2001.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 4; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 774  
ID AAO22929 standard; protein; 855 AA.  
DE Type II transmembrane serine protease 1 protein SEQ ID NO 2.  
PN WO200272786-A2.  
PD 19-SEP-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 775  
ID ADI16816 standard; protein; 855 AA.  
DE Human NOVX protein homologue SegID 352.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 776  
ID ADI16882 standard; protein; 855 AA.  
DE Human NOVX protein homologue SegID 418.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.

Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 777  
ID ADI16875 standard; protein; 855 AA.  
DE Human NOVX protein homologue SegID 411.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.3%; Score 327; DB 5; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 778  
ID AAB56619 standard; protein; 855 AA.  
DE Human membrane-type serine protease MTSP1 protein SEQ ID NO:2.  
PN WO200292841-A2.  
PD 21-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 779  
ID AAO30146 standard; protein; 855 AA.  
DE Human membrane-type serine protease MTSP1 protein.  
PN WO2003044179-A2.  
PD 30-MAY-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 780  
ID AAE29820 standard; protein; 855 AA.  
DE Human membrane-type serine protease 1 (MTSP1) .  
PN WO20027267-A2.  
PD 03-OCT-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 781  
ID AAE29791 standard; protein; 855 AA.  
DE Human membrane-type serine protease, MTSP1.  
PN WO20027263-A2.  
PD 03-OCT-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 782  
ID ABE72376 standard; protein; 855 AA.  
DE Transmembrane serine protease 1 (MTSP1) .  
PN WO2003004681-A2.  
PD 16-JAN-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 6; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 783  
ID ADB97551 standard; protein; 855 AA.  
DE Human MTSP1, SEQ ID NO:2.  
PN WO2003031585-A2.  
PD 17-APR-2003.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 7; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 784  
ID ADI10371 standard; protein; 855 AA.  
DE Human cell surface protease #1.  
PN WO200295007-A2.  
PD 28-NOV-2002.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 7; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 785  
ID ADG65326 standard; protein; 855 AA.  
DE Human MTSP1.  
PN WO2003104394-A2.  
PD 18-DEC-2003.  
PA (DENN-) DENNREON SAN DIEGO LLC.  
Query Match 8.3%; Score 327; DB 8; Length 855;

Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 786  
ID AD128661 standard; protein; 855 AA.  
DE Human matrixinase ( MTSP1) serine protease.  
PN WO2004005471-A2.  
PD 15-JAN-2004.  
PA (DEND-) DENDREON SAN DIEGO LLC.  
Query Match 8.3%; Score 327; DB 8; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 787  
ID AD446895 standard; protein; 855 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #1.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV-) CORVAS INT INC.  
Query Match 8.3%; Score 327; DB 8; Length 855;  
Best Local Similarity 21.6%; Pred. No. 1.3e-09;  
RESULT 788  
ID AAE20788 standard; protein; 3095 AA.  
DE Rat C3b/C4b complement receptor like protein.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.2%; Score 324; DB 5; Length 3095;  
Best Local Similarity 20.1%; Pred. No. 6.4e-09;  
RESULT 789  
ID ADN42162 standard; protein; 757 AA.  
DE Human novel protein NOV 8.  
PN US2004033493-A1.  
PD 19-FEB-2004.  
PA (TCHE/) TCHERNEV V. T.  
PA (SPYT/) SPYTEK K. A.  
PA (ZERR/) ZERHUSEN B. D.  
PA (PATT/) PATTURAJAN M.  
PA (SHIM/) SHIMKETS R. A.  
PA (LILL/) LI L.  
PA (GANG/) GANGOLLI E. A.  
PA (PADI/) PADIGARU M.  
PA (ANDE/) ANDERSON D. W.  
PA (RAST/) RASTELLI L.  
PA (MILL/) MILLER C. E.  
PA (GERL/) GERLACH V.  
PA (TAUP/) TAUPIER R. J.  
PA (GUSE/) GUSEV V. Y.  
PA (COLM/) COLMAN S. D.  
PA (WOLE/) WOLENC A. R.  
PA (PENA/) PENA C. E. A.  
PA (FURT/) FURTAK K.  
PA (GROS/) GROSSE W. M.  
PA (ALSO/) ALSOBROOK J. P.  
PA (LEPL/) LEPLLEY D. M.  
PA (RIEG/) RIEGER D. K.  
PA (BURG/) BURGESS C. E.  
Query Match 8.2%; Score 323; DB 8; Length 757;  
Best Local Similarity 21.6%; Pred. No. 1.9e-09;  
RESULT 790  
ID ADH71146 standard; protein; 3130 AA.  
DE Human protein of the invention NOV46 SEQ ID NO:42.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3130;  
Best Local Similarity 22.6%; Pred. No. 9.4e-09;  
RESULT 791  
ID ADH71144 standard; protein; 3483 AA.  
DE Human protein of the invention NOV4e SEQ ID NO:40.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3483;  
Best Local Similarity 22.6%; Pred. No. 1e-08;  
RESULT 792  
ID ADH71136 standard; protein; 3546 AA.  
DE Human protein of the invention NOV4a SEQ ID NO:32.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 321; DB 8; Length 3546;  
Best Local Similarity 22.6%; Pred. No. 1.1e-08;  
RESULT 793  
ID AAE20787 standard; protein; 3069 AA.  
DE Human C3b/C4b complement receptor like protein #1.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.1%; Score 320.5; DB 5; Length 3069;  
Best Local Similarity 20.7%; Pred. No. 9.8e-09;  
RESULT 794  
ID AAE20789 standard; protein; 3100 AA.  
DE Human C3b/C4b complement receptor like protein #2.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.1%; Score 320.5; DB 5; Length 3100;  
Best Local Similarity 20.7%; Pred. No. 9.9e-09;  
RESULT 795  
ID AAU99088 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant G383N/G385T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.1%; Score 319.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 1.7e-09;  
RESULT 796  
ID AAU99080 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L349N/D351T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.1%; Score 319.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 1.7e-09;  
RESULT 797  
ID ADG8386 standard; protein; 455 AA.  
DE Rough scale snake venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU-) UNIV QUEENSLAND.  
Query Match 8.1%; Score 319.5; DB 8; Length 455;  
Best Local Similarity 23.4%; Pred. No. 1.9e-09;  
RESULT 798  
ID AAU99078 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant I348N/G350T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.1%; Score 318.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2e-09;  
RESULT 799  
ID ADH71142 standard; protein; 2612 AA.  
DE Human protein of the invention NOV4d SEQ ID NO:38.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 2612;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;  
RESULT 800  
ID ABG79169 standard; protein; 2669 AA.  
DE Human cub and sushi domain containing protein #2.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 5; Length 2669;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;

RESULT 801  
ID ADH71140 standard; protein; 2669 AA.  
DE Human protein of the invention NOV4c SEQ ID NO:36.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 2669;  
Best Local Similarity 22.6%; Pred. No. 1.2e-08;  
RESULT 802  
ID ABG79168 standard; protein; 3104 AA.  
DE Human cub and sushi domain containing protein #1.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 5; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 803  
ID ADH71168 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4g SEQ ID NO:64.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 804  
ID ADH71166 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4p SEQ ID NO:62.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 805  
ID ADH71138 standard; protein; 3104 AA.  
DE Human protein of the invention NOV4b SEQ ID NO:34.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.1%; Score 318; DB 8; Length 3104;  
Best Local Similarity 22.6%; Pred. No. 1.4e-08;  
RESULT 806  
ID AAU99006 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D189N/K191T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 317.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 2.2e-09;  
RESULT 807  
ID AAU99066 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T315N/V317T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 317.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.2e-09;  
RESULT 808  
ID AAB57283 standard; protein; 798 AA.  
DE Bovine enterokinase.  
PN WO9416083-A1.  
PD 21-JUL-1994.  
PA (GEMV-) GENETICS INST INC.  
Query Match 8.0%; Score 317.5; DB 2; Length 798;  
Best Local Similarity 24.6%; Pred. No. 4e-09;  
RESULT 809  
ID AAE20900 standard; protein; 3069 AA.  
DE Human C3b/C4b complement receptor like protein #1, alternative version.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.0%; Score 317.5; DB 5; Length 3069;

Best Local Similarity 20.7%; Pred. No. 1.4e-08;  
RESULT 810  
ID AAE20901 standard; protein; 3100 AA.  
DE Human C3b/C4b complement receptor like protein #2, alternative version.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 8.0%; Score 317.5; DB 5; Length 3100;  
Best Local Similarity 20.7%; Pred. No. 1.4e-08;  
RESULT 811  
ID AAU99076 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant M338N/S340T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 316.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.5e-09;  
RESULT 812  
ID AAU99022 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K217N/L219T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 316.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.5e-09;  
RESULT 813  
ID AAU99026 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L220N/R222T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.5e-09;  
RESULT 814  
ID AAU99081 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D351N/Q353S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 815  
ID AAU99071 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S336N/W338S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 2.8e-09;  
RESULT 816  
ID AAU99087 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant G383N/G385S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 817  
ID AAU99079 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L349N/D351S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 8.0%; Score 315.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 2.8e-09;  
RESULT 818

ID AAR62653 standard; protein; 461 AA.  
DE Human protein C.  
PN US5358932-A.  
PD 25-OCT-1994.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 8.0%; Score 315.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 3.1e-09;  
RESULT 819  
ID AAR5760 standard; protein; 419 AA.  
DE Protein C (PC).  
PN WO9309804-A1.  
PD 27-MAY-1993.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 8.0%; Score 314.5; DB 2; Length 419;  
Best Local Similarity 23.3%; Pred. No. 3.2e-09;  
RESULT 820  
ID AAU99053 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant R306N/K308S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 314.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 3.2e-09;  
RESULT 821  
ID AAU99007 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant S190N/K192S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 314.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 3.2e-09;  
RESULT 822  
ID AAU99077 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant I348N/G350S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 314.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 3.2e-09;  
RESULT 823  
ID AAU99043 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant L296N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 314.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 3.2e-09;  
RESULT 824  
ID ADG83832 standard; protein; 454 AA.  
DE Red belly black snake venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYOU) UNIV QUEENSLAND.  
Query Match 8.0%; Score 314.5; DB 8; Length 454;  
Best Local Similarity 23.0%; Pred. No. 3.5e-09;  
RESULT 825  
ID ADM77504 standard; protein; 461 AA.  
DE Human protein C variant #2 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
Query Match 8.0%; Score 314.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 3.5e-09;  
RESULT 826  
ID AAE23083 standard; protein; 855 AA.  
DE Epithelin protein.  
PN WO200203787-A2.  
PD 17-JAN-2002.

PA (DELT-) DELTAGEN INC.  
Query Match 8.0%; Score 314; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
RESULT 827  
ID AD16819 standard; protein; 855 AA.  
DE Murine NOVX protein homologue Segid 355.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.0%; Score 314; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
RESULT 828  
ID AD16877 standard; protein; 855 AA.  
DE Murine NOVX protein homologue Segid 413.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 8.0%; Score 314; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 6.7e-09;  
RESULT 829  
ID AAW72753 standard; protein; 419 AA.  
DE Primary structure of activated human protein C.  
PN EP875563-A2.  
PD 04-NOV-1998.  
PA (BLIL) LILLY & CO ELI.  
Query Match 7.9%; Score 313.5; DB 2; Length 419;  
Best Local Similarity 23.3%; Pred. No. 3.6e-09;  
RESULT 830  
ID AAU99005 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant D189N/K191S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 313.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 3.6e-09;  
RESULT 831  
ID AAU99025 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant L220N/R222S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 313.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 3.6e-09;  
RESULT 832  
ID AAU99065 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant T315N/V317S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 313.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 3.6e-09;  
RESULT 833  
ID AAU99016 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant D214N/S216T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 313.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 3.6e-09;  
RESULT 834  
ID AAU99023 standard; protein; 419 AA.  
DE Human protein C zymogen protein mutant K218N/L220S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 313.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 3.6e-09;  
RESULT 835

ID AAR13083 standard; protein; 509 AA.  
DE PAP-I-Protein C fusion construct.  
PN WO9109953-A.  
PD 11-JUL-1991.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.9%; Score 313; DB 2; Length 509;  
Best Local Similarity 23.5%; Pred. No. 4.6e-09;  
RESULT 836  
ID AD116820 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SegID 356.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 837  
ID AD116881 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SegID 417.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 838  
ID AD116878 standard; protein; 855 AA.  
DE Rat NOVX protein homologue SegID 414.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.9%; Score 313; DB 5; Length 855;  
Best Local Similarity 21.4%; Pred. No. 7.5e-09;  
RESULT 839  
ID AAU99072 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S336N/M338T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 840  
ID AAU99097 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D189N/K191N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.1e-09;  
RESULT 841  
ID AAU99009 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K191N/K193S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.1e-09;  
RESULT 842  
ID AAU99064 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R312N/R314T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.9%; Pred. No. 4.1e-09;  
RESULT 843  
ID AAU99069 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V334N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 844  
ID AAU99048 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D351N/Q353T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 845  
ID AAU99096 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant M338A.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 846  
ID AAU99091 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L387N/N389S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 847  
ID AAU99024 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K218N/L220T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 848  
ID AAU99048 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H303N/S305T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.3%; Pred. No. 4.1e-09;  
RESULT 849  
ID AAU99067 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant F316N/L318S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 850  
ID AAU99075 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant M338N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 851  
ID AAU99092 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L387N/N389T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;



Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 852  
ID AAU99011 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K192N/L194S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 853  
ID AAU99032 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S250N/S252T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.1e-09;  
RESULT 854  
ID ADM77507 standard; protein; 461 AA.  
DE Human protein C variant #5 amino acid sequence.  
PN W02003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 8; Length 461;  
Best Local Similarity 24.3%; Pred. No. 4.5e-09;  
RESULT 855  
ID ADM77505 standard; protein; 461 AA.  
DE Human protein C variant #3 amino acid sequence.  
PN W02003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 312.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 4.5e-09;  
RESULT 856  
ID AAB82677 standard; protein; 419 AA.  
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).  
PN W0200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 312; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.4e-09;  
RESULT 857  
ID AAR13537 standard; protein; 460 AA.  
DE Human Protein C zymogen N.  
PN EP443875-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 312; DB 2; Length 460;  
Best Local Similarity 24.7%; Pred. No. 4.8e-09;  
RESULT 858  
ID ADG83830 standard; protein; 467 AA.  
DE Coesetal taipen venom protease.  
PN W02003082914-A1.  
PD 09-OCT-2003.  
PA (UYOU) UNIV QUEENSLAND.  
Query Match 7.9%; Score 312; DB 8; Length 467;  
Best Local Similarity 23.0%; Pred. No. 4.9e-09;  
RESULT 859  
ID AAB60993 standard; protein; 1031 AA.  
DE Novel human protein. SEQ ID 80.  
PN W0200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK) SMITHKLINE BEECHAM CORP.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 7.9%; Score 312; DB 5; Length 1031;  
Best Local Similarity 22.6%; Pred. No. 1e-08;  
RESULT 860

ID AAU99008 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S190N/K192T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.7e-09;  
RESULT 861  
ID AAU99039 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T254N/N256S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 862  
ID AAU99047 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H303N.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.3%; Pred. No. 4.7e-09;  
RESULT 863  
ID AAU99070 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V334N/S336T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 864  
ID AAU99017 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E215N/K217S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 865  
ID AAU99044 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L296N/T298S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 866  
ID AAU99014 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K193N/A195T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 4.7e-09;  
RESULT 867  
ID AAU99031 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S250N.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 868  
ID AAU99057 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant K308N/A310S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 869  
ID AAU99054 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R306N/K308T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 870  
ID AAU99095 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D214N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 871  
ID AAU99015 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D214N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 4.7e-09;  
RESULT 872  
ID AAP81205 standard; protein; 461 AA.  
DE Human protein C.  
PN EP266190-A.  
PD 04-MAY-1988.  
PA (ZVMO-) ZYMOGENETICS INC.  
Query Match 7.9%; Score 311.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 873  
ID AAR13539 standard; protein; 461 AA.  
DE Human Protein C zymogen LIN.  
PN EP443875-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 874  
ID AAR13997 standard; protein; 461 AA.  
DE Human protein C zymogen Q329.  
PN EP443874-A.  
PD 28-AUG-1991.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 875  
ID ADM77503 standard; protein; 461 AA.  
DE Human protein C variant #1 amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 311.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.1e-09;  
RESULT 876  
ID AAB82678 standard; protein; 419 AA.  
DE Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.

Query Match 7.9%; Score 311; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5e-09;  
RESULT 877  
ID AAB82675 standard; protein; 419 AA.  
DE Human protein C derivative (S11G/Q32E/N33D/L194S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 311; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5e-09;  
RESULT 878  
ID ADC40013 standard; protein; 409 AA.  
DE Human activated protein C-related protein #2.  
PN WO2003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 409;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 879  
ID ADC40012 standard; protein; 410 AA.  
DE Human activated protein C-related protein #1.  
PN WO2003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 410;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 880  
ID AAY56803 standard; protein; 415 AA.  
DE Truncated human protein C polypeptide.  
PN WO9963070-A1.  
PD 09-DEC-1999.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 3; Length 415;  
Best Local Similarity 24.5%; Pred. No. 5.2e-09;  
RESULT 881  
ID AAB82673 standard; protein; 419 AA.  
DE Wild-type human protein C.  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 882  
ID AAB36896 standard; protein; 419 AA.  
DE Human protein C derivative 3.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 883  
ID AAB36894 standard; protein; 419 AA.  
DE Human protein C derivative 1.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 884  
ID AAE08625 standard; protein; 419 AA.  
DE Human mature wild type protein C.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 885  
ID AAU99063 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R312N/R314S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.

Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 886  
ID AAU99012 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant K192N/L194T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 887  
ID AAU99050 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S304N/E306T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 888  
ID AAU99010 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant K191N/K193T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 5.3e-09;  
RESULT 889  
ID AAU99040 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant T254N/N256T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 890  
ID AAU99060 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant E309N/K311T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 891  
ID AAU99055 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant E307N/E309S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 892  
ID AAU99056 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant E307N/E309T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 893  
ID AAU99059 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant E309N/K311S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 894  
ID AAU99052 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S305N/E307S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 895  
ID AAU99051 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S305N/E307S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 896  
ID AAU99052 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S305N/E307T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 897  
ID ABR55547 standard; protein: 419 AA.  
DE Amino acid sequence of mature human protein C (PC).  
PN FR2831170-A1.  
PD 25-APR-2003.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 7.9%; Score 310.5; DB 6; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 898  
ID ADC40014 standard; protein: 419 AA.  
DE Human activated protein C-related protein #3.  
PN W02003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 899  
ID APO18786 standard; protein: 419 AA.  
DE Mature human zymogen-like protein C.  
PN W02004044190-A2.  
PD 27-MAY-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 900  
ID ADG83834 standard; protein: 453 AA.  
DE Mainland tiger snake venom protease.  
PN W02003082914-A1.  
PD 09-OCT-2003.  
PA (UYOU) UNIV QUEBENS LAND.  
Query Match 7.9%; Score 310.5; DB 8; Length 453;  
Best Local Similarity 22.8%; Pred. No. 5.7e-09;  
RESULT 901  
ID AAP81104 standard; protein: 460 AA.  
DE Sequence of human protein C.  
PN JF63263083-A.  
PD 31-OCT-1988.  
PA (FARH) HOECHST JAPAN LTD.  
Query Match 7.9%; Score 310.5; DB 1; Length 460;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 902  
ID AAW25086 standard; protein: 460 AA.  
DE Human protein C.  
PN W09720043-A1.

Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 894  
ID AAU99002 standard; protein: 419 AA.  
DE Human Protein C zymogen protein.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 895  
ID AAU99051 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S305N/E307S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 896  
ID AAU99052 standard; protein: 419 AA.  
DE Human Protein C zymogen protein mutant S305N/E307T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 897  
ID ABR55547 standard; protein: 419 AA.  
DE Amino acid sequence of mature human protein C (PC).  
PN FR2831170-A1.  
PD 25-APR-2003.  
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.  
Query Match 7.9%; Score 310.5; DB 6; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 898  
ID ADC40014 standard; protein: 419 AA.  
DE Human activated protein C-related protein #3.  
PN W02003075834-A2.  
PD 18-SEP-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 7; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 899  
ID APO18786 standard; protein: 419 AA.  
DE Mature human zymogen-like protein C.  
PN W02004044190-A2.  
PD 27-MAY-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.3e-09;  
RESULT 900  
ID ADG83834 standard; protein: 453 AA.  
DE Mainland tiger snake venom protease.  
PN W02003082914-A1.  
PD 09-OCT-2003.  
PA (UYOU) UNIV QUEBENS LAND.  
Query Match 7.9%; Score 310.5; DB 8; Length 453;  
Best Local Similarity 22.8%; Pred. No. 5.7e-09;  
RESULT 901  
ID AAP81104 standard; protein: 460 AA.  
DE Sequence of human protein C.  
PN JF63263083-A.  
PD 31-OCT-1988.  
PA (FARH) HOECHST JAPAN LTD.  
Query Match 7.9%; Score 310.5; DB 1; Length 460;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 902  
ID AAW25086 standard; protein: 460 AA.  
DE Human protein C.  
PN W09720043-A1.

PD 05-JUN-1997.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (PBLT-) PPL THERAPEUTICS.  
Query Match 7.9%; Score 310.5; DB 2; Length 460;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 903  
ID AAB60001 standard; protein; 461 AA.  
DE Sequence of polypeptide with human protein C activity.  
PN EPI91606-A.  
PD 20-AUG-1986.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 904  
ID AAE70855 standard; protein; 461 AA.  
DE Human Protein C.  
PN EPI15548-A.  
PD 25-MAR-1987.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (UNIW ) UNIV WASHINGTON.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 905  
ID AAP90401 standard; protein; 461 AA.  
DE Zymogen form of human protein C.  
PN EP323149-A.  
PD 05-JUL-1989.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 906  
ID AAR13622 standard; protein; 461 AA.  
DE Human protein C.  
PN WO9112320-A.  
PD 22-AUG-1991.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (TEIJ ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 907  
ID AAR13081 standard; protein; 461 AA.  
DE Human protein C.  
PN WO9109953-A.  
PD 11-JUL-1991.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 908  
ID AAR13074 standard; protein; 461 AA.  
DE Protein C precursor.  
PN WO9109951-A.  
PD 11-JUL-1991.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (TEIJ ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 909  
ID AAR34295 standard; protein; 461 AA.  
DE Protein C.  
PN JP05064588-A.  
PD 19-MAR-1993.  
PA (TEIJ ) TEIJIN LTD.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 910  
ID AAM02600 standard; protein; 461 AA.  
DE Human protein C.  
PN USS516650-A.  
PD 14-MAY-1996.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 911

ID AAY9561 standard; protein; 461 AA.  
DE Human lecithin cholesterol acyltransferase protein sequence.  
PN WO9950454-A2.  
PD 07-OCT-1999.  
PA (WHEB ) WIREHEAD INST BIOMEDICAL RES.  
Query Match 7.9%; Score 310.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 912  
ID AAB82674 standard; protein; 461 AA.  
DE Wild-type human protein C.  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 913  
ID AAB36895 standard; protein; 461 AA.  
DE Human protein C derivative 2.  
PN WO200066754-A1.  
PD 09-NOV-2000.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 914  
ID AAB08626 standard; protein; 461 AA.  
DE Human wild type protein C.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310.5; DB 4; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 915  
ID AAU99001 standard; protein; 461 AA.  
DE Human Protein C precursor protein.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 5; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 916  
ID ADW77502 standard; protein; 461 AA.  
DE Human protein C wild-type amino acid sequence.  
PN WO2003106666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 917  
ID ADO18787 standard; protein; 461 AA.  
DE Human zymogen-like protein C.  
PN WO2004044190-A2.  
PD 27-MAY-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.9%; Score 310.5; DB 8; Length 461;  
Best Local Similarity 24.5%; Pred. No. 5.8e-09;  
RESULT 918  
ID AAB82676 standard; protein; 419 AA.  
DE Human protein C derivative (S116/Q32E/N33D/L194S/T234S).  
PN WO200157193-A2.  
PD 09-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 5.6e-09;  
RESULT 919  
ID AAE08630 standard; protein; 419 AA.  
DE Human protein C derivative #4.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.9%; Score 310; DB 4; Length 419;  
RESULT 911

Best Local Similarity 24.5%; Pred. No. 5.6e-09;  
RESULT 920  
ID AAR13538 standard; protein; 460 AA.  
DE Human Protein C zymogen FN.  
PN EP43875-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 310; DB 2; Length 460;  
Best Local Similarity 24.7%; Pred. No. 6.1e-09;  
RESULT 921  
ID AAB36897 standard; protein; 419 AA.  
DE Human protein C derivative 4.  
PN WO2006754-A1.  
PD 09-NOV-2000.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 922  
ID AAB36898 standard; protein; 419 AA.  
DE Human protein C derivative 5.  
PN WO2006754-A1.  
PD 09-NOV-2000.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309.5; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 923  
ID AAU99018 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E215N/K217T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 6e-09;  
RESULT 924  
ID AAU99033 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K251N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 6e-09;  
RESULT 925  
ID AAU99013 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K193N/A195S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 926  
ID AAU99068 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant F316N/K318T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 6e-09;  
RESULT 927  
ID AAU99062 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant A310N/K312T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.8%; Pred. No. 6e-09;  
RESULT 928  
ID AAU99020 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S216N/K218T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 929  
ID AAU99035 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S252N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 6e-09;  
RESULT 930  
ID AAU99085 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E357N/D359S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 931  
ID AAU99058 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K308N/A310T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 932  
ID AAU99019 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S216N/K218S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6e-09;  
RESULT 933  
ID AAU99094 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H388N/Y390T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 6e-09;  
RESULT 934  
ID AAU99089 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L386N/H388S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 309.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 6e-09;  
RESULT 935  
ID AAP90070 standard; protein; 461 AA.  
DE Human protein C.  
PN EP319312-A.  
PD 07-JUN-1989.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309.5; DB 1; Length 461;  
Best Local Similarity 24.5%; Pred. No. 6.5e-09;  
RESULT 936  
ID AAR13540 standard; protein; 461 AA.  
DE Human Protein C zymogen FLIN.  
PN EP43875-A.  
PD 28-AUG-1991.

PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309.5; DB 2; Length 461;  
Best Local Similarity 24.5%; Pred. No. 6.5e-09;  
RESULT 937  
ID AD16874 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SegID 410.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 309.5; DB 5; Length 799;  
Best Local Similarity 21.6%; Pred. No. 1.1e-08;  
RESULT 938  
ID AD16880 standard; protein; 799 AA.  
DE Murine NOVX protein homologue SegID 416.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 7.8%; Score 309.5; DB 5; Length 799;  
Best Local Similarity 21.6%; Pred. No. 1.1e-08;  
RESULT 939  
ID AAE08627 standard; protein; 419 AA.  
DE Human protein C derivative #1.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.4e-09;  
RESULT 940  
ID AAE08629 standard; protein; 419 AA.  
DE Human protein C derivative #3.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 309; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.4e-09;  
RESULT 941  
ID AAU99049 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant S304N/R310S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.1%; Pred. No. 6.8e-09;  
RESULT 942  
ID AAU99061 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant A310N/R312S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.1%; Pred. No. 6.8e-09;  
RESULT 943  
ID AAU99090 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant L386N/H388T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.1%; Pred. No. 6.8e-09;  
RESULT 944  
ID AAU99086 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant E357N/D359T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 945  
ID AAU99036 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant S252N/T254S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 946  
ID AAU99045 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant Y302N.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 947  
ID AAU99034 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K251N/T253S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 948  
ID ADM77506 standard; protein; 461 AA.  
DE Human protein C variant #4 amino acid sequence.  
PN WO200310666-A2.  
PD 24-DEC-2003.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 308.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 6.8e-09;  
RESULT 949  
ID AAE08628 standard; protein; 419 AA.  
DE Human protein C derivative #2.  
PN WO200159084-A1.  
PD 16-AUG-2001.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 308; DB 4; Length 419;  
Best Local Similarity 24.5%; Pred. No. 7.2e-09;  
RESULT 950  
ID AAU99084 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R352N/D354T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.6%; Pred. No. 7.7e-09;  
RESULT 951  
ID AAU99021 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant K217N/L219S.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 7.7e-09;  
RESULT 952  
ID AAU99046 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant Y302N/S304T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 7.7e-09;  
RESULT 953  
ID AAU99093 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant H388N/Y390S.  
PN WO200232461-A2.

PD 25-APR-2002.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.8%; Score 307.5; DB 5; Length 419;  
Best Local Similarity 24.7%; Pred. No. 7.7e-09;  
RESULT 954  
ID AAU99083 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant R352N/D354S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 8.7e-09;  
RESULT 955  
ID AAU99074 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V339T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 8.7e-09;  
RESULT 956  
ID AAU99003 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D172N/K174S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.8%; Score 306.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 8.7e-09;  
RESULT 957  
ID AAR13585 standard; protein; 461 AA.  
DE Human protein C zymogen Q313.  
PN EP43874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.8%; Score 306.5; DB 2; Length 461;  
Best Local Similarity 24.1%; Pred. No. 9.5e-09;  
RESULT 958  
ID AAM83654 standard; protein; 495 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:1903.  
PN W02004023973-A2.  
PD 25-MAR-2004.  
PA (TNCY-) INCTRE CORP.  
Query Match 7.8%; Score 306.5; DB 8; Length 495;  
Best Local Similarity 24.8%; Pred. No. 1e-08;  
RESULT 959  
ID AAU99004 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D172N/K174T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 305.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 9.8e-09;  
RESULT 960  
ID AAU99073 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V339S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 305.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 9.8e-09;  
RESULT 961  
ID AAR13582 standard; protein; 461 AA.  
DE Human protein C zymogen Q097.  
PN EP43874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.7%; Score 304.5; DB 2; Length 461;

Best Local Similarity 24.4%; Pred. No. 1.2e-08;  
RESULT 962  
ID AAR13584 standard; protein; 461 AA.  
DE Human protein C zymogen Q248.  
PN EP43874-A.  
PD 28-AUG-1991.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 7.7%; Score 304.5; DB 2; Length 461;  
Best Local Similarity 24.4%; Pred. No. 1.2e-08;  
RESULT 963  
ID AAU99037 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T253N/D255S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 302.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 1.4e-08;  
RESULT 964  
ID AAU99028 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V243N/V245T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 302.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 1.4e-08;  
RESULT 965  
ID AAU99027 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V243N/V245S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.7%; Score 301.5; DB 5; Length 419;  
Best Local Similarity 24.5%; Pred. No. 1.6e-08;  
RESULT 966  
ID AAU99038 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant T253N/D255T.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 301.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 1.6e-08;  
RESULT 967  
ID AAP93714 standard; protein; 461 AA.  
DE Hybrid protein of protein-C and Factor-X.  
PN EP296413-A.  
PD 28-DEC-1988.  
PA (PARH ) HOECHST JAPAN LTD.  
Query Match 7.6%; Score 301.5; DB 1; Length 461;  
Best Local Similarity 24.7%; Pred. No. 1.8e-08;  
RESULT 968  
ID AAU99041 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D255N/D257S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 299.5; DB 5; Length 419;  
Best Local Similarity 24.2%; Pred. No. 2.1e-08;  
RESULT 969  
ID AAU99029 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant V245N/E247S.  
PN W0200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.6%; Score 298.5; DB 5; Length 419;  
Best Local Similarity 24.4%; Pred. No. 2.3e-08;  
RESULT 970  
ID AAU99030 standard; protein; 419 AA.

DE Human Protein C zymogen protein mutant V245N/E247T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match  
Best Local Similarity 24.4%; Pred. No. 2.3e-08;  
RESULT 971  
ID AA09042 standard; protein; 419 AA.  
DE Human Protein C zymogen protein mutant D255N/D257T.  
PN WO200232461-A2.  
PD 25-APR-2002.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match  
Best Local Similarity 24.2%; Pred. No. 2.3e-08;  
RESULT 972  
ID AD65750 standard; protein; 397 AA.  
DE Human protein encoded by clone UTRU20087070.  
PN EPI308459-A2.  
PD 07-MAY-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match  
Best Local Similarity 24.1%; Pred. No. 2.4e-08;  
RESULT 973  
ID AD117268 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOXV domain Segid 804.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 974  
ID AD117276 standard; protein; 230 AA.  
DE Polypeptide homologous to a human NOXV domain Segid 812.  
PN WO200268649-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 975  
ID AD783075 standard; protein; 230 AA.  
DE Trypsin-like serine protease protein - SEQ ID 66.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J. P.  
PA (TCHE/) TCHERNEV V. T.  
PA (LITU/) LITU X.  
PA (SEYT/) SEYTEK K. A.  
PA (ZERH/) ZERHUSEN B. D.  
PA (PATY/) PATYURAJAN M.  
PA (LEPL/) LEPLLEY D. M.  
PA (BURG/) BURGESS C. E.  
PA (SHIM/) SHIMKETS R. A.  
PA (GROS/) GROSSE W. M.  
PA (SZEK/) SZEKERES E. S.  
PA (VERN/) VERNER C. A. M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S. J.  
PA (BOLD/) BOLDOS F. L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E. A.  
PA (PERN/) FERNANDES E. R.  
PA (RIEG/) RIEGER D. K.  
PA (EDIN/) EDINGER S. R.  
PA (GUNT/) GUNTER E.  
PA (MILT/) MILLER I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J. R.  
PA (SMIT/) SMITSON G.  
Query Match 7.5%; Score 296; DB 5; Length 230;  
7.5%; Score 296; DB 7; Length 230;

Best Local Similarity 32.3%; Pred. No. 1.8e-08;  
RESULT 976  
ID ABG21442 standard; protein; 932 AA.  
DE Novel human diagnostic protein #21433.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 21.0%; Pred. No. 6.7e-08;  
RESULT 977  
ID AAR09290 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue GPe (Leu 66, Asp 67, Thr 68, Gln 117).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match  
Best Local Similarity 23.3%; Pred. No. 5.4e-08;  
RESULT 978  
ID ABU12065 standard; protein; 986 AA.  
DE Human NOV12a CG92293-01 protein SEQ ID 50.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 1e-07;  
RESULT 979  
ID AAR70903 standard; protein; 527 AA.  
DE Human t-PA variant (N103, A432, A434).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GERTH-) GENENTECH INC.  
Query Match  
Best Local Similarity 23.4%; Pred. No. 6.5e-08;  
RESULT 980  
ID AAR70895 standard; protein; 527 AA.  
DE Human t-PA variant (N103, A331, A332).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GERTH-) GENENTECH INC.  
Query Match  
Best Local Similarity 23.5%; Pred. No. 6.5e-08;  
RESULT 981  
ID ADV03787 standard; protein; 516 AA.  
DE Antipsoarctic protein sequence #90.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GERTH-) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 982  
ID AEM80985 standard; protein; 516 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81669, SEQ:2539.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GERTH-) GENENTECH INC.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 983  
ID ADQ39246 standard; protein; 516 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 909.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 6.8e-08;  
RESULT 984  
ID AARI3921 standard; protein; 522 AA.  
DE Delta (466-470) tPA variant with H432A and R434A substns.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GERTH-) GENENTECH INC.  
Query Match 7.4%; Score 291.5; DB 2; Length 522;  
7.4%; Score 291.5; DB 2; Length 522;



Best Local Similarity 22.7%; Pred. No. 6.8e-08;  
RESULT 985  
ID AAR70475 standard; protein: 564 AA.  
DE Sequence of tissue plasminogen (TPA) analogue.  
PN W08703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
PA (MARCO ) MAROTTI K R.  
Query Match  
Best Local Similarity 22.9%; Pred. No. 7.4e-08;  
RESULT 986  
ID A088338 standard; protein: 376 AA.  
DE Rough scale snake venom prothrombin activator, trocacin.  
PN W02003082914-A1.  
PD 09-OCT-2003.  
PA (UYOU ) UNIV QUEENSLAND.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 5.4e-08;  
RESULT 987  
ID AAR60614 standard; protein: 516 AA.  
DE Plasmid pDAP3 encoded sequence.  
PN JP61139386-A.  
PD 26-JUN-1986.  
PA (TOYU ) TOYO SODA MFG CO LTD.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (CENG ) CENTRAL GLASS CO LTD.  
PA (HODO ) HODOGAYA CHEM IND CO LTD.  
Query Match  
Best Local Similarity 23.1%; Pred. No. 7.7e-08;  
RESULT 988  
ID AAR70257 standard; protein: 516 AA.  
DE Sequence of human tissue plasminogen activator (TPA) and leader.  
PN EP211883-A.  
PD 12-AUG-1987.  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (NIPS ) NIPPON SODA CO.  
PA (CENG ) CENTRAL GLASS CO LTD.  
PA (TOYU ) TOYO SODA MFG CO LTD.  
PA (NISC ) NISSAN CHEM IND LTD.  
PA (NISC ) NISSAN CHEMICAL INDS KK.  
Query Match  
Best Local Similarity 7.4%; Score 290.5; DB 1; Length 516;  
RESULT 989  
ID AAR70878 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,D184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.3%; Pred. No. 7.7e-08;  
RESULT 990  
ID AAR70885 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,D184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.3%; Pred. No. 7.7e-08;  
RESULT 991  
ID AAR70894 standard; protein: 527 AA.  
DE Human t-PA variant (N103,A303,A304).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 24.0%; Pred. No. 8.3e-08;  
RESULT 992  
ID AD100357 standard; protein: 520 AA.  
DE Human tissue type plasminogen activator (h-TPA) mutant polypeptide.  
PN CN1397564-A.  
PD 19-FEB-2003.  
PA (LIBB ) LI B.  
Query Match  
7.3%; Score 289.5; DB 7; Length 520;

Best Local Similarity 23.2%; Pred. No. 8.7e-08;  
RESULT 993  
ID AAR12340 standard; protein: 559 AA.  
DE T-PA variant contg. fibrinectin for thrombosis lysis (1).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match  
Best Local Similarity 22.2%; Pred. No. 9.4e-08;  
RESULT 994  
ID AAR22664 standard; protein: 564 AA.  
DE tPA analogue KKZA.  
PN US106741-A.  
PD 21-APR-1992.  
PA (UPJO ) UPJOHN CO.  
Query Match  
Best Local Similarity 23.4%; Pred. No. 9.4e-08;  
RESULT 995  
ID AAR06934 standard; protein: 658 AA.  
DE Human membrane-type serine protease (MTSP) 4-S splice variant.  
PN W0200157194-A2.  
PD 09-AUG-2001.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 22.7%; Pred. No. 1.1e-07;  
RESULT 996  
ID AD110379 standard; protein: 658 AA.  
DE Human cell surface protease #5.  
PN W0200295007-A2.  
PD 28-NOV-2002.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 7.3%; Score 289.5; DB 7; Length 658;  
RESULT 997  
ID ADJ46903 standard; protein: 658 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #5.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 22.7%; Pred. No. 1.1e-07;  
RESULT 998  
ID AAR06933 standard; protein: 802 AA.  
DE Human membrane-type serine protease (MTSP) 4-L splice variant.  
PN W0200157194-A2.  
PD 09-AUG-2001.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 7.3%; Score 289.5; DB 4; Length 802;  
RESULT 999  
ID AD110377 standard; protein: 802 AA.  
DE Human cell surface protease #4.  
PN W0200295007-A2.  
PD 28-NOV-2002.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
RESULT 1000  
ID ADJ46901 standard; protein: 802 AA.  
DE Human transmembrane serine protease (MTSP) polypeptide #4.  
PN US2004001801-A1.  
PD 01-JAN-2004.  
PA (CORV ) CORVAS INT INC.  
Query Match  
Best Local Similarity 7.3%; Score 289.5; DB 8; Length 802;  
RESULT 1001  
ID AAR21598 standard; protein: 527 AA.  
DE tPA variant - T103W, D236A, D238A, K240A.  
PN W09202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 23.4%; Pred. No. 9.4e-08;  
7.3%; Score 289; DB 2; Length 527;

RESULT 1002  
ID AAR09217 standard; protein; 529 AA.  
DE t-PA insertion variant 1304 HR.  
PN MO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 289; DB 2; Length 529;  
Best Local Similarity 23.4%; Pred. No. 9.5e-08;  
RESULT 1003  
ID AAB85076 standard; peptide; 296 AA.  
DE Amino acid sequence of MASP-1 polypeptide.  
PN MO200140451-A2.  
PD 07-JUN-2001.  
PA (JENS//) JENSENIUS J C.  
PA (THIE//) THIEL S.  
Query Match 7.3%; Score 288.5; DB 4; Length 296;  
Best Local Similarity 29.3%; Pred. No. 5.9e-08;  
RESULT 1004  
ID AAY41710 standard; protein; 802 AA.  
DE Human PRO618 protein sequence.  
PN MO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 2; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1005  
ID AAB44266 standard; protein; 802 AA.  
DE Human PRO618 (UNQ354) protein sequence SEQ ID NO:169.  
PN MO200053756-A2.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 3; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1006  
ID AAB24052 standard; protein; 802 AA.  
DE Human PRO618 protein sequence SEQ ID NO:24.  
PN MO200053754-A1.  
PD 14-SEP-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 3; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1007  
ID AAB82755 standard; protein; 802 AA.  
DE Amino acid sequence of novel human protease #54.  
PN MO200200860-A2.  
PD 03-JAN-2002.  
PA (SUGE-) SUGEN INC.  
Query Match 7.3%; Score 288.5; DB 5; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1008  
ID ABO25212 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1009  
ID ABO72231 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1010  
ID ABO84898 standard; protein; 802 AA.  
DE Human secreted and transmembrane polypeptide PRO618.  
PN US200217553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;

RESULT 1011  
ID ABO61096 standard; protein; 802 AA.  
DE Human PRO618 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1012  
ID ABO80365 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein PRO618.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1013  
ID ADA24708 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1014  
ID ABO19667 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane protein PRO618.  
PN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1015  
ID ADA12369 standard; protein; 802 AA.  
DE Human secreted/transmembrane polypeptide PRO618.  
PN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1016  
ID ABO19558 standard; protein; 802 AA.  
DE Novel human secreted and transmembrane polypeptide #26.  
PN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match 7.3%; Score 288.5; DB 6; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1017  
ID ADB73675 standard; protein; 802 AA.  
DE Human PRO polypeptide #26.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1018  
ID ADB76391 standard; protein; 802 AA.  
DE Human PRO polypeptide #26.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1019  
ID ADC43817 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1020  
ID ADC61577 standard; protein; 802 AA.

DE Human secreted/transmembrane protein, PRO618.  
PN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1021  
ID ADC63541 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1022  
ID ADC66641 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1023  
ID ADC68765 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1024  
ID ADC62825 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1025  
ID ADC67890 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1026  
ID ADC41210 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1027  
ID ADC67265 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1028  
ID ADC62201 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1029  
ID ADC41834 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.

PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1030  
ID ADE49203 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1031  
ID ADE35257 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1032  
ID ADE16371 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1033  
ID ADD72986 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1034  
ID ADD72344 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1035  
ID ADE16995 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1036  
ID ADF47009 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1037  
ID ADC52766 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 7; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1038  
ID ADG60086 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003206915-A1.

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PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1039
ID ADI60846 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200307700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 7; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1040
ID ADE48503 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1041
ID ADE89604 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200310181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FLIV/) FLIVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER W A.
PA (PANT/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1042
ID ADF61244 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1043
ID ADF39936 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US200319894-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1044
ID ADF45732 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1045
ID ADF24128 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1046
ID ADF40560 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1047
ID ADF23504 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1048
ID ADF33487 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1049
ID ADF26954 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1050
ID ADF27590 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003198437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1051
ID ADF41184 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1052
ID ADF32863 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 288.5; DB 8; Length 802;
Best Local Similarity 22.7%; Pred. No. 1.5e-07;
RESULT 1053
ID ADF25229 standard; protein; 802 AA.
DE Human secreted/transmembrane protein, PRO618.
PN US2003211092-A1.
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PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1054  
ID ADF26330 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1053  
ID ADF34119 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1056  
ID ADF46356 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1057  
ID ADF50342 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1058  
ID ADG49718 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1059  
ID ADG51590 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1060  
ID ADG49094 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1061  
ID ADG48470 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1062  
ID ADG50966 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004005312-A1.  
PD 08-JAN-2004.

PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1063  
ID ADG58910 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1064  
ID ADG62366 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1065  
ID ADH25391 standard; protein; 802 AA.  
DE Human neurocrinin homologue related protein sequence SEQ ID NO:169.  
PN EP1386931-A1.  
PD 04-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1066  
ID ADM17168 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1067  
ID ADL07002 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1068  
ID ADT91615 standard; protein; 802 AA.  
DE Human secreted/transmembrane protein, PRO618.  
PN AU2002317529-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 7.3%; Score 288.5; DB 8; Length 802;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1069  
ID AAB98507 standard; protein; 902 AA.  
DE Murine epithin.  
PN WO200129056-A1.  
PD 26-APR-2001.  
PA (UYAR ) UNIV ARKANSAS.  
Query Match 7.3%; Score 288.5; DB 4; Length 902;  
Best Local Similarity 21.4%; Pred. No. 1.7e-07;  
RESULT 1070  
ID AAU80517 standard; protein; 902 AA.  
DE Mouse epithillin-like serine protease.  
PN WO200196378-A2.  
PD 20-DEC-2001.  
PA (FARB ) BAYER AG.  
Query Match 7.3%; Score 288.5; DB 5; Length 902;  
Best Local Similarity 21.4%; Pred. No. 1.7e-07;  
RESULT 1071  
ID AAU77549 standard; protein; 902 AA.  
DE Murine type II membrane serine protease, epithin.  
PN WO200212461-A2.  
PD 14-FEB-2002.  
PA (FARB ) BAYER AG.

Query Match 7.3%; Score 288.5; DB 5; Length 902;  
Best Local Similarity 21.4%; Pred. No. 1.7e-07;  
RESULT 1072  
ID AAR05489 standard; protein; 527 AA.  
DE tPA024 precursor protein.  
PN EPJ73896-A.  
PD 20-JUN-1990.  
PA (YAMA) YAMANOUCHI PHARM CO LTD.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.6%; Pred. No. 1.1e-07;  
RESULT 1073  
ID AAR21599 standard; protein; 527 AA.  
DE tPA variant - N117Q, D236A, D238A, K240A.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1074  
ID AAR20220 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-012.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.1e-07;  
RESULT 1075  
ID AAR20219 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-011.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.1e-07;  
RESULT 1076  
ID AAR20217 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-009.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.1e-07;  
RESULT 1077  
ID AAR20218 standard; protein; 527 AA.  
DE t-PA analogue expressed by pCDM8-010.  
PN JP03285680-A.  
PD 16-DEC-1991.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.1e-07;  
RESULT 1078  
ID AAR70901 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A416,A417,A418).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 1.1e-07;  
RESULT 1079  
ID AAR70904 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A440).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 288; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1080  
ID AAY49558 standard; protein; 356 AA.  
DE Human protein C protein sequence.  
PN WO9950544-A2.  
PD 07-OCT-1999.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

Query Match 7.3%; Score 287.5; DB 2; Length 356;  
Best Local Similarity 24.5%; Pred. No. 7.9e-08;  
RESULT 1081  
ID AAM52187 standard; protein; 406 AA.  
DE Human FVII mutant K143N/N145T/R315N/V317T.  
PN WO200158935-A2.  
PD 16-AUG-2001.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.3%; Score 287.5; DB 4; Length 406;  
Best Local Similarity 23.0%; Pred. No. 8.9e-08;  
RESULT 1082  
ID ADJ56078 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant K143N/ N145T/ R290N/ A292T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.3%; Score 287.5; DB 8; Length 406;  
Best Local Similarity 23.0%; Pred. No. 8.9e-08;  
RESULT 1083  
ID AAR13918 standard; protein; 522 AA.  
DE Delta (466-470) tPA variant with K416A, H417A and E418A subctns.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287.5; DB 2; Length 522;  
Best Local Similarity 22.9%; Pred. No. 1.1e-07;  
RESULT 1084  
ID ABP43952 standard; protein; 795 AA.  
DE Human PRO618.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 7.3%; Score 287.5; DB 5; Length 795;  
Best Local Similarity 22.7%; Pred. No. 1.7e-07;  
RESULT 1085  
ID ADG83828 standard; protein; 467 AA.  
DE Coastal taipan venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (UYQU) UNIV QUEENSLAND.  
Query Match 7.3%; Score 287; DB 8; Length 467;  
Best Local Similarity 22.5%; Pred. No. 1.1e-07;  
RESULT 1086  
ID AAR70879 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N103,S184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1087  
ID AAR70883 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N103,K210,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1088  
ID AAR70884 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N103,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1089  
ID AAR70886 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N103,S184,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;

Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1090  
ID AAR70874 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1091  
ID AAR70887 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,K213,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1092  
ID AAR70881 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,R210,A211,R212,R213,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.1e-07;  
RESULT 1093  
ID AAR70882 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,R252,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1094  
ID AAR70889 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,R252,E275,O277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1095  
ID AAR70888 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.1e-07;  
RESULT 1096  
ID AAR70890 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,K210,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1097  
ID AAR70880 standard; protein: 483 AA.  
DE Human tissue PA variant (delta1-44,N103,K213,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 483;  
Best Local Similarity 23.4%; Pred. No. 1.1e-07;  
RESULT 1098  
ID AAR70907 standard; protein: 527 AA.  
DE Human t-PA variant (N103,A460,A462).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.2e-07;  
RESULT 1099  
ID AAR70874 standard; protein: 527 AA.  
DE Human t-PA variant (N67,N103).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.2e-07;  
RESULT 1100  
ID AAR70892 standard; protein: 527 AA.  
DE Human t-PA variant (N103,A283,A287).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 287; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.2e-07;  
RESULT 1101  
ID AAR52182 standard; protein: 406 AA.  
DE Human FVII mutant K143N/N145T.  
PN WO200158935-A2.  
PD 16-AUG-2001.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.3%; Score 286.5; DB 4; Length 406;  
Best Local Similarity 23.0%; Pred. No. 1e-07;  
RESULT 1102  
ID ADJ56073 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant K143N/N145T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.3%; Score 286.5; DB 8; Length 406;  
Best Local Similarity 23.0%; Pred. No. 1e-07;  
RESULT 1103  
ID ADO10589 standard; protein: 406 AA.  
DE Human factor VII/VIII protein mutant #25.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.3%; Score 286.5; DB 8; Length 406;  
Best Local Similarity 23.0%; Pred. No. 1e-07;  
RESULT 1104  
ID ADG83826 standard; protein: 467 AA.  
DE Brown snake venom protease.  
PN WO2003082914-A1.  
PD 09-OCT-2003.  
PA (VYQU) UNIV QUEENSLAND.  
Query Match 7.3%; Score 286.5; DB 8; Length 467;  
Best Local Similarity 22.2%; Pred. No. 1.1e-07;  
RESULT 1105  
ID AAR14486 standard; protein: 522 AA.  
DE Delta (466-470) tPA variant with Y67N substitution.  
PN WO911149-A.  
PD 05-SEP-1991.  
PA (GETH) GENENTECH INC.  
Query Match 7.3%; Score 286.5; DB 2; Length 522;  
Best Local Similarity 22.7%; Pred. No. 1.3e-07;  
RESULT 1106  
ID AAR44816 standard; protein: 527 AA.  
DE Human tPA variant (N67,N103).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
RESULT 1107  
ID AAR44812 standard; protein: 527 AA.  
DE Human tPA variant N103.  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;

RESULT 1108  
ID AAR70868 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A432,A434).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
RESULT 1109  
ID AAR70860 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A331,A332).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.4e-07;  
RESULT 1110  
ID AAR70900 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A410).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.4e-07;  
RESULT 1111  
ID AAR09220 standard; protein; 529 AA.  
DE t-PA insertion variant 1304H, 1305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 286; DB 2; Length 529;  
Best Local Similarity 23.2%; Pred. No. 1.4e-07;  
RESULT 1112  
ID AAR70449 standard; protein; 530 AA.  
DE Sequence encoded by of synthetic gene for mature human tissue plasminogen activator (tPA).  
PN WO8705934-A.  
PD 08-OCT-1987.  
PA (CREA/) CREA R.  
Query Match 7.2%; Score 286; DB 1; Length 530;  
Best Local Similarity 22.9%; Pred. No. 1.4e-07;  
RESULT 1113  
ID AAR12342 standard; protein; 561 AA.  
DE T-PA with -ve charged finger and/or kringle domain (1).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 286; DB 2; Length 561;  
Best Local Similarity 22.1%; Pred. No. 1.4e-07;  
RESULT 1114  
ID AAR09289 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBN12 (Aep 67, Thr 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.2%; Score 286; DB 2; Length 562;  
Best Local Similarity 23.3%; Pred. No. 1.5e-07;  
RESULT 1115  
ID AAR70880 standard; protein; 527 AA.  
DE Thrombolytic proteins 1-9-11 having t-PA activity and R275 is deleted or replaced and containing a modified N-linked glycosylation site.  
PN WO8704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC.  
Query Match 7.2%; Score 285.5; DB 1; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.5e-07;  
RESULT 1116  
ID AAR91683 standard; protein; 527 AA.  
DE Sequence of tissue plasminogen activator (tPA).  
PN WO8911531-A.  
PD 30-NOV-1989.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 1; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.5e-07;  
RESULT 1117  
ID AAR09270 standard; protein; 527 AA.  
DE t-PA variant H331A, H332A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 1.5e-07;  
RESULT 1118  
ID AAR09278 standard; protein; 527 AA.  
DE t-PA variant H432A, R434A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 1.5e-07;  
RESULT 1119  
ID AAR71449 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 285; DB 1; Length 528;  
Best Local Similarity 23.4%; Pred. No. 1.6e-07;  
RESULT 1120  
ID AAR13148 standard; protein; 556 AA.  
DE T-PA variant contg. fibrinectin for thrombosis lysis (2).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 285; DB 2; Length 556;  
Best Local Similarity 21.9%; Pred. No. 1.6e-07;  
RESULT 1121  
ID AAR11710 standard; protein; 264 AA.  
DE Human serine protease BSSPS (hBSSPS) SEQ ID NO:2.  
PN WO200031243-A1.  
PD 02-JUN-2000.  
PA (FUSO ) FUSO PHARM IND LTD.  
Query Match 7.2%; Score 284.5; DB 3; Length 264;  
Best Local Similarity 28.0%; Pred. No. 8.6e-08;  
RESULT 1122  
ID AAR91961 standard; protein; 518 AA.  
DE Sequence of dee 1-44E275 t-PA mutant.  
PN WO8909266-A.  
PD 05-OCT-1989.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284.5; DB 8; Length 629;  
Best Local Similarity 22.9%; Pred. No. 1.6e-07;  
RESULT 1123  
ID ABR84749 standard; protein; 629 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4998.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.2%; Score 284.5; DB 8; Length 629;  
Best Local Similarity 19.5%; Pred. No. 1.9e-07;  
RESULT 1124  
ID ABR82817 standard; protein; 629 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3066.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 7.2%; Score 284.5; DB 8; Length 629;  
Best Local Similarity 19.5%; Pred. No. 1.9e-07;  
RESULT 1125  
ID AAR70851 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N67,D184,E275,I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.



Query Match 7.2%; Score 284; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.6e-07;  
RESULT 1126  
ID AAR70844 standard; protein: 483 AA.  
DE Human tissue PA variant (delccl-44,N67,D184,E275).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 483;  
Best Local Similarity 23.1%; Pred. No. 1.6e-07;  
RESULT 1127  
ID AAR44809 standard; protein: 527 AA.  
DE Human cPA variant (N65, S67).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 1.8e-07;  
RESULT 1128  
ID AAR70908 standard; protein: 527 AA.  
DE Human c-PA variant (N103,A477).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1.8e-07;  
RESULT 1129  
ID AAR70859 standard; protein: 527 AA.  
DE Human c-PA variant (N67,A303,A304).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.8%; Pred. No. 1.8e-07;  
RESULT 1130  
ID AAR70893 standard; protein: 527 AA.  
DE Human c-PA variant (N103,A296,A297,A298,A299).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 1.8e-07;  
RESULT 1131  
ID AAR70891 standard; protein: 527 AA.  
DE Human c-PA variant (N103,A267).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 284; DB 2; Length 527;  
Best Local Similarity 23.7%; Pred. No. 1.8e-07;  
RESULT 1132  
ID AAP70474 standard; protein: 562 AA.  
DE Sequence of tissue plasminogen (TPA) analogue.  
PN W08703906-A.  
PD 02-JUL-1987.  
PA (UPJO ) UPJOHN CO.  
PA (MARO/) MAROTTI K R.  
Query Match 7.2%; Score 284; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 1.9e-07;  
RESULT 1133  
ID AAR09286 standard; protein: 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNTS (Ser 67, Ser 68).  
PN W06912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.2%; Score 284; DB 2; Length 562;  
Best Local Similarity 23.1%; Pred. No. 1.9e-07;  
RESULT 1134  
ID AAR33807 standard; protein: 562 AA.  
DE c-PA (Tyr 297) mutant.  
PN W09206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.

Query Match 7.2%; Score 284; DB 2; Length 562;  
Best Local Similarity 23.2%; Pred. No. 1.9e-07;  
RESULT 1135  
ID ABB80068 standard; protein: 406 AA.  
DE Human coagulation factor VII mutant L305V/M306D/D309S.  
PN W0200183725-A1.  
PD 08-NOV-2001.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 5; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1136  
ID AAG73125 standard; protein: 406 AA.  
DE Human coagulation factor VII mutant polypeptide L305V/M306D/D309S.  
PN W0200277218-A1.  
PD 03-OCT-2002.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 6; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1137  
ID ADJ55852 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant L305V/M306D/D309S.  
PN W0200400366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.2%; Score 283.5; DB 8; Length 406;  
Best Local Similarity 22.7%; Pred. No. 1.5e-07;  
RESULT 1138  
ID ADE83543 standard; protein: 482 AA.  
DE Rat Protein NP\_058639, SEQ ID NO 11161.  
PN W02003016475-A2.  
PD 27-FEB-2003.  
PA (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 7.2%; Score 283.5; DB 7; Length 482;  
Best Local Similarity 22.8%; Pred. No. 1.7e-07;  
RESULT 1139  
ID AAR13917 standard; peptide: 522 AA.  
DE Delta (466-470) cPA variant with K296A, H297A, R298A and R299A  
DE substitutions.  
PN W09113148-A.  
PD 05-SEP-1991.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283.5; DB 2; Length 522;  
Best Local Similarity 22.8%; Pred. No. 1.8e-07;  
RESULT 1140  
ID AAP90169 standard; peptide: 571 AA.  
DE Tissue plasminogen activator mutant 2G.  
PN W08907146-A.  
PD 10-AUG-1989.  
PA (INTE-) INTEG GENETICS INC.  
Query Match 7.2%; Score 283.5; DB 1; Length 571;  
Best Local Similarity 22.4%; Pred. No. 2e-07;  
RESULT 1141  
ID AAR09257 standard; protein: 483 AA.  
DE c-PA variant dl-44, N184D, I210R, G211A, K212R, V213R, T252R, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 1.8e-07;  
RESULT 1142  
ID AAR09269 standard; protein: 527 AA.  
DE c-PA variant E303A, R304A.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 23.7%; Pred. No. 2e-07;  
RESULT 1143  
ID AAR44810 standard; protein: 527 AA.  
DE Human cPA variant (N65, T67).  
PN US5270198-A.  
PD 14-DEC-1993.

PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 2e-07;  
RESULT 1144  
ID AAR44817 standard; protein; 527 AA.  
DE Human tPA variant (N67,A236,A297,A298,A299).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 2e-07;  
RESULT 1145  
ID AAR44814 standard; protein; 527 AA.  
DE Human tPA variant (N105,T107).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 23.6%; Pred. No. 2e-07;  
RESULT 1146  
ID AAR70899 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A408).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 283; DB 2; Length 527;  
Best Local Similarity 22.9%; Pred. No. 2e-07;  
RESULT 1147  
ID AAR12341 standard; protein; 560 AA.  
DE T-PA variant congl. fibrinectin for chromobasis lysis (3).  
PN JP03061482-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 283; DB 2; Length 560;  
Best Local Similarity 22.1%; Pred. No. 2.1e-07;  
RESULT 1148  
ID AAR12367 standard; protein; 561 AA.  
DE T-PA with -ve charged finger and/or kringle domain (7).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.2%; Score 283; DB 2; Length 561;  
Best Local Similarity 22.1%; Pred. No. 2.1e-07;  
RESULT 1149  
ID AAR09231 standard; protein; 524 AA.  
DE t-PA deletion variant d297-299.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.2%; Score 282.5; DB 2; Length 524;  
Best Local Similarity 22.8%; Pred. No. 2.1e-07;  
RESULT 1150  
ID AAR09246 standard; protein; 483 AA.  
DE t-PA variant d1-44, N184D, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 2.1e-07;  
RESULT 1151  
ID AAR09254 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211H, K212Q, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 483;  
Best Local Similarity 22.8%; Pred. No. 2.1e-07;  
RESULT 1152  
ID AAR09230 standard; protein; 525 AA.  
DE t-PA deletion variant d297-298.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.

Query Match 7.1%; Score 282; DB 2; Length 525;  
Best Local Similarity 23.4%; Pred. No. 2.2e-07;  
RESULT 1153  
ID AAR09255 standard; protein; 527 AA.  
DE t-PA variant I210R, G211H, K212Q, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 527;  
Best Local Similarity 22.8%; Pred. No. 2.2e-07;  
RESULT 1154  
ID AAR21600 standard; protein; 527 AA.  
DE tPA variant - B94A, D95A, T103N.  
PN WO9202612-A.  
PD 20-FEB-1992.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.2e-07;  
RESULT 1155  
ID AAR70866 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A416,A417,A418).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 2.2e-07;  
RESULT 1156  
ID AAR70902 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A426,A427,A429,A430).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 2.2e-07;  
RESULT 1157  
ID AAR70869 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A440).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 282; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.2e-07;  
RESULT 1158  
ID AAR82582 standard; protein; 562 AA.  
DE Tissue plasminogen activator with S-119 substd for M and QG196-98 substd  
DE for NGT.  
PN JP63230083-A.  
PD 26-SEP-1988.  
PA (ETSA ) ETSAI CO LTD.  
Query Match 7.1%; Score 282; DB 2; Length 562;  
Best Local Similarity 23.2%; Pred. No. 2.4e-07;  
RESULT 1159  
ID AAR09287 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator analogue BBNT6 (Thr 67, Asp 68).  
PN WO8912681-A.  
PD 28-DEC-1989.  
PA (BRBI-) BRIT BIO-TECHN LTD.  
Query Match 7.1%; Score 282; DB 2; Length 562;  
Best Local Similarity 23.1%; Pred. No. 2.4e-07;  
RESULT 1160  
ID AAR23808 standard; protein; 562 AA.  
DE t-PA (Glu 298) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 282; DB 2; Length 562;  
Best Local Similarity 23.5%; Pred. No. 2.4e-07;  
RESULT 1161  
ID AAR23810 standard; protein; 562 AA.  
DE t-PA (Gly 301) mutant.  
PN WO9206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.

Query Match 7.1%; Score 282; DB 2; Length 562;  
Best Local Similarity 23.6%; Pred. No. 2.4e-07;  
RESULT 1162  
ID AAB84869 standard; protein: 406 AA.  
DE Mutant blood coagulant factor VII (FVII-30).  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA) 2H KAGAKU & KESSEI RYOHO KENKYUSHO.  
Query Match 7.1%; Score 281.5; DB 4; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;  
RESULT 1163  
ID HAM52185 standard; protein: 406 AA.  
DE Human FVII mutant G291N.  
PN WO200158935-A2.  
PD 16-AUG-2001.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 281.5; DB 4; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;  
RESULT 1164  
ID AAO30584 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158D/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1165  
ID AAO30626 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1166  
ID AAO30582 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1167  
ID AAO30616 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1168  
ID AAO30572 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1169  
ID AAO30628 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158D/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1170  
ID ADJ55926 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;

Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1171  
ID ADJ55927 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1172  
ID ADJ55915 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1173  
ID ADJ55970 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1174  
ID ADJ56063 standard; protein: 406 AA.  
DE Human factor VII protein mutant F374Y/ V158D/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1175  
ID ADJ55959 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1176  
ID ADJ56067 standard; protein: 406 AA.  
DE Human factor VII protein mutant F374Y/ V158T/ M298Q/ L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1177  
ID ADJ55971 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1178  
ID ADJ56033 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 1.9e-07;  
RESULT 1179  
ID ADJ56076 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant G291N.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;

RESULT 1180  
ID ADOI0585 standard; protein; 406 AA.  
DE Human factor VII/VIII protein mutant #21.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.8%; Pred. No. 1.9e-07;  
RESULT 1181  
ID ADOI0626 standard; protein; 406 AA.  
DE Human factor VII/VIII protein mutant #62.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 1.9e-07;  
RESULT 1182  
ID ADS12886 standard; protein; 406 AA.  
DE Human factor VII G237L mutant.  
PN WO2004083361-A2.  
PD 30-SEP-2004.  
PA (MAXY-) MAXYGEN HOLDINGS LTD.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 281.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 1.9e-07;  
RESULT 1183  
ID AAR09233 standard; protein; 522 AA.  
DE t-PA deletion variant d397-301.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 522;  
Best Local Similarity 23.4%; Pred. No. 2.4e-07;  
RESULT 1184  
ID AAR13919 standard; protein; 522 AA.  
DE Delta (466-470) tPA variant with E426A, R427A, K429A and E430A substitutions.  
PN WO9113149-A.  
PD 05-SEP-1991.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 522;  
Best Local Similarity 22.7%; Pred. No. 2.4e-07;  
RESULT 1185  
ID AAR09239 standard; protein; 524 AA.  
DE t-PA deletion variant d300-302.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281.5; DB 2; Length 524;  
Best Local Similarity 23.2%; Pred. No. 2.4e-07;  
RESULT 1186  
ID AAR12366 standard; protein; 562 AA.  
DE T-PA with -ve charged finger and/or kringles domain (5).  
PN JPO3061483-A.  
PD 18-MAR-1991.  
PA (FUJI) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 2.5e-07;  
RESULT 1187  
ID AAR09249 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213K, F305H.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.3%; Pred. No. 2.3e-07;  
RESULT 1188  
ID AAR70855 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, K210, E275, I277).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1189  
ID AAR70845 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, S184, E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1190  
ID AAR70848 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, R252, E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1191  
ID AAR70849 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, K210, E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1192  
ID AAR70854 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, R252, E275, I277).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1193  
ID AAR70843 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1194  
ID AAR70846 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, K213, E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1195  
ID AAR79144 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, S184, E275, I277).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1196  
ID AAR70850 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, E275, I277).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1197  
ID AAR70852 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44, N67, K213, E275, I277).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.2%; Pred. No. 2.3e-07;  
RESULT 1198  
ID AAR70847 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 2.3e-07;  
RESULT 1199  
ID AAR70853 standard; protein; 483 AA.  
DE Human tissue PA variant (delta1-44,N67,R210,A211,R212,R213,E275,1277).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 2.3e-07;  
RESULT 1200  
ID AAR60518 standard; protein; 487 AA.  
DE Cattle Factor-Xa.  
PN WO9418227-A2.  
PD 18-AUG-1994.  
PA (DENZ-) DENZYME APS.  
Query Match 7.1%; Score 281; DB 2; Length 487;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1201  
ID AAR76216 standard; protein; 488 AA.  
DE Human Factor X protein.  
PN WO9838317-A1.  
PD 03-SEP-1998.  
PA (IMMO ) IMMUNO AG.  
Query Match 7.1%; Score 281; DB 2; Length 488;  
Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
RESULT 1202  
ID AAR76217 standard; protein; 488 AA.  
DE Human Factor X protein analogue.  
PN WO9838317-A1.  
PD 03-SEP-1998.  
PA (IMMO ) IMMUNO AG.  
Query Match 7.1%; Score 281; DB 2; Length 488;  
Best Local Similarity 22.6%; Pred. No. 2.4e-07;  
RESULT 1203  
ID AAR76218 standard; protein; 488 AA.  
DE Human Factor X protein.  
PN WO9838318-A1.  
PD 03-SEP-1998.  
PA (IMMO ) IMMUNO AG.  
Query Match 7.1%; Score 281; DB 2; Length 488;  
Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
RESULT 1204  
ID AAB70411 standard; protein; 488 AA.  
DE Human factor X protein sequence SEQ ID NO:2.  
PN WO200110896-A2.  
PD 15-FEB-2001.  
PA (BAXTER ) BAXTER AG.  
Query Match 7.1%; Score 281; DB 4; Length 488;  
Best Local Similarity 24.0%; Pred. No. 2.4e-07;  
RESULT 1205  
ID AAR60502 standard; protein; 492 AA.  
DE Serine protease for fusion protein cleavage.  
PN WO9418227-A2.  
PD 18-AUG-1994.  
PA (DENZ-) DENZYME APS.  
Query Match 7.1%; Score 281; DB 2; Length 492;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1206  
ID AAR09238 standard; protein; 525 AA.  
DE t-PA deletion variant d300-301.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 525;

Best Local Similarity 22.8%; Pred. No. 2.5e-07;  
RESULT 1207  
ID AAR09276 standard; protein; 527 AA.  
DE t-PA variant K416A, H417A, E418A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1208  
ID AAR09279 standard; protein; 527 AA.  
DE t-PA variant R440A.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.5e-07;  
RESULT 1209  
ID AAR70875 standard; protein; 527 AA.  
DE Human t-PA variant (N60,N103).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1210  
ID AAR70876 standard; protein; 527 AA.  
DE Human t-PA variant (N60,N67,N103).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1211  
ID AAR70857 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A283,A287).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1212  
ID AAR70898 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A364,A365,A366).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1213  
ID AAR70906 standard; protein; 527 AA.  
DE Human t-PA variant (N103,A449,A453).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 2.5e-07;  
RESULT 1214  
ID AAR70872 standard; protein; 527 AA.  
DE Human t-PA variant (N67,A460,A462).  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;  
RESULT 1215  
ID AAR70842 standard; protein; 527 AA.  
DE Wild type tissue plasminogen activator protein.  
PN US3385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 281; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 2.5e-07;

RESULT 1216  
ID AAB13150 standard; protein: 558 AA.  
DE T-PA with -ve charged finger and/or kringle domain (3).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281; DB 2; Length 558;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1217  
ID AAB13152 standard; protein: 559 AA.  
DE T-PA with -ve charged finger and/or kringle domain (6).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 281; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1218  
ID AAP06091 standard; protein: 1087 AA.  
DE Hybrid plasminogen/-C-PA compound 1.  
PN EP292326-A.  
PD 23-NOV-1988.  
PA (BEC ) BECHAM GROUP PLC.  
Query Match 7.1%; Score 281; DB 1; Length 1087;  
Best Local Similarity 22.3%; Pred. No. 5e-07;  
RESULT 1219  
ID ABM1778 standard; protein: 264 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 280.5; DB 8; Length 264;  
Best Local Similarity 27.2%; Pred. No. 1.4e-07;  
RESULT 1220  
ID ABM84054 standard; protein: 279 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4303.  
PN \*WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY ) INCYTE CORP.  
Query Match 7.1%; Score 280.5; DB 8; Length 279;  
Best Local Similarity 27.2%; Pred. No. 1.5e-07;  
RESULT 1221  
ID AAO30575 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1222  
ID AAO30604 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158T/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1223  
ID AAO30577 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/V158T/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1224  
ID AAO30594 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1225

ID AAO30569 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1226  
ID AAO30606 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/V158D/K337A/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1227  
ID AAO30613 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1228  
ID AAO30621 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1229  
ID AAO30619 standard; protein: 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158D/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1230  
ID ADJ55876 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant / M298Q/L305V/K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1231  
ID ADJ55937 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant M298Q/L305V/K316H/K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1232  
ID ADJ56047 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant F374Y/V158D/M298Q/L305V/S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1233  
ID ADJ55949 standard; protein: 406 AA.  
DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K316H/K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 280.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
RESULT 1234  
ID ADJ55965 standard; protein: 406 AA.

DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1235  
 ID ADJ55948 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K316H/ K337A.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1236  
 ID ADJ56057 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ S314E.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1237  
 ID ADJ55885 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ K337A.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1238  
 ID ADJ55921 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V/ S314E.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1239  
 ID ADJ55958 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant M298Q/ L305V/ K316Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1240  
 ID ADJ55963 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K316Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1241  
 ID ADJ56016 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/ L305V/ M298Q/ S314E.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1242  
 ID ADJ56046 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/ V158D/ M298Q/ L305V/ K337A.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1243  
 ID ADJ55919 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ S314E.

PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1244  
 ID ADJ56056 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ L305V/ K337A.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1245  
 ID ADJ55887 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V/ K337A.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1246  
 ID ADJ55914 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant M298Q/ L305V/ S314E.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1247  
 ID ADJ56004 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ M298Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1248  
 ID ADJ010616 standard; protein; 406 AA.  
 DE Human factor VII/VIIa protein mutant #52.  
 PN W02004029091-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1249  
 ID ADJ010607 standard; protein; 406 AA.  
 DE Human factor VII/VIIa protein mutant #43.  
 PN W02004029091-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN APS.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1250  
 ID AAR09221 standard; protein; 526 AA.  
 DE c-PA deletion variant d297.  
 PN W09002798-A.  
 PD 22-MAR-1990.  
 PA (GEHTH ) GENENTECH INC.  
 Query Match 7.1%; Score 280.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.1e-07;  
 RESULT 1251  
 ID AAV70020 standard; protein; 561 AA.  
 DE Sequence of tissue plasminogen activator (tPA).  
 PN EP242836-A.  
 PD 28-CCR-1987.  
 PA (BOERF ) BOEHRINGER MANNHEIM GMBH.  
 Query Match 7.1%; Score 280.5; DB 1; Length 561;  
 Best Local Similarity 21.7%; Pred. No. 2.9e-07;  
 RESULT 1252  
 ID ABR62449 standard; protein; 583 AA.

DE Bovine recombinant prothrombin, expressed in *Escherichia coli*.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.1%; Score 280.5; DB 7; Length 583;  
 Best Local Similarity 21.9%; Pred. No. 3e-07;  
 RESULT 1253  
 ID ABR62451 standard; protein; 635 AA.  
 DE Bovine recombinant prothrombin, expressed in CHO cells.  
 PN WO2003052059-A2.  
 PD 26-JUN-2003.  
 PA (ELIL ) LILLY & CO ELI.  
 Query Match 7.1%; Score 280.5; DB 7; Length 635;  
 Best Local Similarity 21.9%; Pred. No. 3.2e-07;  
 RESULT 1254  
 ID AAR37402 standard; protein; 448 AA.  
 DE Factor X.  
 PN WO9309803-A1.  
 PD 27-MAY-1993.  
 PA (SCHAF ) SCHAFER S C.  
 PA (SCRI ) SCRIPPS RES INST.  
 Query Match 7.1%; Score 280; DB 2; Length 448;  
 Best Local Similarity 24.0%; Pred. No. 2.5e-07;  
 RESULT 1255  
 ID AAN66092 standard; peptide; 448 AA.  
 DE Human factor X variant.  
 PN WO9839456-A1.  
 PD 11-SEP-1998.  
 PA (UNIV ) UNIV WASHINGTON.  
 Query Match 7.1%; Score 280; DB 2; Length 448;  
 Best Local Similarity 24.0%; Pred. No. 2.5e-07;  
 RESULT 1256  
 ID AAR09245 standard; protein; 525 AA.  
 DE t-PA deletion variant d297, d305.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 2; Length 525;  
 Best Local Similarity 23.1%; Pred. No. 2.9e-07;  
 RESULT 1257  
 ID AAR05488 standard; protein; 527 AA.  
 DE tPA024 precursor protein.  
 PN EP973896-A.  
 PD 20-JUN-1990.  
 PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
 PA (YAMA ) NIPPON STEEL CORP.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1258  
 ID AAR09267 standard; protein; 527 AA.  
 DE t-PA variant D283A, H287A.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1259  
 ID AAR09282 standard; protein; 527 AA.  
 DE t-PA variant D460A, R462A.  
 PN WO9002798-A.  
 PD 22-MAR-1990.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1260  
 ID AAR13911 standard; protein; 527 AA.  
 DE t-PA deriv. (II).  
 PN EP445464-A.  
 PD 11-SEP-1991.  
 PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1261

ID AAR13914 standard; protein; 527 AA.  
 DE t-PA deriv. (V).  
 PN EP445464-A.  
 PD 11-SEP-1991.  
 PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1262  
 ID AAR13912 standard; protein; 527 AA.  
 DE t-PA deriv. (III).  
 PN EP445464-A.  
 PD 11-SEP-1991.  
 PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1263  
 ID AAR13910 standard; protein; 527 AA.  
 DE t-PA deriv. (I).  
 PN EP445464-A.  
 PD 11-SEP-1991.  
 PA (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1264  
 ID AAR21594 standard; protein; 527 AA.  
 DE tPA variant - D95A.  
 PN WO9202612-A.  
 PD 20-FEB-1992.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1265  
 ID AAR21593 standard; protein; 527 AA.  
 DE tPA variant - E94A.  
 PN WO9202612-A.  
 PD 20-FEB-1992.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.4%; Pred. No. 2.9e-07;  
 RESULT 1266  
 ID AAR20221 standard; protein; 527 AA.  
 DE t-PA analogue expressed by pCDM6-013.  
 PN JP03285680-A.  
 PD 16-DEC-1991.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1267  
 ID AAR20215 standard; protein; 527 AA.  
 DE R462S t-PA analogue.  
 PN JP03285680-A.  
 PD 16-DEC-1991.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1268  
 ID AAR20216 standard; protein; 527 AA.  
 DE R462G t-PA analogue.  
 PN JP03285680-A.  
 PD 16-DEC-1991.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1269  
 ID AAR20222 standard; protein; 527 AA.  
 DE t-PA analogue expressed by pCDM6-014.  
 PN JP03285680-A.  
 PD 16-DEC-1991.  
 PA (SUMU ) SUMITOMO SEIYAKU KK.  
 Query Match 7.1%; Score 280; DB 2; Length 527;  
 Best Local Similarity 23.0%; Pred. No. 2.9e-07;  
 RESULT 1270  
 ID AAR20223 standard; protein; 527 AA.



DE t-PA analogue expressed by pCDM8-018.  
 PN JF03285680-A.  
 PD 16-DEC-1991.  
 PA (SUMU ) SUMITOMO SEIRYAKU KK.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 527;  
 RESULT 1271  
 ID AAR44811 standard; protein; 527 AA.  
 DE Human tPA variant N67.  
 PN US5270198-A.  
 PD 14-DEC-1993.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 527;  
 RESULT 1272  
 ID AAR70865 standard; protein; 527 AA.  
 DE Human t-PA variant (N67,A410).  
 PN US5385732-A.  
 PD 31-JAN-1995.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 527;  
 RESULT 1273  
 ID AAW57778 standard; protein; 527 AA.  
 DE R275E,H417D human tissue-type plasminogen activator protein mutant.  
 PN WO9821320-A2.  
 PD 22-MAY-1998.  
 PA (SCRI ) SCRIPPS RES INST.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 527;  
 RESULT 1274  
 ID AAW45907 standard; peptide; 527 AA.  
 DE Single chain form of the intact t-PA molecule.  
 PN WO9802454-A2.  
 PD 22-JAN-1998.  
 PA (ADPR-) ADPOTECHE PLC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 527;  
 RESULT 1275  
 ID AAE24190 standard; protein; 527 AA.  
 DE Human tissue plasminogen activator (tPA) protein.  
 PN WO200240656-A2.  
 PD 23-MAY-2002.  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 5; Length 527;  
 RESULT 1276  
 ID AAG79362 standard; protein; 527 AA.  
 DE Human tissue plasminogen activator.  
 PN WO200243747-A2.  
 PD 06-JUN-2002.  
 PA (ISIS-) ISIS INNOVATION LTD.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 5; Length 527;  
 RESULT 1277  
 ID AAE25044 standard; protein; 527 AA.  
 DE Human tissue plasminogen activator (tPA) protein.  
 PN WO200240650-A2.  
 PD 23-MAY-2002.  
 PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 5; Length 527;  
 RESULT 1278  
 ID ADL92126 standard; protein; 527 AA.  
 DE Alteplase protein sequence.  
 PN WO200309862-A1.  
 PD 04-DEC-2003.  
 PA (NANO-) APPLIED NANOSYSTEMS BV.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 8; Length 527;  
 RESULT 1279  
 ID AAM82630 standard; protein; 534 AA.  
 DE Human diagnostic and therapeutic protein SEQ ID NO.2879.

PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 8; Length 534;  
 RESULT 1280  
 ID AAM82821 standard; protein; 534 AA.  
 DE Human diagnostic and therapeutic protein SEQ ID NO.3070.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 8; Length 534;  
 RESULT 1281  
 ID AAR13020 standard; protein; 557 AA.  
 DE T-PA variant contg. fibronectin for thrombosis lysis (4).  
 PN JF03061482-A.  
 PD 18-MAR-1991.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 557;  
 RESULT 1282  
 ID AAR13149 standard; protein; 557 AA.  
 DE T-PA variant contg. fibronectin for thrombosis lysis (4).  
 PN JF03061482-A.  
 PD 18-MAR-1991.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 2; Length 557;  
 RESULT 1283  
 ID AAP50219 standard; protein; 561 AA.  
 DE Tissue plasminogen activator encoded by cDNA clone.  
 PN EP143081-A.  
 PD 29-MAY-1985.  
 PA (CIBA ) CIBA GEIGY AG.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 1; Length 561;  
 RESULT 1284  
 ID AAP60790 standard; protein; 562 AA.  
 DE Sequence of human pre-tissue plasminogen activator (pre-t-PA).  
 PN G82173804-A.  
 PD 22-OCT-1986.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 1; Length 562;  
 RESULT 1285  
 ID AAP60810 standard; protein; 562 AA.  
 DE Sequence of modified human tissue plasminogen activator (t-PA).  
 PN FR2581652-A.  
 PD 14-NOV-1986.  
 PA (GETH ) GENENTECH INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 1; Length 562;  
 RESULT 1286  
 ID AAP60214 standard; protein; 562 AA.  
 DE Sequence of active human uterine tissue plasminogen activator (UTPA).  
 PN EP178105-A.  
 PD 16-APR-1986.  
 PA (INTE-) INTEG GENETICS INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 1; Length 562;  
 RESULT 1287  
 ID AAP81913 standard; protein; 562 AA.  
 DE Tissue plasminogen activator encoded by pEM1-tPA.  
 PN WO8800242-A.  
 PD 14-JAN-1988.  
 PA (DAMO-) DAMON BIOTECH INC.  
 Query Match  
 Best Local Similarity 7.1%; Score 280; DB 1; Length 562;  
 RESULT 1288  
 ID AAP80655 standard; protein; 562 AA.  
 DE Tissue plasminogen activator analogue.  
 PN EP293934-A.

PD 07-DEC-1988.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PA (NOVO ) NOVO IND AS.  
 PA (EISA ) EISA CO LTD.  
 Query Match 7.1%; Score 280; DB 1; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1289  
 ID AAP94406 standard; protein; 562 AA.  
 DE Sequence encoded by native cPA of plasmid pST112.  
 PN EP302456-A.  
 PD 08-FEB-1989.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match 7.1%; Score 280; DB 1; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1290  
 ID AAP93716 standard; protein; 562 AA.  
 DE Human melanoma t-PA encoded by plasmid pKG12.  
 PN EP297066-A.  
 PD 28-DEC-1988.  
 PA (KABI ) KABIGEN AB.  
 Query Match 7.1%; Score 280; DB 1; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1291  
 ID AAP90916 standard; protein; 562 AA.  
 DE Human tissue plasminogen activator.  
 PN JP01174388-A.  
 PD 10-JUL-1989.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match 7.1%; Score 280; DB 1; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1292  
 ID AAR09288 standard; protein; 562 AA.  
 DE Sequence of tissue plasminogen activator analogue BBWT11 (Ser 67, Leu 68).  
 PN WO8912681-A.  
 PD 28-DEC-1989.  
 PA (BBBI-) BRIT BIO-TECHN LTD.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1293  
 ID AAR06237 standard; protein; 562 AA.  
 DE Novel tissue plasminogen activator (t-PA) encoded by plasmid pST112.  
 PN EP379890-A.  
 PD 01-AUG-1990.  
 PA (FUJI ) FUJISAWA PHARM CO LTD.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1294  
 ID AAR04700 standard; protein; 562 AA.  
 DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S, H420S with altered residues 419 and 420.  
 PN EP351246-A.  
 PD 17-JAN-1990.  
 PA (NOVO ) NOVO-NORDISK AS.  
 PA (NOVO ) NOVO-NORDISK AS.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1295  
 ID AAR04701 standard; protein; 562 AA.  
 DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA K419S with altered residue 419.  
 PN EP351246-A.  
 PD 17-JAN-1990.  
 PA (NOVO ) NOVO-NORDISK AS.  
 PA (NOVO ) NOVO-NORDISK AS.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1296  
 ID AAR04699 standard; protein; 562 AA.  
 DE Native tissue plasminogen activator (t-PA).  
 PN EP351246-A.  
 PD 17-JAN-1990.  
 PA (NOVO ) NOVO-NORDISK AS.

PA (NOVO ) NOVO-NORDISK AS.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1297  
 ID AAR13727 standard; protein; 562 AA.  
 DE T-PA67+ mutant with supernumerary N-linked oligosaccharide side chain.  
 PN US5041376-A.  
 PD 20-AUG-1991.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1298  
 ID AAR12847 standard; protein; 562 AA.  
 DE T-PA Kringle 1 domain substitution mutant.  
 PN JP03127987-A.  
 PD 31-MAY-1991.  
 PA (KANF ) KANEGARUFUCHI CHEM KK.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1299  
 ID AAR23811 standard; protein; 562 AA.  
 DE t-PA (Glu 296, Glu 298, Glu 299) triple mutant.  
 PN WO9206203-A.  
 PD 16-APR-1992.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.5%; Pred. No. 3.1e-07;  
 RESULT 1300  
 ID AAR23806 standard; protein; 562 AA.  
 DE t-PA (Glu 296) mutant.  
 PN WO9206203-A.  
 PD 16-APR-1992.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1301  
 ID AAR23804 standard; protein; 562 AA.  
 DE t-PA (Glu 304) mutant.  
 PN WO9206203-A.  
 PD 16-APR-1992.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1302  
 ID AAR34426 standard; protein; 562 AA.  
 DE Sequence of human pre-pro tissue plasminogen activator (t-PA).  
 PN US5200340-A.  
 PD 06-APR-1993.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1303  
 ID AAR96220 standard; protein; 562 AA.  
 DE Full-length tissue plasminogen activator.  
 PN US5504001-A.  
 PD 02-APR-1996.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 7.1%; Score 280; DB 2; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1304  
 ID AAY50868 standard; protein; 562 AA.  
 DE Human tissue plasminogen activator protein fragment.  
 PN WO9957251-A2.  
 PD 11-NOV-1999.  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 Query Match 7.1%; Score 280; DB 3; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1305  
 ID AAY43397 standard; protein; 562 AA.  
 DE Human tissue plasminogen activator protein sequence.  
 PN US5985607-A.  
 PD 16-NOV-1999.

PA (CANG-) CANGENE CORP.  
 Query Match 7.1%; Score 280; DB 3; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1306  
 ID AAY9590 standard; protein; 562 AA.  
 DE Human tissue-type plasminogen activator t-PA.  
 PN W0200032759-A1.  
 PD 08-JUN-2000.  
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
 Query Match 7.1%; Score 280; DB 3; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1307  
 ID AAU97700 standard; protein; 562 AA.  
 DE Human tissue plasminogen activator (t-PA) protein sequence.  
 PN W0200232446-A2.  
 PD 25-APR-2002.  
 PA (PFIZ ) PFIZER LTD.  
 Query Match 7.1%; Score 280; DB 5; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1308  
 ID AAE37130 standard; protein; 562 AA.  
 DE Human tissue-type plasminogen activator (tPA) protein.  
 PN W02003033009-A2.  
 PD 24-APR-2003.  
 PA (OMNI-) OMNIO AB.  
 Query Match 7.1%; Score 280; DB 6; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1309  
 ID ABR55851 standard; protein; 562 AA.  
 DE Human tissue-type plasminogen activator (TPA) .  
 PN W02003031464-A2.  
 PD 17-APR-2003.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Query Match 7.1%; Score 280; DB 6; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1310  
 ID ABUS7646 standard; protein; 562 AA.  
 DE Differentially expressed breast cancer associated protein #33.  
 PN US2002156263-A1.  
 PD 24-OCT-2002.  
 PA (CHEN/) CHEN H.  
 Query Match 7.1%; Score 280; DB 6; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1311  
 ID ADN95624 standard; protein; 562 AA.  
 DE Human BEC/Lec-related protein sequence SeqID547.  
 PN W02003080640-A1.  
 PD 02-OCT-2003.  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 Query Match 7.1%; Score 280; DB 7; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1312  
 ID ADNA9698 standard; protein; 562 AA.  
 DE Human tissue type plasminogen activator TPA protein SeqID 26.  
 PN W02004033651-A2.  
 PD 22-APR-2004.  
 PA (NEOS-) NEOSE TECHNOLOGIES INC.  
 Query Match 7.1%; Score 280; DB 8; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1313  
 ID ADO28679 standard; protein; 562 AA.  
 DE Human tPA protein SEQ ID NO:108.  
 PN W02004044178-A2.  
 PD 27-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 8; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1314  
 ID AAM80983 standard; protein; 562 AA.  
 DE Tumour-associated antigenic target (TAR) polypeptide PRO4, SEQ:2535.  
 PN W02004030615-A2.

PD 15-APR-2004.  
 PA (GETH ) GENENTECH INC.  
 Query Match 7.1%; Score 280; DB 8; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1315  
 ID ADQ3248 standard; protein; 562 AA.  
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 911.  
 PN W02004058052-A2.  
 PD 15-JUL-2004.  
 PA (APPL-) APPLERA CORP.  
 Query Match 7.1%; Score 280; DB 8; Length 562;  
 Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
 RESULT 1316  
 ID AAO30591 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316H/L305V/M298Q) .  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1317  
 ID AAO30599 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316H/L305V/V158T/M298Q) .  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1318  
 ID AAO30597 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316H/L305V/V158D/M298Q) .  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1319  
 ID ADJ55873 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant M298Q/L305V.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1320  
 ID ADJ55985 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/L305V/M298Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1321  
 ID ADJ55941 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158D/M298Q/L305V/K316H.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1322  
 ID ADJ55943 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant V158T/M298Q/L305V/K316H.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.1%; Score 279.5; DB 8; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
 RESULT 1323  
 ID ADJ56009 standard; protein; 406 AA.  
 DE Human factor VII polypeptide mutant F374Y/L305V/V158D/M298Q.  
 PN W02004000366-A1.  
 PD 31-DEC-2003.

PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1324  
ID AD55879 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ M298Q/ L305V.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1325  
ID AD556014 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158T/ M298Q.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1326  
ID AD55881 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ M298Q/ L305V.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1327  
ID AD55936 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ L305V/ K316H.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1328  
ID AD010619 standard; protein; 406 AA.  
DE Human factor VII/VIII protein mutant #55.  
PN W02004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 279.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.4e-07;  
RESULT 1329  
ID AAR74689 standard; protein; 520 AA.  
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by QRLASQA).  
PN CN1082111-A.  
PD 16-FEB-1994.  
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
Query Match 7.1%; Score 279.5; DB 2; Length 520;  
Best Local Similarity 23.3%; Pred. No. 3e-07;  
RESULT 1330  
ID AAR09229 standard; protein; 526 AA.  
DE t-PA deletion variant d305.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1331  
ID AAR09228 standard; protein; 526 AA.  
DE t-PA deletion variant d304.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1332  
ID AAR09218 standard; protein; 528 AA.  
DE t-PA insertion variant i305 H, T, N, K, R, Q.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279.5; DB 2; Length 528;  
Best Local Similarity 23.0%; Pred. No. 3.1e-07;  
RESULT 1333  
ID AAG96427 standard; protein; 782 AA.  
DE Human ovarian cancer marker OV82.  
PN W0200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 7.1%; Score 279.5; DB 5; Length 782;  
Best Local Similarity 20.8%; Pred. No. 4.4e-07;  
RESULT 1334  
ID AAB84871 standard; protein; 401 AA.  
DE Mutant blood coagulant factor VII (FVII-39).  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSHI RYOHO KENKYUSHO.  
Query Match 7.1%; Score 279; DB 4; Length 401;  
Best Local Similarity 22.8%; Pred. No. 2.5e-07;  
RESULT 1335  
ID AAR09250 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1336  
ID AAR09248 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210R, G211A, K212R, V213R, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 22.8%; Pred. No. 3e-07;  
RESULT 1337  
ID AAR09247 standard; protein; 483 AA.  
DE t-PA variant d1-44, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1338  
ID AAR09251 standard; protein; 483 AA.  
DE t-PA variant d1-44, T252R, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1339  
ID AAR09263 standard; protein; 483 AA.  
DE t-PA variant Y67N, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1340  
ID AAR09252 standard; protein; 483 AA.  
DE t-PA variant d1-44, V213K, T252R, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1341  
ID AAR09253 standard; protein; 483 AA.  
DE t-PA variant d1-44, I210K, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 483;  
Best Local Similarity 23.0%; Pred. No. 3e-07;  
RESULT 1342  
ID AAR09243 standard; protein; 525 AA.  
DE t-PA deletion variant d304-305.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 525;  
Best Local Similarity 23.0%; Pred. No. 3.2e-07;  
RESULT 1343  
ID AAR04186 standard; protein; 527 AA.  
DE Plasmidogen activator.  
PN EP365468-A.  
PD 25-APR-1990.  
PA (CIBA) CIBA GEIGY AG.  
PA (UCPG-) UCP GEN-PHARMA AG.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 3.3e-07;  
RESULT 1344  
ID AAR06236 standard; protein; 527 AA.  
DE Novel tissue plasminogen activator (tPA) encoding plasmid PTPA102.  
PN EP379890-A.  
PD 01-AUG-1990.  
PA (FUJ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.3e-07;  
RESULT 1345  
ID AAR09256 standard; protein; 527 AA.  
DE t-PA variant I210R, G211A, K212R, V213R, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 22.8%; Pred. No. 3.3e-07;  
RESULT 1346  
ID AAR09275 standard; protein; 527 AA.  
DE t-PA variant E410A.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 22.8%; Pred. No. 3.3e-07;  
RESULT 1347  
ID AAR09215 standard; protein; 527 AA.  
DE t-PA variant F305 H, T, N, K, R, Q.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1348  
ID AAR09262 standard; protein; 527 AA.  
DE t-PA variant Y67N, F305H.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1349  
ID AAR21596 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, N117Q.  
PN W09202612-A.  
PD 20-FEB-1992.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1350  
ID AAR21595 standard; protein; 527 AA.  
DE tPA variant - D95G.  
PN W09202612-A.  
PD 20-FEB-1992.  
PA (GETH) GENENTECH INC.

Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1351  
ID AAR21597 standard; protein; 527 AA.  
DE tPA variant - E94A, D95A, D236A, D238A, K240A.  
PN W09202612-A.  
PD 20-FEB-1992.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.3e-07;  
RESULT 1352  
ID AAR44813 standard; protein; 527 AA.  
DE Human tPA variant (N105, S107).  
PN US5270198-A.  
PD 14-DEC-1993.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.4%; Pred. No. 3.3e-07;  
RESULT 1353  
ID AAR70905 standard; protein; 527 AA.  
DE Human t-PA variant (N103, A445, A449).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1354  
ID AAM57779 standard; protein; 527 AA.  
DE R275E, H417E human tissue-type plasminogen activator protein mutant.  
PN W09821320-A2.  
PD 22-MAY-1998.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 7.1%; Score 279; DB 2; Length 527;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1355  
ID AAR25435 standard; protein; 528 AA.  
DE t-PA variant R299D.  
PN W09211377-A1.  
PD 09-JUL-1992.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 528;  
Best Local Similarity 23.5%; Pred. No. 3.3e-07;  
RESULT 1356  
ID AAR09219 standard; protein; 529 AA.  
DE t-PA insertion variant 1305 HH.  
PN W09002798-A.  
PD 22-MAR-1990.  
PA (GETH) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 529;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1357  
ID AAP70882 standard; protein; 530 AA.  
DE Thrombolytic protein 1-19-1-21 having t-PA activity, deleted or replaced  
DE R275 is and containing a modified N-linked glycosylation site.  
PN W08704722-A.  
PD 13-AUG-1987.  
PA (GEMV) GENETICS INST INC.  
PA (LARS/) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1358  
ID AAP71659 standard; protein; 530 AA.  
DE Thrombolytic protein with t-PA activity where R275 is deleted or replaced  
DE and containing a modified N-linked glycosylation site.  
PN W08704722-A.  
PD 13-AUG-1987.  
PA (GEMV) GENETICS INST INC.  
PA (LARS/) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1359  
ID AAP70879 standard; protein; 530 AA.  
DE Thrombolytic proteins 1-1-1-7 having t-PA activity, where R275 is deleted

DE or replaced.  
PN W08704722-A.  
PD 13-AUG-1987.  
PA (GEMV ) GENETICS INST INC.  
PA (LARS/) LARSEN G R.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1360  
ID AAP92377 standard; protein; 530 AA.  
DE Sequence of modified tPA-type thrombolytic proteins.  
PN W08810119-A.  
PD 29-DEC-1988.  
PA (GEMV ) GENETICS INST INC.  
Query Match 7.1%; Score 279; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.3e-07;  
RESULT 1361  
ID AAP30001 standard; protein; 562 AA.  
DE Sequence of full length tissue plasminogen activator (t-Pa).  
PN EP93619-A.  
PD 09-NOV-1983.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 1; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.5e-07;  
RESULT 1362  
ID AAP94238 standard; protein; 562 AA.  
DE Human tissue plasminogen activator (t-Pa) gene.  
PN W08900197-A.  
PD 12-JAN-1989.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 1; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1363  
ID AAR23803 standard; protein; 562 AA.  
DE t-Pa (Ser 304) mutant.  
PN W09206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1364  
ID AAR23801 standard; protein; 562 AA.  
DE Zymogen-like t-Pa (His 305).  
PN W09206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1365  
ID AAW47536 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant R275E.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1366  
ID AAW47537 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant I276P.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1367  
ID AAW47535 standard; protein; 562 AA.  
DE Tissue plasminogen activator variant R275G.  
PN US5714372-A.  
PD 03-FEB-1998.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 279; DB 2; Length 562;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1368  
ID AAW48426 standard; protein; 562 AA.

DE Tissue type plasminogen activator, tPA.  
PN KRI41262-B1.  
PD 15-JUN-1998.  
PA (GLDS ) LG CHEM LTD.  
Query Match 7.1%; Score 279; DB 3; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.5e-07;  
RESULT 1369  
ID ADR43718 standard; protein; 932 AA.  
DE Human protease PRS-6, SEQ ID 6.  
PN W0200220736-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 7.1%; Score 279; DB 5; Length 932;  
Best Local Similarity 23.4%; Pred. No. 5.5e-07;  
RESULT 1370  
ID AAU82743 standard; protein; 970 AA.  
DE Amino acid sequence of novel human protease #42.  
PN W0200200860-A2.  
PD 03-JAN-2002.  
PA (SUG-) SUGEN INC.  
Query Match 7.1%; Score 279; DB 5; Length 970;  
Best Local Similarity 23.4%; Pred. No. 5.8e-07;  
RESULT 1371  
ID ABR39439 standard; protein; 264 AA.  
DE Human GENSET polypeptide clone name vCTRL-1.  
PN W02003014151-A2.  
PD 20-FEB-2003.  
PA (GEST ) GENSET SA.  
Query Match 7.1%; Score 278.5; DB 6; Length 264;  
Best Local Similarity 27.2%; Pred. No. 1.8e-07;  
RESULT 1372  
ID AAB84867 standard; protein; 406 AA.  
DE Mutant blood coagulant factor VII (FVII-5).  
PN JP2001061479-A.  
PD 13-MAR-2001.  
PA (KAGA ) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.  
Query Match 7.1%; Score 278.5; DB 4; Length 406;  
Best Local Similarity 23.0%; Pred. No. 2.7e-07;  
RESULT 1373  
ID AAM52183 standard; protein; 406 AA.  
DE Human FVII mutant V253N.  
PN W0200158935-A2.  
PD 16-AUG-2001.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 278.5; DB 4; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1374  
ID AAO30631 standard; protein; 406 AA.  
DE Human factor VII variant (K316Q/L305V/V158T/E296V/M298Q/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1375  
ID AAO30610 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1376  
ID AAO30615 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1377  
ID AAO30587 standard; protein; 406 AA.  
DE Human factor VII variant (S314E/L305V/V158T/E296V/M298Q/K337A).

PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1378  
ID AAO30571 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158T).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1379  
ID AAO30630 standard; protein; 406 AA.  
DE Human factor VII variant (K316Q/L305V/V158D/E296V/M298Q/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1380  
ID AAO30574 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A/V158D).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1381  
ID AAO30618 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/K337A/V158D).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1382  
ID AAO30586 standard; protein; 406 AA.  
DE Human factor VII variant (S314E/L305V/V158D/E296V/M298Q/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1383  
ID AAO30566 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/L305V/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1384  
ID ADJ55962 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1385  
ID ADJ55651 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158T/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1386  
ID ADJ55918 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1387  
ID ADJ56069 standard; protein; 406 AA.  
DE Human factor VII mutant F374Y/ V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1388  
ID ADJ55917 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1389  
ID ADJ55931 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1390  
ID ADJ55972 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316Q/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1391  
ID ADJ56005 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A/ S314E.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1392  
ID ADJ56039 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158DK337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1393  
ID ADJ556041 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158D/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1394  
ID ADJ55928 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1395  
ID ADJ56064 standard; protein; 406 AA.  
DE Human factor VII mutant F374Y/ V158D/ E296V/ M298Q/ L305V/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.

PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1396  
ID ADJ56074 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V253N.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1397  
ID ADJ55961 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1398  
ID ADJ56017 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ M298Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 2.7e-07;  
RESULT 1399  
ID ADJ55954 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1400  
ID ADJ55910 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1401  
ID ADJ55975 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 2.7e-07;  
RESULT 1402  
ID ADJ56050 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ V158T/ M298Q/ S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 2.7e-07;  
RESULT 1403  
ID ADJ010592 standard; protein; 406 AA.  
DE Human factor VII/Vita protein mutant #28.  
PN WO2004029091-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN APS.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1404  
ID ADJ010602 standard; protein; 406 AA.  
DE Human factor VII/Vita protein mutant #38.  
PN WO2004029091-A2.  
PD 08-APR-2004.

PA (MAXY-) MAXYGEN HOLDINGS LTD.  
Query Match 7.1%; Score 278.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 2.7e-07;  
RESULT 1405  
ID AAP60056 standard; protein; 466 AA.  
DE Factor VII peptide encoded by cDNA clone lambda VII2463.  
PN EP200421-A.  
PD 10-DEC-1986.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 7.1%; Score 278.5; DB 1; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1406  
ID AAR52562 standard; protein; 466 AA.  
DE Factor VIII.  
PN WO9323074-A1.  
PD 25-NOV-1993.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
Query Match 7.1%; Score 278.5; DB 2; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1407  
ID AAW69606 standard; protein; 466 AA.  
DE Human Factor VIIa.  
PN WO9831394-A2.  
PD 23-JUL-1998.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.1%; Score 278.5; DB 2; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1408  
ID AAB36327 standard; protein; 466 AA.  
DE Human factor VII (F7) protein reference sequence.  
PN US2003087244-A1.  
PD 08-MAY-2003.  
PA (VITI-) VITIVITY INC.  
Query Match 7.1%; Score 278.5; DB 7; Length 466;  
Best Local Similarity 22.0%; Pred. No. 3.1e-07;  
RESULT 1409  
ID AAR74682 standard; protein; 521 AA.  
DE t-PA mutein (N117Q, N184Q, delta 296-302, 44-50 replaced by ERHSTVQT).  
PN CN1082111-A.  
PD 16-FEB-1994.  
PA (BIOE-) BIOENGINEERING INST ACAD MILITARY.  
Query Match 7.1%; Score 278.5; DB 2; Length 521;  
Best Local Similarity 22.9%; Pred. No. 3.4e-07;  
RESULT 1410  
ID AAR09222 standard; protein; 526 AA.  
DE t-PA deletion variant d298.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GERTH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1411  
ID AAR09224 standard; protein; 526 AA.  
DE t-PA deletion variant d300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GERTH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1412  
ID AAR09223 standard; protein; 526 AA.  
DE t-PA deletion variant d299.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GERTH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.3%; Pred. No. 3.5e-07;  
RESULT 1413  
ID AAR09225 standard; protein; 526 AA.  
DE t-PA deletion variant d301.  
PN WO9002798-A.  
PD 22-MAR-1990.



PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.1%; Pred. No. 3.5e-07;  
RESULT 1414  
ID AAR09227 standard; protein: 526 AA.  
DE t-PA deletion variant d303.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.1%; Score 278.5; DB 2; Length 526;  
Best Local Similarity 23.0%; Pred. No. 3.5e-07;  
RESULT 1415  
ID AAR12343 standard; protein: 562 AA.  
DE t-PA with -ve charged finger and/or kringle domain (2).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1416  
ID AAR12423 standard; protein: 562 AA.  
DE T-PA variant having Lys416 substitution (1).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1417  
ID AAR12424 standard; protein: 562 AA.  
DE T-PA variant having Lys416 substitution (3).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.1%; Score 278.5; DB 2; Length 562;  
Best Local Similarity 21.9%; Pred. No. 3.7e-07;  
RESULT 1418  
ID ADU57511 standard; protein: 701 AA.  
DE Human FVII-19G1 Fc domain fusion protein.  
PN WO2004006962-A2.  
PD 22-JAN-2004.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.1%; Score 278.5; DB 8; Length 701;  
Best Local Similarity 22.0%; Pred. No. 4.5e-07;  
RESULT 1419  
ID ABB71752 standard; protein: 408 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 42048.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 7.0%; Score 278; DB 4; Length 408;  
Best Local Similarity 25.2%; Pred. No. 2.9e-07;  
RESULT 1420  
ID AAR35762 standard; protein: 448 AA.  
DE Factor X (X).  
PN WO9309804-A1.  
PD 27-MAY-1993.  
PA (SCRI ) SCRIPPS RES INST.  
Query Match 7.0%; Score 278; DB 2; Length 448;  
Best Local Similarity 24.0%; Pred. No. 3.2e-07;  
RESULT 1421  
ID AAR22511 standard; protein: 488 AA.  
DE Human Factor Xa1.  
PN WO9204378-A.  
PD 19-MAR-1992.  
PA (CORT-) COR THERAPEUTICS IN.  
Query Match 7.0%; Score 278; DB 2; Length 488;  
Best Local Similarity 24.0%; Pred. No. 3.4e-07;  
RESULT 1422  
ID ADO117444 standard; protein: 488 AA.  
DE Human bone tissue sarcoma-upregulated protein - SEQ ID 261.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.

Query Match 7.0%; Score 278; DB 8; Length 488;  
Best Local Similarity 24.0%; Pred. No. 3.4e-07;  
RESULT 1423  
ID AAR09232 standard; protein: 523 AA.  
DE t-PA deletion variant d297-300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 523;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1424  
ID AAR09244 standard; protein: 525 AA.  
DE t-PA deletion variant d297, d300.  
PN WO9002798-A.  
PD 22-MAR-1990.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 525;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1425  
ID AAR05806 standard; protein: 527 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen  
DE activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1426  
ID AAR22621 standard; protein: 527 AA.  
DE Mutated recombinant tPA.  
PN JP04094684-A.  
PD 26-MAR-1992.  
PA (KANF ) KANEKA CORP.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.1%; Pred. No. 3.7e-07;  
RESULT 1427  
ID AAR70896 standard; protein: 527 AA.  
DE Human t-PA variant (N103,A339,A342).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1428  
ID AAR70858 standard; protein: 527 AA.  
DE Human t-PA variant (N67,A296,A297,A298,A299).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.3%; Pred. No. 3.7e-07;  
RESULT 1429  
ID AAR70897 standard; protein: 527 AA.  
DE Human t-PA variant (N103,A347,A348,A349,A351).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1430  
ID AAR70856 standard; protein: 527 AA.  
DE Human t-PA variant (N67,A267).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.5%; Pred. No. 3.7e-07;  
RESULT 1431  
ID AAR70873 standard; protein: 527 AA.  
DE Human t-PA variant (N67,A177).  
PN US5385732-A.  
PD 31-JAN-1995.  
PA (GETH ) GENENTECH INC.

Query Match 7.0%; Score 278; DB 2; Length 527;  
Best Local Similarity 23.2%; Pred. No. 3.7e-07;  
RESULT 1432  
ID AAF71450 standard; protein; 528 AA.  
DE Modified human tissue plasminogen activator.  
PN EP238304-A.  
PD 23-SEP-1987.  
PA (GETH ) GENENTECH INC.  
Query Match 7.0%; Score 278; DB 1; Length 528;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1433  
ID AAR07033 standard; protein; 528 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 528;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1434  
ID AAF70881 standard; protein; 530 AA.  
DE Thrombolytic protein 1-12-18 having t-PA activity, deleted or replaced DE R275 is and containing a modified N-linked glycosylation site.  
PN W08704722-A.  
PD 13-AUG-1987.  
PA (GENY ) GENETICS INST INC.  
PA (LARS ) LARSEN G R.  
Query Match 7.0%; Score 278; DB 1; Length 530;  
Best Local Similarity 23.0%; Pred. No. 3.7e-07;  
RESULT 1435  
ID AAR07034 standard; protein; 531 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 531;  
Best Local Similarity 22.9%; Pred. No. 3.7e-07;  
RESULT 1436  
ID AAR13153 standard; protein; 558 AA.  
DE T-PA with -ve charged finger and/or kringle domain (8).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 558;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1437  
ID AAR13151 standard; protein; 559 AA.  
DE T-PA with -ve charged finger and/or kringle domain (4).  
PN JP03061483-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1438  
ID AAR13155 standard; protein; 559 AA.  
DE T-PA variant having Lys416 substitution (4).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1439  
ID AAR13154 standard; protein; 559 AA.  
DE T-PA variant having Lys416 substitution (2).  
PN JP03061484-A.  
PD 18-MAR-1991.  
PA (FUJI ) FUJISAWA PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 559;  
Best Local Similarity 23.0%; Pred. No. 3.9e-07;  
RESULT 1440  
ID AAF81359 standard; protein; 562 AA.  
DE Pre-pro tissue plasminogen activator.  
PN EP293934-A.  
PD 07-DEC-1988.  
PA (ZYMO ) ZYMOGENETICS INC.  
PA (NOVO ) NOVO IND AS.  
PA (EISA ) EISA CO LTD.  
Query Match 7.0%; Score 278; DB 1; Length 562;  
Best Local Similarity 23.2%; Pred. No. 3.9e-07;  
RESULT 1441  
ID AAR07079 standard; protein; 562 AA.  
DE Thrombolytic protein with secondary structure of human tissue plasminogen activator.  
PN JP02145184-A.  
PD 04-JUN-1990.  
PA (YAMA ) YAMANOUCHI PHARM CO LTD.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 22.9%; Pred. No. 3.9e-07;  
RESULT 1442  
ID AAR04702 standard; protein; 562 AA.  
DE Sequence of tissue plasminogen activator (t-PA) analogue t-PA C87S; K419S DE with altered residues 87 and 419.  
PN EP351246-A.  
PD 17-JAN-1990.  
PA (NOVO ) NOVO-NORDISK AS.  
PA (NOVO ) NOVO-NORDISK AS.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 22.7%; Pred. No. 3.9e-07;  
RESULT 1443  
ID AAR23809 standard; protein; 562 AA.  
DE t-PA (Glu 299) mutant.  
PN W09206203-A.  
PD 16-APR-1992.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 7.0%; Score 278; DB 2; Length 562;  
Best Local Similarity 23.5%; Pred. No. 3.9e-07;  
RESULT 1444  
ID ADI27177 standard; protein; 1113 AA.  
DE Mouse LRP binding family protein #17.  
PN W0200310657-A2.  
PD 24-DEC-2003.  
PA (STOW ) STOWERS INST MEDICAL RES.  
Query Match 7.0%; Score 278; DB 8; Length 1113;  
Best Local Similarity 20.7%; Pred. No. 7.4e-07;  
RESULT 1445  
ID ADR29372 standard; protein; 1113 AA.  
DE Murine Lrp4 dopaminergic neuronal marker SEQ ID NO:3.  
PN W0200406559-A1.  
PD 05-AUG-2004.  
PA (EISA ) EISA CO LTD.  
Query Match 7.0%; Score 278; DB 8; Length 1113;  
Best Local Similarity 20.7%; Pred. No. 7.4e-07;  
RESULT 1446  
ID AAO30596 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316H/L305V/K337A/V158D).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1447  
ID AAO30549 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (S314E/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1448  
ID AAO30561 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1449  
ID AAO30561 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/K337A).  
PN W02003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;

Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
 RESULT 1449  
 ID AAO30570 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V/V158T).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1450  
 ID AAO30588 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316H/L305V/K337A).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1451  
 ID AAO30623 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316Q/L305V/E296V/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1452  
 ID AAO30611 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316Q/L305V/V158D).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1453  
 ID AAO30567 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V/V158D).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1454  
 ID AAO30529 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/K316Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
 RESULT 1455  
 ID AAO30548 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1456  
 ID AAO30564 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316Q/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
 RESULT 1457  
 ID AAO30609 standard; protein; 406 AA.  
 DE Human factor VII variant (K316H/L305V/V158T/E296V/M298Q/K337A).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1467

RESULT 1458  
 ID AAO30579 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V/E296V/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1459  
 ID AAO30581 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1460  
 ID AAO30593 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316H/L305V/K337A/V158T).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1461  
 ID AAO30624 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316Q/L305V/V158D/E296V/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1462  
 ID AAO30632 standard; protein; 406 AA.  
 DE Human factor VII variant (L305V/K337A).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1463  
 ID AAO30552 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
 RESULT 1464  
 ID AAO30580 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (S314E/L305V/V158T/E296V/M298Q).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1465  
 ID AAO30614 standard; protein; 406 AA.  
 DE Human coagulation factor VII variant (K316Q/L305V/V158T).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1466  
 ID AAO30608 standard; protein; 406 AA.  
 DE Human factor VII variant (K316H/L305V/V158D/E296V/M298Q/K337A).  
 PN W02003037932-A2.  
 PD 08-MAY-2003.  
 PA (NOVO ) NOVO NORDISK AS.  
 Query Match 7.0%; Score 277.5; DB 6; Length 406;  
 Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
 RESULT 1467

ID AA030625 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V/V158T/E296V/M298Q).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1468  
ID AA030560 standard; protein; 406 AA.  
DE Human coagulation factor VII variant (K316Q/L305V).  
PN WO2003037932-A2.  
PD 08-MAY-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 6; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1469  
ID ADJ55906 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1470  
ID ADJ56001 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ M298Q/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1471  
ID ADJ56022 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158D.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1472  
ID ADJ56024 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ M298Q/ V158T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1473  
ID ADJ55878 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1474  
ID ADJ55983 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1475  
ID ADJ56019 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158T.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1476  
ID ADJ56037 standard; protein; 406 AA.

DE Human factor VII polypeptide mutant F374Y/ S314E/ E296V/ M298Q/ L305V.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1477  
ID ADJ55909 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant K316Q/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1478  
ID ADJ55953 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158T/ E296V/ M298Q/ L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1479  
ID ADJ55955 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1480  
ID ADJ55893 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant S314E/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1481  
ID ADJ55932 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K316H/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1482  
ID ADJ55897 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant M298Q/ S314E.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1483  
ID ADJ55956 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316Q.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1484  
ID ADJ56036 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ E296V/ M298Q/ L305V/ K337A.  
PN WO2004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO ) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1485  
ID ADJ55875 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K337A.

PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1486  
ID ADJ55912 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ S314E.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1487  
ID ADJ55940 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ L305V/ K316H/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1488  
ID ADJ56029 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298QV158T.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1489  
ID ADJ55609 standard; protein; 406 AA.  
DE Human factor VII protein mutant F374Y/ V158D/ E296V/ M298Q/ S314E/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.1%; Pred. No. 3.1e-07;  
RESULT 1490  
ID ADJ55891 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant S314E/ K316Q.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;  
RESULT 1491  
ID ADJ55923 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant E296V/ M298Q/ L305V/ S314E.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1492  
ID ADJ55925 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ S314E.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1493  
ID ADJ55939 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ L305V/ K316H/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1494  
ID ADJ55968 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158D/ E296V/ M298Q/ L305V/ K316Q.  
PN W02004000366-A1.

PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1495  
ID ADJ55969 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant V158T/ E296V/ M298Q/ L305V/ K316Q.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1496  
ID ADJ56010 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ L305V/ V158D/ S314E.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1497  
ID ADJ56026 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ S314E/ M298Q/ V158D.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.3%; Pred. No. 3.1e-07;  
RESULT 1498  
ID ADJ55861 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant L305V/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1499  
ID ADJ55950 standard; protein; 406 AA.  
DE Human factor VII protein mutant V158D/ E296V/ M298Q/ L305V/ K316H/ K337A.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.5%; Pred. No. 3.1e-07;  
RESULT 1500  
ID ADJ56020 standard; protein; 406 AA.  
DE Human factor VII polypeptide mutant F374Y/ K337A/ S314E/ V158D.  
PN W02004000366-A1.  
PD 31-DEC-2003.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 7.0%; Score 277.5; DB 8; Length 406;  
Best Local Similarity 22.6%; Pred. No. 3.1e-07;

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:08:11 ; Search time 43 Seconds  
(without alignments)  
1611.071 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945  
Sequence: 1 MEIGCWTLQGLTFLLQULLIS.....LSTAFKVLPRFDMIERNNK 720

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR 79:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949	24.1	181	2 T08805	hypothetical prote
2	672	17.0	1039	2 A38738	coagulation factor
3	482	12.2	699	1 I54763	Ra-reactive factor
4	403.5	10.2	705	1 C1HURB	complement subcomp
5	400.5	10.2	686	1 A59271	Ra-reactive factor
6	378.5	9.6	695	1 S05008	complement subcomp
7	354	9.0	1524	2 T30337	polyprotein - Afri
8	340.5	8.6	694	2 JC6554	complement subcomp
9	334	8.5	688	1 C1HUS	complement subcomp
10	331.5	8.4	1019	1 A56318	enteropeptidase (E
11	330.5	8.4	1034	1 A53663	enteropeptidase (E
12	320	8.1	461	1 JX0210	protein C (activat
13	317.5	8.0	1035	1 A43090	enteropeptidase (E
14	314.5	8.0	475	1 EXCH	coagulation factor
15	313	7.9	855	2 JC7731	membrane-bound arg
16	310.5	7.9	461	1 KKHU	protein C (activat
17	299.5	7.6	443	2 A46332	coagulation factor
18	293.5	7.4	407	1 KFB07	coagulation factor
19	292	7.4	461	1 A18994	protein C (activat
20	285.5	7.2	452	1 A30351	coagulation factor
21	283.5	7.2	482	1 EXRT	coagulation factor
22	282	7.1	456	1 KXBO	protein C (activat
23	281.5	7.1	558	2 JC5878	plasma hyaluronan-
24	281	7.1	492	1 EXBO	coagulation factor
25	280.5	7.1	264	2 I38136	chymotrypsin-like
26	280	7.1	362	1 UKHUT	t-plasminogen acti
27	278.5	7.1	466	1 KFHU7	coagulation factor
28	278	7.0	488	1 EXHU	coagulation factor
29	278	7.0	1113	2 JEO315	low-density lipopr

30	277	7.0	559	1 A29941	t-plasminogen acti
31	277	7.0	559	1 A35029	t-plasminogen acti
32	276.5	7.0	555	1 A46888	hepatocyte growth
33	274.5	7.0	625	1 TBBO	thrombin (EC 3.4.2
34	273	6.9	560	1 JC4795	plasma hyaluronan-
35	270	6.8	477	2 JS0597	t-plasminogen acti
36	264.5	6.7	431	2 JS0599	t-plasminogen acti
37	264.5	6.7	431	2 A35827	thrombin (EC 3.4.2
38	262.5	6.7	461	1 KFHU	coagulation factor
39	262	6.6	477	2 JS0598	t-plasminogen acti
40	261.5	6.6	442	1 UKPG	u-plasminogen acti
41	261	6.6	431	1 UKHU	u-plasminogen acti
42	261	6.6	433	1 UN0560	u-plasminogen acti
43	260	6.6	477	1 A34369	t-plasminogen acti
44	259	6.6	244	2 JS2219	chymotrypsin B - A
45	259	6.6	416	1 KFB0	coagulation factor
46	258.5	6.6	786	1 A47547	serine proteinase
47	258	6.5	251	2 PC1235	29K serine protein
48	258	6.5	433	1 UKBAY	u-plasminogen acti
49	257.5	6.5	1004	2 T30338	oviductin (EC 3.4.
50	255.5	6.5	763	2 I50807	complement factor
51	254	6.4	617	2 S10511	thrombin (EC 3.4.2
52	253	6.4	1070	2 T31069	colloid-BMP-1 like
53	249.5	6.3	400	1 A48050	coagulation factor
54	249.5	6.3	986	1 B58788	procollagen C-endo
55	248.5	6.3	459	2 JU0419	coagulation factor
56	248	6.3	263	2 A31299	chymotrypsin (EC 3
57	248	6.3	638	1 KOHUP	plasma kallikrein
58	247.5	6.3	991	2 I49540	procollagen C-endo
59	247	6.3	275	2 A32410	trypsin (EC 3.4.2
60	247	6.3	764	1 BBHU	complement factor
61	246.5	6.2	347	2 G00006	haptoglobin - blac
62	246.5	6.2	622	1 TBHU	thrombin (EC 3.4.2
63	246	6.2	236	2 C42696	thrombin (EC 3.4.2
64	246	6.2	812	1 PLBO	plasma (EC 3.4.21
65	245	6.2	234	2 F42696	thrombin (EC 3.4.2
66	244	6.2	638	1 KOMSPL	plasma kallikrein
67	242.5	6.1	730	1 BMHUI	procollagen C-endo
68	241.5	6.1	823	1 A58788	procollagen C-endo
69	240	6.1	242	2 A54989	trypsin (EC 3.4.21
70	239.5	6.1	406	1 HPHU2	haptoglobin precur
71	239	6.1	245	1 KYBOA	chymotrypsin (EC 3
72	238	6.0	237	1 TRCY1	trypsin (EC 3.4.21
73	238	6.0	263	2 A21195	chymotrypsin (EC 3
74	238	6.0	347	1 HPHUI	haptoglobin precur
75	238	6.0	375	1 A23689	limulus clotting e
76	237.5	6.0	810	2 I46260	plasma (EC 3.4.21
77	237	6.0	263	1 KYRTB	chymotrypsin (EC 3
78	236.5	6.0	274	2 JC2118	trypsin (EC 3.4.2
79	236.5	6.0	707	2 JC2218	procollagen C-endo
80	235	6.0	270	2 S56160	mast cell trypsin
81	235	6.0	345	2 I36941	haptoglobin - chim
82	235	6.0	1420	2 A32869	apolipoprotein(a)
83	233.5	5.9	263	2 S47537	chymotrypsin (EC 3
84	232	5.9	416	1 S33777	hepsin (EC 3.4.21
85	232	5.9	638	1 KORRPL	plasma kallikrein
86	229.5	5.8	329	1 HPDG	haptoglobin precur
87	228.5	5.8	225	2 E42696	thrombin (EC 3.4.2
88	228.5	5.8	347	1 HPMS	haptoglobin precur
89	228.5	5.8	861	2 A46825	Notch homolog Motc
90	228.5	5.8	2531	2 A46019	notch-1 protein -
91	228	5.8	812	1 PLMS	plasma (EC 3.4.21
92	227.5	5.8	242	2 S11775	trypsin (EC 3.4.21
93	227.5	5.8	349	2 I36944	haptoglobin - chim
94	227	5.8	242	2 S31776	trypsin (EC 3.4.21
95	227	5.8	1464	2 S58984	development protei
96	226.5	5.7	238	2 S31779	trypsin (EC 3.4.21
97	226.5	5.7	761	2 JC5759	brain-specific ser
98	226	5.7	394	2 JS0600	t-plasminogen acti
99	226	5.7	625	1 KFHUI	coagulation factor
100	225	5.7	615	1 KFHUI2	coagulation factor
101	224.5	5.7	271	1 ELRT2-	pancreatic elasta
102	224	5.7	245	1 KYBOB	chymotrypsin (EC 3

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptogloblin-relate	177	198.5	5.0	229	1	TRBOTR	trypsin (EC 3.4.21
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21.	178	198.5	5.0	222	1	KQPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S55378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21	180	198	5.0	259	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastas	181	198	5.0	270	2	B29934	pancreatic elastas
109	222	5.6	275	2	B35863	tryptase (EC 3.4.2	182	198	5.0	760	2	C2MS	classical-compleme
110	221.5	5.6	2531	2	S18168	notch protein homo	183	197.5	5.0	250	1	T01179	trypsin (EC 3.4.21
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21	184	197.5	5.0	258	2	I36947	haptogloblin Hpp -
112	220.5	5.6	274	2	A45754	tryptase (EC 3.4.2	185	196.5	5.0	269	2	C26823	pancreatic elastas
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropelein C prec
114	220	5.6	235	2	A35863	thrombin (EC 3.4.2	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	pancreatic elastas	188	196.5	5.0	2524	2	A35844	Notch protein - Af
116	219.5	5.6	271	2	A25528	complement factor	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBMS	prostaasin (EC 3.4.	190	195.5	4.9	432	1	S18932	factor IX - pig (f
118	219	5.6	343	1	A57014	serine proteinase (	191	195	4.9	246	1	TRRT1	u-plasminogen acti
119	218	5.5	271	2	S41308	venom proteinase (	192	194.5	4.9	246	2	A25606	trypsin (EC 3.4.21
120	217.5	5.5	243	2	A56338	tissue kallikrein	193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	pancreatic elastas	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21
122	217	5.5	268	2	S68825	tryptase (EC 3.4.2	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	coagulation factor	196	193.5	4.9	347	1	HPRT	haptogloblin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24430	notch protein - fr	198	193	4.9	240	1	CPBOA3	procaboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2	199	193	4.9	246	1	DBHU	complement factor
127	216.5	5.5	346	2	I36942	haptogloblin - chlm	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21
128	216.5	5.5	2616	2	A57096	mdel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	PLHU	plasmin (EC 3.4.21	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	TRDG	trypsin (EC 3.4.21	203	190.5	4.8	579	2	JC7629	membrane-type fritz
131	215.5	5.5	248	1	S55066	trypsin (EC 3.4.21	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.5	241	2	S39048	trypsin (EC 3.4.21	205	190.5	4.8	1064	2	A40136	fibropelein Ia - 8
133	215	5.4	268	2	S68826	pancreatic elastas	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21	207	189.5	4.8	1737	2	T00209	MG68 protein - hu
135	214.5	5.4	366	2	JE0105	teuticulin serine	208	189	4.8	246	2	UQ1472	trypsin (EC 3.4.21
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21
137	214	5.4	275	2	C35863	tryptase (EC 3.4.2	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	235	2	D12686	thrombin (EC 3.4.2	211	189	4.8	258	4	S70439	pancreatic elastas
139	213.5	5.4	2352	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	260	2	I65559	neutropsin - mouse	213	189	4.8	646	2	UN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	tryptase (EC 3.4.2	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	mat cell proteina	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A66136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21
145	210	5.3	2437	2	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	UQ1471	trypsin (EC 3.4.21
147	208.5	5.3	258	2	I36945	thrombin (EC 3.4.2	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	haptogloblin Hp - c	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastas	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.3	238	1	TRW5Y	trypsin-like prote	223	185.5	4.7	927	1	J00948	AS antigen precurs
151	206.5	5.2	246	1	TRRT2	trypsin (EC 3.4.21	224	185.5	4.7	256	1	NGMSA	7S nerve growth fa
152	206.5	5.2	256	2	T10109	trypsin (EC 3.4.21	225	185	4.7	1372	2	T25933	hypothetical prote
153	206	5.2	430	1	A24702	serine proteinase	226	183.5	4.6	392	1	J05092	tissue kallikrein
154	206	5.2	4548	1	S00657	apoptoteina(a) (EC	227	183	4.6	265	1	KORP	serine proteinase
155	205.5	5.2	269	2	B32410	matocytoma protei	228	183	4.6	482	2	J05092	E-selectin - pig
156	205.5	5.2	460	2	B61545	plasmin (EC 3.4.21	229	182.5	4.6	722	2	I48324	notch homolog - be
157	204.5	5.2	367	2	JE0104	testicular serine	230	182.5	4.6	2531	2	T31070	tissue kallikrein
158	204.5	5.2	752	1	C2HU	complement C2 prec	231	182.5	4.6	261	1	PRMSM5	granzyme B (EC 3.4
159	204.5	5.2	1203	1	A49175	Morch B protein -	232	182	4.6	247	2	PRMSCL	trypsin (EC 3.4.21
160	203.5	5.2	247	1	B25852	trypsin (EC 3.4.21	233	181.5	4.6	247	2	S12764	serine proteinase
161	203.5	5.2	263	1	I55608	complement factor	234	181.5	4.6	259	2	A45161	acrosin (EC 3.4.21
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	437	2	S18407	7S nerve growth fa
163	203.5	5.2	309	2	B49878	intrinsic factor-B	236	181	4.6	261	1	NGMSG	acrosin (EC 3.4.21
164	203.5	5.2	3623	2	T09456	probable trypsin V	237	181	4.6	418	2	A37344	hypothetical prote
165	203	5.1	403	2	C82228	trypsin (EC 3.4.21	238	181	4.6	1291	2	T21694	trypsin (EC 3.4.21
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21	239	181	4.6	248	2	S55067	factor IX - rabbit
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	275	2	I46712	acrosin (EC 3.4.21
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21	241	180.5	4.6	436	2	UX0172	trypsin-like prote
169	200.5	5.1	226	1	KCPU	brechhyurin (EC 3.4	242	180.5	4.6	254	2	S49329	tissue kallikrein
170	200.5	5.1	231	1	TRPGTR	trypsin (EC 3.4.21	243	180	4.6	261	2	S01971	trypsin (EC 3.4.21
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21	244	180	4.6	275	2	S40005	trypsin (EC 3.4.21
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21	245	180	4.6	243	1	A35871	trypsin (EC 3.4.21
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	259	2	WMMS28	complement factor
174	199.5	5.1	258	2	G02959	haptogloblin - thes	247	179.5	4.6	274	2	I47078	coagulation factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21	248	179.5	4.6				



249	179.5	4.6	728	2	150719	C-Delta-1 - chick	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	maequeride precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	BLPG	pancreatic elastase	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repetit
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	1	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFH013	coagulation factor
257	177	4.5	268	2	JQ1473	pancreatic elastase	330	160	4.1	262	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin I precur
259	177	4.5	747	2	IS1579	complement factor	332	159.5	4.0	1722	2	E89752	protein P11C7.4 (l
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A44284	tissue kallikrein
261	176	4.5	261	2	A29745	tissue kallikrein	334	159	4.0	261	2	A48062	gamma-tenin (EC 3.
262	176	4.5	261	2	A31136	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precur
263	176	4.5	264	2	S32794	trypsin-like prote	336	158.5	4.0	247	2	S59135	mast cell proteina
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	385	2	S53718	homeotic protein d
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protei
266	175	4.4	270	2	A29934	pancreatic elastase	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precur
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	apern-egg recognit
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	gip1 protein precu	345	156.5	4.0	282	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin V	346	156.5	4.0	275	2	UC6506	tumor necrosis fac
274	173	4.4	229	1	TRDPS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homeotic protein 1
275	173	4.4	768	2	IS3821	P-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRM5C2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTN	tonin (EC 3.4.21.-
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T11632	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibrinolytic prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	UC7985	brain-specific CUB
282	172	4.4	435	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	Cab-binding protei
285	171.5	4.3	2403	2	A59386	saako - human	358	154	3.9	669	2	S65551	Factor H - bovine
286	171	4.3	257	2	A45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	B45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	endothelial leukoc
288	171	4.3	266	1	ELRRT1	pancreatic elastase	361	153.5	3.9	551	2	I46709	laminin beta-1 cha
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMMSB1	complement factor
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	trypsin-like prote
291	170	4.3	268	2	S33756	granzyme-like prote	364	153	3.9	254	1	TRWV3Y	fibrillin I - bovi
292	170	4.3	246	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	Delta-4 protein -
293	169.5	4.3	251	2	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65603	granzyme 3 (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	560	2	T116833	hypothetical prote	369	152.5	3.9	422	1	KXHU2	plasma protein Z p
297	169	4.3	214	2	S17680	fibrinolytic prote	370	152	3.9	281	3	A61021	tissue kallikrein
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	hypothetical prote
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	261	2	A34079	granzyme-like prote
300	169	4.3	504	2	S56745	muclin (clone pM31	373	151.5	3.8	716	1	A40332	cisue kallikrein
301	168.5	4.3	597	2	S33755	granzyme-like prote	374	151.5	3.8	977	2	I52657	macrophage-stimula
302	168	4.3	248	2	S71352	metalloproteinase	375	151	3.8	249	1	A35842	seizure-related pr
303	168	4.3	2014	2	I36936	complement recepto	376	151	3.8	1620	2	T27283	chymase (EC 3.4.21
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	248	2	S41359	tissue kallikrein
305	167.5	4.2	383	2	SS3716	delta-like homeoti	378	150.5	3.8	277	2	A41735	hypothetical prote
306	167	4.2	247	2	S45113	granzyme-like prote	379	150.5	3.8	285	2	T35195	granzyme-like prote
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	hyaluronate-bindin
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	UC7570	problee serine pr
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	Delta-4 protein -
310	164.5	4.2	449	1	NBHUNS	complement factor	383	150	3.8	263	1	MMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUNS	complement factor	384	150	3.8	267	1	ELHUL	leukocyte elastase
312	164	4.2	230	2	I48685	mast cell proteina	385	150	3.8	601	2	B36346	fibrulin 1 precurs
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precur	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog PS4	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnetin precursor	390	149.5	3.8	13288	2	T03099	muclin, submaxillar
318	162.5	4.1	2083	2	T42721	CNP-ductin-alpha p	391	149	3.8	216	1	KIVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibrulin 1 precurs
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KTVH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	proteinase 7 - buf
397	148	3.8	1469	2	B36655	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36655	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A34910	mast cell proteina	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	CdBP alpha chain p	474	132	3.3	246	2	A36578	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	UCS377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	CdBP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	150421	aggreccan precursor
405	147	3.7	259	2	D33863	tiasee kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	UC4803	venomobin A (EC 3.4	479	131.5	3.3	302	1	MMBS1E	secretory compleme
407	147	3.7	716	1	UCS061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	129.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	venomobin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B26359	decay-accelerating
414	145	3.7	263	1	C36838	trypsin-like prote	487	129.5	3.3	440	2	A26359	decay-accelerating
415	145	3.7	732	1	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	venomobin AB (EC 3.
416	145	3.7	382	2	A51625	tenascin-like prot	489	128.5	3.3	255	2	A27122	cathepsin G (EC 3.
417	144.5	3.7	245	2	B38678	mast cell proteina	490	128.5	3.3	321	2	T33161	hypothetical prote
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRPGXZ	azurocidin - pig
419	144.5	3.7	360	2	T42921	complement control	492	128	3.2	5147	1	LUFTFM	cadherin-related c
420	144	3.7	683	2	B72152	B1BL protein - var	493	127.5	3.2	1531	2	T42218	slit-1 protein hom
421	144	3.7	263	2	B78040	fibulin, eplice fo	494	127	3.2	258	2	156220	trypsinase 2 - rat
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin gamma-1 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUBH	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	2	S53868	laminin alpha-2 ch
425	142	3.6	272	2	UC4170	trypsin-like prote	498	126.5	3.2	1025	1	T42626	secreted leucine-r
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	A38894	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	285	2	JS0260	serine proteinase
428	141	3.6	225	2	S45356	probable serine pr	501	126	3.2	330	2	156100	complement factor
429	141	3.6	246	2	A32692	cytotoxic T-lympho	502	125	3.2	642	2	S53433	plasma protein S p
430	140.5	3.6	246	1	A46504	chymase (EC 3.4.21	503	125	3.2	254	2	S35585	chymotrypsin-like
431	140.5	3.6	1234	1	NMWSH	complement factor	504	125.5	3.2	265	2	I48679	neutrophil elastas
432	140.5	3.6	2406	2	A54148	odt protein - fruit	505	125.5	3.2	597	1	NBHUC4	Cd-binding proteol
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140	3.5	396	1	KXBOZ	plasma protein 2 -	507	125	3.2	323	1	SO9702	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	1	NMFPB1	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	548	2	T16642	cytotoxic T-lympho
437	139.5	3.5	319	2	151569	UVS.2 protein - Af	510	124.5	3.2	330	2	T46256	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	710	1	151283	brevican - human (
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	883	2	S49126	heparocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	1221	2	A49457	fibulin-2 precursor
441	138.5	3.5	705	2	S34968	fibulin, eplice fo	514	124	3.1	1523	2	T13953	MEGFS protein - ra
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1584	2	T22674	hypothetical prote
443	137.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	808	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	258	2	S57960	CdBP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	372	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S49129	chymotrypsin (EC 3
447	137	3.5	2823	2	P87908	protein T22A3.8 [i	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	T23064	hypothetical prote	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precursor
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	1	T42017	cysteine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	360	1	NMBE2E	membrane-bound com	525	123	3.1	340	2	156234	decay-accelerating
453	136	3.4	676	2	A45900	complement c3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JEO151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	146002	CdBP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NMMSCA	Cd-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	1	NBHU	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBHU	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	146001	Cd-binding protei
464	134.5	3.4	601	2	T23025	hypothetical prote	537	121.5	3.1	5376	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	D89711	protein F40E10.4 [	538	121	3.1	647	2	A43902	tenascin - easerat
466	134	3.4	232	1	A54361	venomobin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	versican precursor

541	120.5	3.1	247	2	S64708	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	616	112	2.8	918	2	UC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	615	112	2.8	1155	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	1353	112	2.8	1353	1	JH0675	restictin precurs
545	120.5	3.1	646	2	S38819	618	112	2.8	1639	1	MMFPR2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42950	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60165	621	112	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	MMRTS	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	624	111.5	2.8	1338	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	625	111.5	2.8	1797	2	A55677	laminin beta-2 cha
553	120	3.0	493	2	UC5621	626	111.5	2.8	2019	1	UQ1322	tenascin precursor
554	120	3.0	589	2	T43210	627	111.5	2.8	2531	2	T16743	hypothetical prote
555	120	3.0	912	2	A54423	628	111.5	2.8	4351	2	T00252	MEGF1 protein - ra
556	120	3.0	1548	2	S34583	629	111	2.8	231	2	A60468	venombin A (EC 3.4
557	120	3.0	1643	2	T14274	630	111	2.8	915	2	T21773	hypothetical prote
558	120	3.0	2397	1	A55535	631	110.5	2.8	234	1	S20407	venombin A (EC 3.4
559	120	3.0	3381	2	T42389	632	110.5	2.8	297	1	NBRT	apolipoprotein H p
560	119.5	3.0	161	2	T48158	633	110.5	2.8	408	2	T22801	hypothetical prote
561	119.5	3.0	482	2	A43924	634	110.5	2.8	583	2	A29154	complement factor
562	119.5	3.0	675	1	KXBOS	635	110.5	2.8	678	2	B48089	growth arrest-spec
563	119.5	3.0	835	1	JP0076	636	110.5	2.8	692	2	T32980	hypothetical prote
564	119.5	3.0	1247	1	MMHUND	637	110.5	2.8	961	1	TSMDP4	thrombospondin 4 p
565	119.5	3.0	1506	2	T30886	638	110.5	2.8	1217	1	EGMSNG	dermal growth f
566	119.5	3.0	258	2	A57290	639	110.5	2.8	1894	2	JC4980	plexin 1 precursor
567	119	3.0	513	2	D88991	640	110	2.8	266	2	T19292	hypothetical prote
568	118.5	3.0	674	2	I55476	641	110	2.8	1134	1	I58388	protein-tyrosine k
569	118.5	3.0	728	1	A35644	642	110	2.8	1905	2	I51553	plexin - African c
570	118.5	3.0	728	1	UH0579	643	109.5	2.8	198	2	S06176	cytotoxic T-lympho
571	118	3.0	133	2	S21114	644	109.5	2.8	2215	2	T00348	IKK1 protein - mou
572	118	3.0	196	2	T08808	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	646	1808	2.8	1808	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	647	109	2.8	2610	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	649	108.5	2.8	2825	1	T14271	Doc4 protein, bre
577	117.5	3.0	259	2	T21011	650	108	2.7	251	1	TRHDA2	azurocidin precurs
578	117.5	3.0	642	2	S53434	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	JE0237	652	108	2.7	1700	2	S08167	Balblani ring 3 pr
580	117.5	3.0	1160	2	P88369	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRH01	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	658	107	2.7	280	2	G02741	skeletal muscle Li
586	116.5	3.0	384	2	S01896	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	661	106.5	2.7	362	2	UC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	UC0164	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	I37278	667	106	2.7	927	2	T21772	hypothetical prote
595	114.5	2.9	349	2	G02913	668	106	2.7	1133	1	EGRT	epidermal growth f
596	114.5	2.9	369	2	I57988	669	106	2.7	1142	2	T30272	hypothetical prote
597	114.5	2.9	369	2	S53869	670	106	2.7	1522	2	H88380	protein T22F7.3 [i
598	114	2.9	255	1	A28169	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	672	106	2.7	2195	2	T34264	hypothetical prote
600	114	2.9	846	2	A30889	673	105.5	2.7	346	2	T46914	variant-specific s
601	114	2.9	1069	2	T42681	674	105.5	2.7	596	2	A45664	growth arrest-spec
602	113.5	2.9	502	2	T22919	675	105.5	2.7	673	2	A48089	IDL receptor precu
603	113.5	2.9	502	2	T20130	676	105	2.7	860	2	ORHND	hypothetical prote
604	113.5	2.9	558	2	T17324	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	ORRTD	679	105	2.7	2201	1	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	680	104.5	2.6	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	681	104.5	2.6	1360	2	T33922	hypothetical prote
609	112.5	2.9	264	2	A28942	682	104	2.6	345	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	UC7591	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	C42125	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	685	104	2.6	473	2	T32326	hypothetical prote
613	112.5	2.9	1797	2	T21889	686	104	2.6	2101	2	S57245	insulin receptor (

687	104	2.6	4135	2	T42629	tenascin-X - bovin
688	103.5	2.6	383	2	T21946	hypothetical prote
689	103	2.6	311	2	A45222	complement factor
690	103	2.6	412	2	S72579	hypothetical prote
691	103	2.6	1296	2	T16859	hypothetical prote
692	103	2.6	2148	1	A56081	insulin receptor -
693	102.5	2.6	153	2	S35204	proteinase 4 - buf
694	102.5	2.6	473	2	I49283	ADAM 4 protein pre
695	102.5	2.6	565	2	T16408	hypothetical prote
696	102.5	2.6	873	1	QRRVD	VDL receptor prec
697	102	2.6	149	2	S35208	serine proteinase
698	102	2.6	280	2	G01884	LIM protein FHL-1,
699	102	2.6	380	2	G01639	transmembrane proc
700	102	2.6	411	2	D88087	protein B0454.7 [i
701	102	2.6	718	2	T29448	hypothetical prote
702	102	2.6	863	1	S51789	VDL receptor prec
703	102	2.6	1168	2	I56985	kelinin B1 - mouse
704	102	2.6	1713	2	A55347	adhesive ligand ep
705	102	2.6	4006	2	T09070	probable tenascin
706	101.5	2.6	379	2	T16213	APX-1 protein homo
707	101.5	2.6	1106	2	T18739	hypothetical prote
708	101.5	2.6	1959	1	AGRT	agrin - rat
709	101.5	2.6	2415	1	A39086	aggreacan precursor
710	101	2.6	377	2	C68710	protein C43G2.5 [i
711	101	2.6	463	2	T26655	hypothetical prote
712	101	2.6	557	2	A48434	variant-specific s
713	101	2.6	1371	2	A33837	insulin-like growt
714	101	2.6	1378	1	I48751	protein-tyrosine k
715	101	2.6	1875	2	A36429	integrin beta-4 ch
716	100.5	2.5	417	2	T20199	hypothetical prote
717	100.5	2.5	670	2	S77463	transketolase [EC
718	100.5	2.5	802	2	T24293	hypothetical prote
719	100.5	2.5	949	2	T24294	hypothetical prote
720	100.5	2.5	956	1	A46016	thrombospondin 3 -
721	100.5	2.5	1252	2	S36016	occynt wall protei
722	100.5	2.5	1356	2	A45445	janusin precursor,
723	100	2.5	152	2	S35203	serine proteinase
724	100	2.5	421	2	T25383	hypothetical prote
725	100	2.5	667	2	A48579	trophozoite surfac
726	100	2.5	873	1	A49729	VDL receptor prec
727	100	2.5	1122	2	I54237	protein-tyrosine k
728	100	2.5	1123	1	UN0712	protein-tyrosine k
729	100	2.5	1125	1	UH0771	protein-tyrosine k
730	100	2.5	1151	2	I38004	M130 antigen precu
731	100	2.5	1156	2	I38005	M130 antigen precu
732	100	2.5	1251	2	A57293	latent transformin
733	100	2.5	1299	2	T43251	furin (EC 3.4.21.7
734	99.5	2.5	330	2	I55975	X/Y protein - mus
735	99.5	2.5	640	1	A30452	urmodulin precurs
736	99.5	2.5	686	2	S43562	KOBE5.3 protein -
737	99.5	2.5	914	1	S07047	iodide peroxidase
738	99.5	2.5	1280	2	A39117	170K lectin precu
739	99.5	2.5	1350	2	S00647	finger protein - A
740	99.5	2.5	1766	2	A42125	trophozoite cystei
741	99.5	2.5	1847	2	T18308	probable vitelloge
742	99.5	2.5	1984	2	T13171	probable vitelloge
743	99	2.5	589	2	B38128	epithelin/granulin
744	99	2.5	591	2	I48141	acroganin - guine
745	99	2.5	675	1	KXMS	plasma protein S p
746	99	2.5	675	1	KXRTS	plasma protein S p
747	99	2.5	805	2	S68441	leptin receptor, s
748	99	2.5	892	2	S68439	leptin receptor, s
749	99	2.5	894	2	S68437	leptin receptor, s
750	99	2.5	900	2	S68440	leptin receptor, s
751	99	2.5	1162	2	S68438	leptin receptor, s
752	99	2.5	1558	2	AB2457	two-component hyb
753	99	2.5	2809	2	T30213	G-cadherin - sea u
754	98.5	2.5	317	2	T28605	hypothetical prote
755	98.5	2.5	317	2	F72172	H7R protein - vari
756	98.5	2.5	317	2	G36855	B7R protein - vari
757	98.5	2.5	427	2	S74211	PAS-6/7 protein pr
758	98.5	2.5	1178	1	A39804	thrombospondin pre
759	98	2.5	82	2	T46510	hypothetical prote
760	98	2.5	102	2	B55885	chondroitin sulfat
761	98	2.5	357	2	S23403	sperm surface prot
762	98	2.5	909	1	QRXLL1	LDL receptor 1 pre
763	98	2.5	937	2	I53282	gene PACB4 protein
764	98	2.5	1087	2	T31100	probable potassium
765	98	2.5	1748	1	UN0786	integrin beta-4 ch
766	98	2.5	2588	2	T14342	NSD1 protein - mou
767	98	2.5	4660	2	T42737	gp330 protein prec
768	97.5	2.5	577	1	A60501	thrombospondin pre
769	97.5	2.5	837	1	A29512	LDL receptor precu
770	97.5	2.5	878	2	B71460	probable outer mem
771	97.5	2.5	884	2	T18649	hypothetical prote
772	97.5	2.5	1162	2	T21557	hypothetical prote
773	97.5	2.5	2946	2	T13840	hypothetical prote
774	97	2.5	146	2	A23473	chymotrypsin-like
775	97	2.5	379	2	T27350	hypothetical prote
776	97	2.5	429	2	T21113	hypothetical prote
777	97	2.5	626	2	T27319	hypothetical prote
778	97	2.5	799	1	IUMSFB	fibronectin recept
779	97	2.5	808	2	T23129	hypothetical prote
780	97	2.5	862	2	S43922	versican - pig-tal
781	97	2.5	915	1	A48225	subtilisin-like pr
782	97	2.5	1138	1	S24066	protein-tyrosine k
783	97	2.5	1193	2	A44018	laminin B2t chain
784	97	2.5	1292	2	T09229	galactose binding
785	96.5	2.4	149	1	KQMSN	tissue kallikrein
786	96.5	2.4	317	2	D42526	BSR protein - vacc
787	96.5	2.4	613	2	A69535	aldehyde ferredoxi
788	96.5	2.4	956	2	A57121	thrombospondin 3 p
789	96.5	2.4	1149	2	I38006	M130 antigen precu
790	96.5	2.4	1193	2	T21133	hypothetical prote
791	96.5	2.4	1297	2	T30274	proteolipaisin - be
792	96.5	2.4	116	2	S39434	hemocytin - silkw
793	96	2.4	3133	2	S52093	AGN-3 protein - pi
794	96	2.4	116	2	S17567	AGN-3 protein - pi
795	96	2.4	256	2	A56593	cyprin-related pr
796	96	2.4	392	2	T25213	hypothetical prote
797	96	2.4	798	2	A28193	integrin beta-1 ch
798	96	2.4	798	2	B28193	probable hormone r
799	96	2.4	886	2	A57172	LDL-receptor-relat
800	96	2.4	4753	1	A47437	chymase (EC 3.4.21
801	95.5	2.4	177	2	S23505	probable regulator
802	95.5	2.4	218	2	H70770	probable serine pr
803	95.5	2.4	330	2	B82415	aga protein precu
804	95.5	2.4	427	2	JC4915	hypothetical prote
805	95.5	2.4	561	2	T27318	mucin 5AC (clone L
806	95.5	2.4	1042	2	A57534	G2-G1 polyprotein
807	95.5	2.4	1135	1	J01928	hypothetical prote
808	95.5	2.4	1270	2	T22615	hypothetical prote
809	95.5	2.4	3191	2	T22945	hypothetical prote
810	95	2.4	463	2	T39621	peptidyl prollyl ci
811	95	2.4	850	2	S56015	gastric mucin MUC5
812	95	2.4	869	1	JC4858	VDL receptor prec
813	95	2.4	989	2	T01519	hypothetical prote
814	95	2.4	1245	1	MMMSUD	nidogen precursor
815	95	2.4	1321	2	JB0352	mucin MUC5B, trach
816	94.5	2.4	111	2	S21211	spermadhesin AGN-1
817	94.5	2.4	643	2	T25473	hypothetical prote
818	94.5	2.4	736	2	S47645	TMDC 1 protein - c
819	94.5	2.4	862	1	QRMSUD	LDL receptor precu
820	94.5	2.4	1216	2	T26104	hypothetical prote
821	94.5	2.4	1416	1	E88550	protein ZC84.1 [im
822	94.5	2.4	1717	1	A45558	epidermal growth f
823	94	2.4	258	1	B37252	insulin-like growt
824	94	2.4	370	2	JC7998	platelet-derived g
825	94	2.4	634	2	T02594	hypothetical prote
826	94	2.4	713	2	T44447	neuregulin-3 [limo
827	94	2.4	736	2	T06757	hypothetical prote
828	94	2.4	899	2	G02428	subtilisin-like pr
829	94	2.4	915	2	JC6148	subtilisin-like pr
830	94	2.4	932	2	I52527	PACB4 - mouse (fr
831	94	2.4	1381	2	T31083	paranodin - rat
832	94	2.4	1385	2	T14158	neurexin IV - mou

833	94	2.4	3097	2	T00021	906	89.5	2.3	854	1	QRHYLD	LDL receptor precu
834	93.5	2.4	258	2	A45403	907	89.5	2.3	1164	2	T01871	RNA-directed DNA p
835	93.5	2.4	317	2	J01799	908	89.5	2.3	1258	2	A12155	WD-repeat protein
836	93.5	2.4	449	2	T35048	909	89.5	2.3	1364	2	T00250	MEGF2 protein - hu
837	93.5	2.4	456	2	T31483	910	89	2.3	319	2	A53502	foliistatin - Afri
838	93.5	2.4	486	2	S49820	911	89	2.3	354	2	T22274	hypothetical prote
839	93.5	2.4	612	2	JH0799	912	89	2.3	369	2	F81178	histone deacetylase
840	93.5	2.4	739	2	B88553	913	89	2.3	390	2	C90208	hypothetical prote
841	93.5	2.4	1115	2	S40241	914	89	2.3	469	1	NM1V27	exo-alpha-sialidas
842	93.5	2.4	1136	1	S57845	915	89	2.3	525	2	T21357	hypothetical prote
843	93	2.4	104	2	T19868	916	89	2.3	907	2	I50404	p50b/p97 (lyt-10)
844	93	2.4	329	2	A48805	917	89	2.3	977	2	I50404	G2-G1 polyprotein
845	93	2.4	873	1	I48952	918	89	2.3	1110	1	B42544	chromospondin 1 p
846	93	2.4	995	2	A56599	919	88.5	2.2	317	2	T37442	BEV gp42,ps/hr pro
847	93	2.4	2767	1	UIHU	920	88.5	2.2	356	2	T20656	hypothetical prote
848	93	2.4	4545	1	S25111	921	88.5	2.2	438	2	T40509	lim domain protein
849	92.5	2.3	211	2	A46458	922	88.5	2.2	633	2	I37570	zinc finger protei
850	92.5	2.3	736	2	T19366	923	88.5	2.2	754	2	T47886	transketolase-like
851	92.5	2.3	756	2	S47656	924	88.5	2.2	905	2	S55059	feritin alpha-I -
852	92.5	2.3	803	1	IUCH3	925	88.5	2.2	1077	2	T41146	probable cysteine-
853	92.5	2.3	955	2	A45441	926	88.5	2.2	1096	2	T16875	hypothetical prote
854	92.5	2.3	1367	1	TGHU1	927	88.5	2.2	1170	2	TSHP1	chromospondin 1 p
855	92	2.3	334	2	T23027	928	88.5	2.2	1978	2	T07081	acetyl-CoA carboxy
856	92	2.3	650	2	A34498	929	88	2.2	621	2	I38467	low density lipopr
857	92	2.3	719	2	T00266	930	88	2.2	656	2	JC2005	integrin beta-5 ch
858	92	2.3	915	2	B48225	931	88	2.2	798	2	B27079	fibronectin recept
859	92	2.3	964	2	JC5545	932	88	2.2	799	2	A38308	integrin beta-5 ch
860	92	2.3	1097	2	S68685	933	88	2.2	962	2	JC5571	subtilisin-like pr
861	92	2.3	1444	2	T18856	934	88	2.2	1085	2	C96797	unknown protein [i
862	92	2.3	1895	2	T15881	935	88	2.2	1175	2	S52417	E-selectin ligand-
863	92	2.3	2533	2	T28675	936	88	2.2	1192	2	S69000	laminin gamma 2 ch
864	92	2.3	3869	2	A48205	937	87.5	2.2	554	2	A45818	cytolysin precursor
865	91.5	2.3	237	2	I47031	938	87.5	2.2	580	2	A37107	spermatogenesis pr
866	91.5	2.3	250	2	T30124	939	87.5	2.2	584	1	C8HUA	complement C8 alph
867	91.5	2.3	303	2	H35068	940	87.5	2.2	667	2	T01899	hypothetical prote
868	91.5	2.3	511	2	T17298	941	87.5	2.2	914	1	JC0550	iodide peroxidase
869	91.5	2.3	588	2	T33815	942	87.5	2.2	1807	2	JC6319	integrin beta-4 ch
870	91.5	2.3	640	2	S49932	943	87.5	2.2	1816	2	S68960	laminin alpha-4 ch
871	91.5	2.3	1101	2	T16840	944	87	2.2	387	2	I38449	extracellular prot
872	91.5	2.3	1161	2	D83076	945	87	2.2	706	2	S74610	hypothetical prote
873	91.5	2.3	2144	2	S71490	946	87	2.2	743	2	T40521	hypothetical prote
874	91.5	2.3	2672	2	A48126	947	87	2.2	860	2	T16892	hypothetical prote
875	91.5	2.3	2910	2	T42214	948	87	2.2	970	2	I78842	receptor protein-c
876	91	2.3	94	2	PC2013	949	87	2.2	975	2	JC5570	subtilisin-like pr
877	91	2.3	293	2	T09065	950	87	2.2	1042	2	T26644	hypothetical prote
878	91	2.3	319	1	I50370	951	87	2.2	1056	2	A53767	muclin MUC5B, trach
879	91	2.3	398	2	E71539	952	87	2.2	1134	1	JN0711	protein-tyrosine k
880	91	2.3	435	2	I54182	953	87	2.2	1945	2	T13937	plexin A - fruit f
881	91	2.3	478	2	S47040	954	87	2.2	2481	2	A43908	fibronectin - Afri
882	91	2.3	909	1	ORXL2	955	87	2.2	3968	2	A44265	trithorax homolog
883	91	2.3	2543	2	T31687	956	86.5	2.2	222	2	S72795	hypothetical prote
884	91	2.3	4543	1	A53102	957	86.5	2.2	264	2	T16271	hypothetical prote
885	90.5	2.3	53	2	S17294	958	86.5	2.2	336	2	D69074	polyferredoxin 4x2
886	90.5	2.3	330	1	JN0561	959	86.5	2.2	391	2	T34284	hypothetical prote
887	90.5	2.3	642	1	JP0079	960	86.5	2.2	471	2	I79528	alkaline phosphata
888	90.5	2.3	746	1	HYHUMA	961	86.5	2.2	585	2	I46686	complement compo
889	90.5	2.3	776	2	S28258	962	86.5	2.2	632	2	T22288	hypothetical prote
890	90.5	2.3	960	2	JB0356	963	86.5	2.2	632	2	T21602	hypothetical prote
891	90.5	2.3	1104	2	I38869	964	86.5	2.2	638	2	AF3463	flagellar protein
892	90.5	2.3	1148	1	GNVUNE	965	86.5	2.2	651	2	F71810	type III DNA modif
893	90.5	2.3	1357	2	T16860	966	86.5	2.2	651	2	T05869	hypothetical prote
894	90.5	2.3	1436	2	A46496	967	86.5	2.2	700	2	A32392	protein kinase C (
895	90.5	2.3	2813	1	VMHU	968	86.5	2.2	734	2	C81399	isocitrate dehydro
896	90	2.3	156	2	B23863	969	86.5	2.2	1172	2	A42887	chromospondin 2 p
897	90	2.3	340	2	T34423	970	86.5	2.2	1376	1	J01534	E2 glycoprotein pr
898	90	2.3	409	2	T11743	971	86.5	2.2	1418	2	D75281	ribonucleoside-dip
899	90	2.3	417	2	T29864	972	86.5	2.2	1473	2	A20872	ovostatin precursor
900	90	2.3	522	2	T29767	973	86.5	2.2	3712	1	YGCEVC	alpha-aminoadipyl-
901	90	2.3	577	1	B37057	974	86	2.2	445	2	B82525	conserved hypotet
902	90	2.3	814	1	I39627	975	86	2.2	713	2	A35502	major surface-labe
903	90	2.3	2533	1	T28674	976	86	2.2	738	2	S40992	hypothetical prote
904	89.5	2.3	417	2	T39939	977	86	2.2	905	2	T23229	hypothetical prote
905	89.5	2.3	748	2	S24134	978	86	2.2	906	2	A71438	probable resistanc

979	86	2.2	933	1	OPHUT	1052	83.5	2.1	311	2	JC7873	l-rhamnose-binding
980	86	2.2	969	1	A39490	1053	83.5	2.1	344	2	A32141	follietatin 1 prec
981	86	2.2	1487	2	S48719	1054	83.5	2.1	348	2	T28623	hypothetical prote
982	86	2.2	1572	2	T00027	1055	83.5	2.1	354	2	G64475	GTP-binding protei
983	86	2.2	1650	2	S53457	1056	83.5	2.1	358	1	A55973	transcription fact
984	86	2.2	2233	2	T28669	1057	83.5	2.1	366	2	I53035	trithorax homolog
985	85.5	2.2	317	2	A38493	1058	83.5	2.1	481	2	H83770	hypothetical prote
986	85.5	2.2	340	2	B55973	1059	83.5	2.1	579	2	B84192	pyruvate kinase [i
987	85.5	2.2	344	1	A27701	1060	83.5	2.1	589	2	C38128	epithelin/granulin
988	85.5	2.2	358	2	B64427	1061	83.5	2.1	697	2	H86457	78.1K hypothetical
989	85.5	2.2	463	1	A36479	1062	83.5	2.1	873	2	D88482	protein C05D11.8 f
990	85.5	2.2	515	2	T05863	1063	83.5	2.1	1106	2	T13938	gene shuttle craft
991	85.5	2.2	638	2	S22491	1064	83.5	2.1	2120	2	T30243	alpha tectorin - c
992	85.5	2.2	663	2	T21010	1065	83.5	2.1	2704	2	S09118	G surface protein
993	85.5	2.2	798	2	S01659	1066	83.5	2.1	4302	2	A38971	polyestic kidney
994	85.5	2.2	1162	2	PC4184	1067	83.5	2.1	13055	2	T16580	hypothetical prote
995	85.5	2.2	1229	2	H84465	1068	83.5	2.1	304	2	A83513	probable transcrip
996	85.5	2.2	2452	1	RWZ021	1069	83	2.1	351	2	S20078	NOV protein - chic
997	85.5	2.2	2457	2	T18492	1070	83	2.1	372	2	T39244	probable phospho-2
998	85	2.2	200	2	T42678	1071	83	2.1	451	2	F83747	denosylmethionine-
999	85	2.2	291	2	I38098	1072	83	2.1	492	2	D35114	anthranilate synth
1000	85	2.2	318	2	H86342	1073	83	2.1	593	1	GYHU	granulin precursor
1001	85	2.2	343	2	S55369	1074	83	2.1	770	2	S04847	leukocyte adhesion
1002	85	2.2	359	1	T51734	1075	83	2.1	770	2	D89447	protein P57C12.1 f
1003	85	2.2	413	2	T23098	1076	83	2.1	800	2	A45839	leukocyte adhesion
1004	85	2.2	542	2	A84554	1077	83	2.1	800	2	S54623	probable microend
1005	85	2.2	552	2	F83417	1078	83	2.1	816	2	C69493	hypothetical prote
1006	85	2.2	606	2	S43118	1079	83	2.1	1046	2	F71432	hypothetical prote
1007	85	2.2	638	2	S22490	1080	83	2.1	1066	2	B95037	hyaluronidase [imp
1008	85	2.2	653	2	G96675	1081	83	2.1	1111	2	T00324	hypothetical prote
1009	85	2.2	671	1	UTPV15	1082	83	2.1	1373	2	JE0095	gastric mucin MUC5
1010	85	2.2	752	2	T26508	1083	83	2.1	1216	1	ZLVNSY	genome polypeptin
1011	85	2.2	794	2	F88508	1084	83	2.1	3020	2	A43932	mucin 2 precursor,
1012	85	2.2	895	2	S74225	1085	82.5	2.1	328	2	F83599	hypothetical prote
1013	85	2.2	1021	2	S26985	1086	82.5	2.1	429	2	A42972	coagulation factor
1014	85	2.2	1078	2	P97907	1087	82.5	2.1	466	2	S29302	alliin lyase (EC 4
1015	85	2.2	1148	1	UQ1604	1088	82.5	2.1	591	1	C6HUB	complement C8 beta
1016	85	2.2	1533	2	T00344	1089	82.5	2.1	753	2	T19338	hypothetical prote
1017	85	2.2	1538	2	S73296	1090	82.5	2.1	761	2	B82223	ribonucleoside-dip
1018	85	2.2	2150	2	T32497	1091	82.5	2.1	781	2	S43521	integrin beta3 - c
1019	85	2.2	271	2	S12783	1092	82.5	2.1	984	2	T00326	hypothetical prote
1019	85	2.2	271	2	S12783	1093	82.5	2.1	1175	2	I57549	adenosine deaminas
1020	84.5	2.1	337	2	I47079	1094	82.5	2.1	1372	2	A34157	insulin receptor p
1021	84.5	2.1	344	2	I45894	1095	82	2.1	188	2	A39787	teratocarcinoma de
1022	84.5	2.1	429	2	T16656	1096	82	2.1	235	2	AE0114	deoxyribonuclease
1023	84.5	2.1	494	2	A99683	1097	82	2.1	318	2	S65019	chitinase [EC 3.2.
1024	84.5	2.1	494	2	B85533	1098	82	2.1	343	2	S45321	follietatin - mous
1025	84.5	2.1	505	2	A46570	1099	82	2.1	349	2	D72175	G2R protein - vari
1026	84.5	2.1	615	2	S06546	1100	82	2.1	432	2	D83904	carbon storage regu
1027	84.5	2.1	654	2	T30136	1101	82	2.1	528	2	B42560	4-chlorodenzotate-C
1028	84.5	2.1	696	2	A12849	1102	82	2.1	583	2	T34121	steroid/thyroid/re
1029	84.5	2.1	696	2	G97626	1103	82	2.1	599	2	B82439	formate-tetrahydro
1030	84.5	2.1	744	2	A43353	1104	82	2.1	711	2	T27358	hypothetical prote
1031	84.5	2.1	746	2	F87243	1105	82	2.1	866	2	T02635	D2 protein homolog
1032	84.5	2.1	760	2	A40195	1106	82	2.1	1530	2	I45944	neurexin I -alpha
1033	84.5	2.1	788	2	A26547	1107	82	2.1	1609	2	S44821	PAE2.4 protein -
1034	84.5	2.1	789	2	S28259	1108	82	2.1	1661	2	T31330	head-activator bin
1035	84.5	2.1	864	2	T49574	1109	82	2.1	2214	2	T16305	hypothetical prote
1036	84.5	2.1	917	2	I48950	1110	82	2.1	4861	2	S71752	giant protein p619
1037	84.5	2.1	950	2	T28793	1111	82	2.1	209	2	T02394	hypothetical prote
1038	84	2.1	278	2	T21718	1112	81.5	2.1	251	2	A55035	cysteine-rich prot
1039	84	2.1	335	2	T32657	1113	81.5	2.1	349	2	S57453	polyesterdioxin 4x2
1040	84	2.1	349	2	D36858	1114	81.5	2.1	383	2	D88633	protein f56b3.2 [i
1041	84	2.1	413	2	T34123	1115	81.5	2.1	429	2	S01919	klirps protein - f
1042	84	2.1	471	2	A84741	1116	81.5	2.1	432	2	A25483	env polyprotein, r
1043	84	2.1	520	2	G88846	1117	81.5	2.1	443	2	T29147	hypothetical prote
1044	84	2.1	567	2	T49492	1118	81.5	2.1	460	2	S67174	hypothetical prote
1045	84	2.1	572	2	A30363	1119	81.5	2.1	482	2	A83655	lysine decarboxyla
1046	84	2.1	1034	2	JC5598	1120	81.5	2.1	496	2	T08674	probable finger pr
1047	84	2.1	1047	2	T34946	1121	81.5	2.1	519	2	S54300	transketolase (EC
1048	84	2.1	1599	2	T16210	1122	81.5	2.1	604	1	HMNZCD	hemagglutinin - ca
1049	84	2.1	2153	2	T14893	1123	81.5	2.1	625	2	S35317	proto-oncogene - m
1050	83.5	2.1	202	2	A44247	1124	81.5	2.1	626	2	S37622	
1051	83.5	2.1	278	2	AH0282							

1125	81.5	2.1	724	2	A48569	antigen Em100 - E1	1198	80	2.0	644	2	184634	Tamm-Horsfall prot
1126	81.5	2.1	977	2	S49004	tyrosine kinase Mp	1199	80	2.0	656	1	S59631	endo-1,4-beta-xyla
1127	81.5	2.1	1187	2	T18355	hypothetical prote	1200	80	2.0	680	1	PN0510	integrin beta-3 ch
1128	81.5	2.1	1210	2	D88013	protein K10B4.1 [1	1201	80	2.0	713	2	GC6012	glutamine-fructose
1129	81.5	2.1	1507	2	A40238	neurexin I -alpha p	1202	80	2.0	741	2	GC4888	probable transkeo
1130	81	2.1	180	2	AE1010	conserved hypochet	1203	80	2.0	746	2	GC4505	hypothetical prote
1131	81	2.1	296	2	C81906	hypothetical prote	1204	80	2.0	753	2	UC7386	retinovin - chicke
1132	81	2.1	348	2	C56247	natural killer cel	1205	80	2.0	817	2	T27063	hypothetical prote
1133	81	2.1	428	2	T04472	probable porphobil	1206	80	2.0	902	2	T01127	curly leaf protein
1134	81	2.1	491	2	T40455	penicillin binding	1207	80	2.0	1138	2	T36406	hypothetical prote
1135	81	2.1	501	2	JC7181	maternal transcrip	1208	80	2.0	1184	2	A96638	hypothetical prote
1136	81	2.1	554	2	A31300	perforin precursor	1209	80	2.0	1342	2	A36223	kinase-related tra
1137	81	2.1	560	2	S25092	jasmonate-induced	1210	80	2.0	1385	2	H88569	protein K03H1.5 [1
1138	81	2.1	732	2	T52588	wall-associated ce	1211	80	2.0	1409	2	S41028	hypothetical prote
1139	81	2.1	735	2	G02937	fertilin beta - cr	1212	80	2.0	2219	2	T27684	hypothetical prote
1140	81	2.1	735	2	T48101	ADAM 6 protein pre	1213	80	2.0	2239	2	T16199	hypothetical prote
1141	81	2.1	769	2	JC1121	leukocyte adhesion	1214	80	2.0	2643	2	T29149	hypothetical prote
1142	81	2.1	787	2	T49614	related to tol pro	1215	80	2.0	3140	2	S47508	genome polyprotein
1143	81	2.1	799	2	JC4126	integrin beta olig	1216	79.5	2.0	71	2	A59412	KGD-bearing platel
1144	81	2.1	821	1	A39667	brain-derived neur	1217	79.5	2.0	217	2	D90033	conserved hypochet
1145	81	2.1	1166	1	S06142	protein-tyrosine k	1218	79.5	2.0	254	2	I48599	insulin-like growt
1146	81	2.1	1344	2	H84557	hypothetical prote	1219	79.5	2.0	254	2	JC1464	insulin-like growt
1147	81	2.1	1365	2	T00833	RNA-directed DNA p	1220	79.5	2.0	317	2	D64167	transaldolase (EC
1148	81	2.1	1438	2	A48216	neurexin III -alpha	1221	79.5	2.0	318	2	S43317	chitinase (EC 3.2.
1149	81	2.1	1471	2	B48218	neurexin III -alpha	1222	79.5	2.0	334	2	S20981	chitinase (EC 3.2.
1150	81	2.1	1578	2	T48216	neurexin III -alpha	1223	79.5	2.0	356	2	A25918	chromomodulin - b
1151	81	2.1	1895	2	T06609	disease resistance	1224	79.5	2.0	391	2	S49300	hypothetical prote
1152	81	2.1	3898	2	S57437	genome polyprotein	1225	79.5	2.0	457	2	C86464	hypothetical prote
1153	80.5	2.0	371	2	B72461	hypothetical prote	1226	79.5	2.0	474	2	A57480	tubulointerstitial
1154	80.5	2.0	390	2	T27256	hypothetical prote	1227	79.5	2.0	614	2	T40652	hypothetical prote
1155	80.5	2.0	409	2	B87661	conserved hypochet	1228	79.5	2.0	661	2	C85758	hypothetical prote
1156	80.5	2.0	416	2	A37877	hemorrhagic protei	1229	79.5	2.0	661	2	B90861	hypothetical prote
1157	80.5	2.0	431	2	S49821	PR2 protein - Ara	1230	79.5	2.0	694	2	S58083	transketolase (EC
1158	80.5	2.0	454	2	T26554	hypothetical prote	1231	79.5	2.0	700	1	HYHMB	mepirin A (EC 3.4.2
1159	80.5	2.0	471	1	PAECA	alkaline phosphata	1232	79.5	2.0	713	2	I65253	disintegrin-like t
1160	80.5	2.0	479	2	D86182	protein F13W7.11 [	1233	79.5	2.0	741	2	T09015	transketolase (EC
1161	80.5	2.0	502	2	T16716	hypothetical prote	1234	79.5	2.0	868	2	G84674	probable selenium-
1162	80.5	2.0	509	2	T22238	hypothetical prote	1235	79.5	2.0	952	2	T28792	diacylglycerol kin
1163	80.5	2.0	516	2	S53007	citrate synthase -	1236	79.5	2.0	1161	1	S31213	nitrogen precursor
1164	80.5	2.0	555	2	T21028	hypothetical prote	1237	79.5	2.0	1178	2	S08405	hypothetical prote
1165	80.5	2.0	570	2	T46261	hypothetical prote	1238	79.5	2.0	1260	2	A86323	protein F14D16.3 [
1166	80.5	2.0	604	2	T15796	hypothetical prote	1239	79.5	2.0	1390	2	S51564	sperm tail-specific
1167	80.5	2.0	627	2	T00603	hypothetical prote	1240	79.5	2.0	1402	2	T24664	hypothetical prote
1168	80.5	2.0	656	2	B49423	semaphorin I - fru	1241	79.5	2.0	2261	2	T07084	acetyl-CoA carboxy
1169	80.5	2.0	658	2	A86828	transketolase (EC	1242	79.5	2.0	2499	1	A30788	mannose 6-phosphat
1170	80.5	2.0	673	2	A49878	coagulation factor	1243	79	2.0	171	2	S57894	lamnin - Hydra vu
1171	80.5	2.0	704	2	A48040	mepirin A (EC 3.4.2	1244	79	2.0	188	2	A30362	teratocarcinoma-de
1172	80.5	2.0	741	2	B81143	isocitrate dehydro	1245	79	2.0	192	1	B57143	chitosulfate-dithio
1173	80.5	2.0	742	2	I37225	leucocyte antigen	1246	79	2.0	192	2	AC0763	chitosulfate reduct
1174	80.5	2.0	773	2	T46059	beta-1 integrin su	1247	79	2.0	206	2	D97285	ribosomal protein
1175	80.5	2.0	1055	2	T05653	hypothetical prote	1248	79	2.0	360	2	S32595	Mnt-2 protein - Ca
1176	80.5	2.0	1119	2	A88481	protein C16A3.6 [1	1249	79	2.0	364	2	T24153	hypothetical prote
1177	80.5	2.0	1245	1	VHW82	structural polypro	1250	79	2.0	392	2	T33444	hypothetical prote
1178	80.5	2.0	1376	1	VG1HJ2	E2 glycoprotein pr	1251	79	2.0	393	2	A64036	hypothetical prote
1179	80.5	2.0	1382	1	INHUR	insulin receptor p	1252	79	2.0	415	2	D87020	probable membrane
1180	80.5	2.0	1526	2	T19473	hypothetical prote	1253	79	2.0	417	2	T08724	hypothetical prote
1181	80.5	2.0	1558	2	C89114	protein C37C3.6a [	1254	79	2.0	587	2	C85044	hypothetical prote
1182	80.5	2.0	1611	2	G84493	probable retroelem	1255	79	2.0	602	2	B81420	GTP-binding protei
1183	80.5	2.0	2167	2	T34395	hypothetical prote	1256	79	2.0	606	2	T22105	hypothetical prote
1184	80.5	2.0	2262	2	T30890	calcium channel al	1257	79	2.0	630	2	T48369	hypothetical prote
1185	80.5	2.0	211	1	CYRTB3	beta-crystallin B3	1258	79	2.0	660	2	S71949	metalloproteinase
1186	80	2.0	243	2	T27036	hypothetical prote	1259	79	2.0	687	2	T16352	hypothetical prote
1187	80	2.0	284	2	T25938	hypothetical prote	1260	79	2.0	729	2	A45716	leukemia virus cel
1188	80	2.0	290	2	T46470	hypothetical prote	1261	79	2.0	738	2	T41730	hypothetical prote
1189	80	2.0	335	2	A39743	u-plasminogen acti	1262	79	2.0	753	2	B36268	platelet glycoprot
1190	80	2.0	395	2	S64299	polymerizable mem	1263	79	2.0	773	2	JB0387	exo-alpha-sialidas
1191	80	2.0	398	1	S24802	polyferidoxin 6x2	1264	79	2.0	788	2	A60798	platelet glycoprot
1192	80	2.0	437	2	S05478	properdin - mouse	1265	79	2.0	788	2	I77349	phenylalanine-tRNA
1193	80	2.0	464	2	H82928	ATP synthase beta	1266	79	2.0	790	2	D61568	monocyte surface a
1194	80	2.0	500	2	A36388	RNA-directed RNA p	1267	79	2.0	826	2	A60385	hypothetical prote
1195	80	2.0	589	2	I38598	zinc finger protei	1268	79	2.0	871	2	T04867	disintegrin and me
1196	80	2.0	642	2	C89124	protein K07C11.9 [	1269	79	2.0	952	2	T18900	
1197	80	2.0	644	1	A40212	uromodulin precurs	1270	79	2.0	1023	2	T30257	IgG Fc binding pro

1271	79	2.0	1289	1	BMXRR3	mRNA guanylyltrans	1344	78	2.0	4085	2	S28600	hypothetical prote
1272	79	2.0	1391	2	T20406	hypothetical prote	1345	77.5	2.0	46	2	OT0747	epiregulin - rat
1273	79	2.0	1513	2	A54895	myc2, intestina	1346	77.5	2.0	162	2	S68401	epiregulin precurs
1274	79	2.0	1522	2	T00028	brain-specific ang	1347	77.5	2.0	244	2	AB2505	histidine kinase-1
1275	79	2.0	1642	2	T19130	hypothetical prote	1348	77.5	2.0	255	2	H96705	hypothetical prote
1276	79	2.0	1777	2	T00490	nonstructural prot	1349	77.5	2.0	295	2	JC5559	lectin-B - Virgin
1277	79	2.0	1777	2	AC2088	seirine/threonine k	1350	77.5	2.0	296	2	G81111	conserved hypotet
1278	79	2.0	1166	2	S65875	spermadhesin PSP-1	1351	77.5	2.0	400	2	A55647	phyllipod - fruit
1279	78.5	2.0	307	1	S18523	fructokinase (EC 2	1352	77.5	2.0	402	2	S02099	phosphotrioxikinas
1280	78.5	2.0	327	2	A55356	urokinase-type pla	1353	77.5	2.0	407	2	C82438	glucose-1-phosphat
1281	78.5	2.0	341	2	I61725	natural killer ass	1354	77.5	2.0	413	4	FOHJ2	retrovirus-related
1282	78.5	2.0	344	2	I57698	folliclatin - rat	1355	77.5	2.0	457	2	B85749	ATP-dependent RNA
1283	78.5	2.0	355	2	C70457	hypothetical prote	1356	77.5	2.0	457	2	G90869	ATP-dependent RNA
1284	78.5	2.0	363	1	C55973	transcription fact	1357	77.5	2.0	457	2	B64884	ATP-dependent RNA
1285	78.5	2.0	376	2	E70361	chaperone DnaJ - A	1358	77.5	2.0	459	2	T36362	probable DNA repai
1286	78.5	2.0	389	2	D75180	hypothetical prote	1359	77.5	2.0	488	2	T21701	hypothetical prote
1287	78.5	2.0	401	2	S65138	glycoprotein antig	1360	77.5	2.0	546	2	B75375	probable amidase -
1288	78.5	2.0	436	2	S06884	viLD2 protein - Ag	1361	77.5	2.0	548	2	S38864	Ig epsilon chain C
1289	78.5	2.0	474	2	B38634	tumor necrosis fac	1362	77.5	2.0	569	2	B85076	probable transposo
1290	78.5	2.0	495	2	A57053	germ cell nuclear	1363	77.5	2.0	645	2	S20138	probable protein k
1291	78.5	2.0	507	2	T06452	probable legumin A	1364	77.5	2.0	717	2	B32838	DNA-directed RNA p
1292	78.5	2.0	517	1	FMPMLA	legumin A precurs	1365	77.5	2.0	729	2	A39707	erythrocyte membra
1293	78.5	2.0	552	2	C45710	R transactivator h	1366	77.5	2.0	729	2	A69202	conserved hypotet
1294	78.5	2.0	600	2	I49281	fertilin alpha pre	1367	77.5	2.0	767	2	B85079	hypothetical prote
1295	78.5	2.0	638	2	D86477	protein F1504.27 l	1368	77.5	2.0	809	2	A57283	integrin beta chai
1296	78.5	2.0	658	2	F85024	probable CHP-rich	1369	77.5	2.0	845	2	G82773	phage-related proc
1297	78.5	2.0	662	2	I37892	IL12 receptor comp	1370	77.5	2.0	848	2	AF0020	nitrite reductase
1298	78.5	2.0	717	2	T25431	hypothetical prote	1371	77.5	2.0	933	2	A31930	cytoactin - chick
1299	78.5	2.0	748	2	T00732	hypothetical prote	1372	77.5	2.0	1017	2	D75028	h-transporing AT
1300	78.5	2.0	757	2	T05688	hypothetical prote	1373	77.5	2.0	1079	1	TVFMI	gag-RmlI-env polyp
1301	78.5	2.0	763	2	T49089	hypothetical prote	1374	77.5	2.0	1142	2	A45031	cysteine-rich fibr
1302	78.5	2.0	842	2	T04555	hypothetical prote	1375	77.5	2.0	1323	2	E88257	protein let-23 lim
1303	78.5	2.0	819	2	T16720	probable membrane	1376	77.5	2.0	1374	2	S70712	protein-cytosine k
1304	78.5	2.0	1121	2	S57058	hypothetical prote	1377	77.5	2.0	2895	2	T08437	hyperplastic discs
1305	78.5	2.0	1137	2	T18625	hypothetical prote	1378	77.5	2.0	3085	2	T00327	polyprotein - infe
1306	78.5	2.0	1137	2	T30951	hypothetical prote	1379	77	2.0	194	2	S70663	lectin heavy chain
1307	78.5	2.0	1188	2	UC4889	actial natriuretic	1380	77	2.0	230	2	T31722	hypothetical prote
1308	78.5	2.0	3473	1	A46112	phosphatidylinosit	1381	77	2.0	230	2	A44074	probable EGF-like
1309	78.5	2.0	3473	2	S27927	genome polyprotein	1382	77	2.0	279	2	T16201	hypothetical prote
1310	78.5	2.0	3864	2	D87757	polyprotein - rice	1383	77	2.0	317	2	T45984	hypothetical prote
1311	78	2.0	247	2	T27778	protein C44E4.1a l	1384	77	2.0	375	2	F70691	hypothetical prote
1312	78	2.0	334	2	T20357	hypothetical prote	1385	77	2.0	452	2	H84772	probable serine ca
1313	78	2.0	360	2	G82937	probable capid as	1386	77	2.0	476	2	T19786	hypothetical prote
1314	78	2.0	360	2	G82934	glycine-cleavage s	1387	77	2.0	500	2	AE2032	glycerol kinase li
1315	78	2.0	372	2	T31060	hypothetical prote	1388	77	2.0	502	2	T41148	trp-asp repeat con
1316	78	2.0	385	2	A81926	hypothetical prote	1389	77	2.0	535	2	T19706	hypothetical prote
1317	78	2.0	401	2	C89102	protein P25E5.10 l	1390	77	2.0	540	1	OYHUCR	natriuretic peptide
1318	78	2.0	404	2	T40553	Trp-Asp repeat pro	1391	77	2.0	591	2	S33542	catechol oxidase (
1319	78	2.0	415	2	E83377	probable alcohol d	1392	77	2.0	713	2	T40729	wp repeat-containi
1320	78	2.0	441	2	AH2930	oxidoreductase Atu	1393	77	2.0	729	2	A49120	fibroblast growth
1321	78	2.0	446	2	F98351	tumor necrosis fac	1394	77	2.0	768	2	A87722	protein ZC13.1 li
1322	78	2.0	454	1	GQWST1	neurexin I-beta pr	1395	77	2.0	821	1	S06943	brain-derived neur
1323	78	2.0	468	2	B40228	transmembrane glyc	1396	77	2.0	1019	2	JC7538	neuronal different
1324	78	2.0	468	2	S25741	T-cell glycoprotei	1397	77	2.0	1019	2	T00038	hypothetical prote
1325	78	2.0	482	2	T17250	hypothetical prote	1398	77	2.0	1498	2	B97355	DNA segregation AT
1326	78	2.0	522	2	A46103	conserved hypotet	1399	77	2.0	1552	2	G86344	T2211.2 protein -
1327	78	2.0	523	2	C95303	importin alpha - t	1400	77	2.0	1723	2	T26859	receptor DEC-205 -
1328	78	2.0	527	2	T04329	integrin beta-3 ch	1401	77	2.0	2165	2	T21371	hypothetical prote
1329	78	2.0	599	2	JH0259	hypothetical prote	1402	77	2.0	2165	2	T21371	hypothetical prote
1330	78	2.0	723	2	T27148	hypothetical prote	1403	77	2.0	2584	2	T24158	hypothetical prote
1331	78	2.0	725	2	T27148	hypothetical prote	1404	77	2.0	2606	2	T24157	hypothetical prote
1332	78	2.0	843	2	A27131	epidermal growth f	1405	77	2.0	2769	1	UIBO	thyroglobulin prec
1333	78	2.0	857	2	T15976	hypothetical prote	1406	77	2.0	3033	1	GNMWV8	genome polyprotein
1334	78	2.0	989	2	T47503	hypothetical prote	1407	77	2.0	3660	1	S02041	dystrrophin, muscle
1335	78	2.0	989	2	G86295	hypothetical prote	1408	77	2.0	4957	2	T03455	AR protein - huma
1336	78	2.0	1016	2	T38744	hypothetical prote	1409	77	2.0	5262	2	T03454	AR protein - huma
1337	78	2.0	1245	1	VHNVB	structural polyp	1410	77	1.9	771	2	A59413	platelet-aggregati
1338	78	2.0	1260	1	TVRTNU	protein-tyrosine k	1411	76.5	1.9	146	2	G95995	hypothetical prote
1339	78	2.0	1330	1	GQFPE	epidermal growth f	1412	76.5	1.9	216	2	JX0265	platelet aggregati
1340	78	2.0	1339	2	JC4387	epidermal growth f	1413	76.5	1.9	224	2	AD2115	phosphoribosylform
1341	78	2.0	1369	2	S70713	protein-tyrosine k	1414	76.5	1.9	254	2	I48603	insulin-like growt
1342	78	2.0	1658	2	D75489	hypothetical prote	1415	76.5	1.9	264	2	T22380	hypothetical prote
1343	78	2.0	3224	1	S58884	Ran-binding protei	1416	76.5	1.9	272	2	E97451	hypothetical prote



1417	76.5	1.9	272	2	AG2669	enoyl-(acyl)-carrie
1418	76.5	1.9	279	2	JC6565	four-and-a-half LI
1419	76.5	1.9	292	2	E86267	hypothetical prote
1420	76.5	1.9	322	1	S37344	chitinase (EC 3.2.
1421	76.5	1.9	323	2	T24836	hypothetical prote
1422	76.5	1.9	327	2	AC0156	probable cobalamin
1423	76.5	1.9	359	2	T36050	probable histidin
1424	76.5	1.9	359	2	E83262	hypothetical prote
1425	76.5	1.9	385	2	AH0793	probable lipopolys
1426	76.5	1.9	386	2	T12527	hypothetical prote
1427	76.5	1.9	388	1	EHMS	ig epsilon chain C
1428	76.5	1.9	420	2	S74388	gamma-glutamyl pho
1429	76.5	1.9	435	2	T25350	hypothetical prote
1430	76.5	1.9	481	2	A56346	transcription fact
1431	76.5	1.9	483	2	T48328	importin alpha-1ik
1432	76.5	1.9	487	2	T21384	hypothetical prote
1433	76.5	1.9	504	2	T34404	hypothetical prote
1434	76.5	1.9	518	2	G88861	protein F59A7.8 (I
1435	76.5	1.9	520	2	C70311	hypothetical prote
1436	76.5	1.9	536	1	A39036	H+-transporting tw
1437	76.5	1.9	545	1	PMBYA	hypothetical prote
1438	76.5	1.9	601	2	T34396	H+-transporting tw
1439	76.5	1.9	623	2	S56206	probable membrane
1440	76.5	1.9	658	2	T47960	hypothetical prote
1441	76.5	1.9	707	2	S68858	finger protein - m
1442	76.5	1.9	712	2	T16338	hypothetical prote
1443	76.5	1.9	772	2	S32659	integrin beta 2 ch
1444	76.5	1.9	837	2	A42112	mucln-like peptide
1445	76.5	1.9	849	2	I50617	protein-tyrosine k
1446	76.5	1.9	1000	2	S47243	starch phosphoryl
1447	76.5	1.9	1004	2	T31655	hypothetical prote
1448	76.5	1.9	1056	2	T33167	hypothetical prote
1449	76.5	1.9	1071	2	T18307	suppressor protein
1450	76.5	1.9	1153	2	T00615	DNA polymerase III
1451	76.5	1.9	1201	2	AD1107	RNA polymerase (be
1452	76.5	1.9	1349	2	T01659	aldelyde oxidase (
1453	76.5	1.9	1561	2	S46200	acetyl-CoA carboxy
1454	76.5	1.9	1660	2	T18561	vitellogenin vit-6
1455	76.5	1.9	1738	2	C84507	hypothetical prote
1456	76.5	1.9	1985	2	T61776	Munc13-2 - rat
1457	76.5	1.9	2098	2	T18397	protein CTRP - mal
1458	76.5	1.9	2155	2	T30197	alpha tectorin - m
1459	76.5	1.9	2395	1	S50820	surface protein ty
1460	76.5	1.9	2562	2	T14266	xin protein - chic
1461	76.5	1.9	3828	2	T13857	retinoblastoma p
1462	76.5	1.9	4550	2	T18440	hypothetical prote
1463	76.5	1.9	4836	2	T14346	herc2 protein - mo
1464	76	1.9	96	2	A05308	tiase kallikrein
1465	76	1.9	136	2	S72508	sperm motility inh
1466	76	1.9	171	2	T49612	teratocarcinoma-de
1467	76	1.9	233	2	T22396	hypothetical prote
1468	76	1.9	261	2	G97190	rRNA methylase, YS
1469	76	1.9	269	2	S36166	paired box transcr
1470	76	1.9	287	2	A11072	conserved hypochet
1471	76	1.9	333	2	T15257	hypothetical prote
1472	76	1.9	349	1	T51739	transcription fact
1473	76	1.9	374	2	A42264	membrane-associate
1474	76	1.9	415	2	T32467	hypothetical prote
1475	76	1.9	418	2	T24350	hypothetical prote
1476	76	1.9	450	2	D75446	oxidoreductase - D
1477	76	1.9	494	2	T35948	probable ADA-like
1478	76	1.9	512	1	DTBSPH	purh bifunctional
1479	76	1.9	531	2	T22021	hypothetical prote
1480	76	1.9	603	2	S22402	2-aminobenzozate-Co
1481	76	1.9	605	2	S71650	metalloproteinase
1482	76	1.9	612	2	T39666	WD-repeat protein
1483	76	1.9	616	1	RRVQWA	probable RNA-direc
1484	76	1.9	626	2	T09345	hypothetical prote
1485	76	1.9	634	2	AG0252	probable DEAD box
1486	76	1.9	670	2	A12223	transketolase (imp
1487	76	1.9	837	2	S43656	turin (EC 3.4.21.7
1488	76	1.9	860	2	JC5702	EBB kinase activa
1489	76	1.9	897	2	S67283	hypothetical prote

1490	76	1.9	908	2	T27117	hypothetical prote
1491	76	1.9	925	2	T37475	lipoprotein recept
1492	76	1.9	926	1	OPPGIT	iodide peroxidase
1493	76	1.9	934	1	A34372	complement C6 prec
1494	76	1.9	967	2	T48210	hypothetical prote
1495	76	1.9	1001	2	AG1879	hypothetical prote
1496	76	1.9	1084	2	T18292	hypothetical prote
1497	76	1.9	1097	2	S17308	nicotinamide nucle
1498	76	1.9	1206	2	T18557	probable hydrogena
1499	76	1.9	1245	1	VHWVB2	structural polypro
1500	76	1.9	1385	2	S34230	156k protein - pla

## ALIGNMENTS

RESULT 1  
 T08805  
 hypothetical protein DKFZp566H2123.1 - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 A:Accession: T08805  
 R:Ansoyge, W.; Warkner, U.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.  
 Submitted to the Protein Sequence Database, May 1999  
 A:Reference number: Z16472  
 A:Accession: T08805  
 A:Molecule type: mRNA  
 A:Residues: 1-181 <ANS>  
 A:Cross-references: UNIPROT:Q9Y432; EMBL:AL050214  
 A:Experimental source: adult uterus; clone DKFZp566H2123  
 C:Genetics:  
 A>Note: DKFZp566H2123.1

Query Match 24.1%; Score 949; DB 2; Length 181;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-56;  
 Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	540	SLQISAIILHPNDPILLDADIAIILKLDKARISTRVOPICLAASRDLSFQESHITVA	599
DB	1	SLAISAIILHPNDPILLDADIAIILKLDKARISTRVOPICLAASRDLSFQESHITVA	60
QY	600	GNMVLADVRSPPGKNDTLRSQVSVVDSLLCEQHEHDGI PVSVTNMFCAWEPAPSD	659
DB	61	GNMVLADVRSPPGKNDTLRSQVSVVDSLLCEQHEHDGI PVSVTNMFCAWEPAPSD	120
QY	660	ICTAETGGIINAASFPPGRASPEPRWHLMGVSNVYDTCSHRLSTATKULPFDQWIERNM	719
DB	121	ICTAETGGIINAASFPPGRASPEPRWHLMGVSNVYDTCSHRLSTATKULPFDQWIERNM	180
QY	720	K 720	
DB	181	K 181	

## RESULT 2

A38738  
 coagulation factor C precursor - horseshoe crab (Tachypleus tridentatus)  
 N:Alternate names: coagulation-complement factor C; Limulus factor C  
 N:Contains: coagulation factor C heavy chain; coagulation factor C light chain peptide A,  
 C:Species: Tachypleus tridentatus  
 C:Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
 A:Accession: A38738; B38738; S00105  
 R:Muta, T.; Miyara, T.; Minami, Y.; Tokunaga, F.; Nakamura, T.; Toh, Y.; Ikehara, Y.; Iwe  
 U. Biol. Chem. 266, 6534-6561, 1991  
 A:Title: Limulus factor C. An endotoxin-sensitive serine protease zymogen with a mosaic  
 A:Reference number: A38738; MUID:91177916; PMID:2007602  
 A:Accession: A38738  
 A:Molecule type: mRNA  
 A:Residues: 1-1019 <MUT>  
 A:Cross-references: UNIPROT:P28175; GB:D90271; NID:g217396; PID:d1015020; PID:g217397  
 A:Accession: B38738  
 A:Molecule type: mRNA  
 A:Residues: 1-466, 616, 'DN', 619-620, 'A', 622 <MUT>

A:Cross-references: GB:D90272  
R:Tokunaga, F.; Miyata, T.; Nakamura, T.; Morita, T.; Kume, K.I.; Miyata, T.; Iwanaga, S  
Eur. J. Biochem. 167, 405-416, 1987  
A:Title: Lipopolysaccharide-sensitive serine-protease zymogen (factor C) of horseshoe cr  
is a novel type of serine protease.  
A:Reference number: S00105; MUID:88004461; PMID:3308457  
A:Accession: S00105  
A:Molecule type: protein  
A:Residues: 'S', 27-39, 'S', 41, 'T', 43-54, 'E', 691-782, 950-977 <TOK>  
C:Superfamily: coagulation factor C; C-type lectin homology; complement factor H repeat  
C:Keywords: alternative splicing; glycoprotein; hemolymph coagulation; hydrolase; serine  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-690/Product: coagulation factor C heavy chain #status experimental <RCH>  
F:136-195/Domain: complement factor H repeat homology <FH01>  
F:199-254/Domain: complement factor H repeat homology <FH02>  
F:260-321/Domain: complement factor H repeat homology <FH03>  
F:436-564/Domain: C-type lectin homology <LCH>  
F:576-634/Domain: complement factor H repeat homology <FH04>  
F:685-747/Domain: complement factor H repeat homology #status atypical <FH05>  
F:691-762/Product: coagulation factor C light chain peptide A #status experimental <PPA>  
F:763-1019/Product: coagulation factor C light chain peptide B #status experimental <PPB>  
F:523-534, 624-912/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:767/Binding site: carbohydrate (Asn) (covalent) #status experimental  
F:809, 865, 966/Active site: His, Asp, Ser #status predicted

Query Match 17.0%; Score 672; DB 2; Length 1019;  
Best Local Similarity 25.6%; Pred. No. 4.5e-37;  
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

34 PGAEWNIN-----CRECCYDQIE---CYCPGKREYVGTITCCRNNEECSCLIHQCT 86  
184 PNCQMSPPPCIRCEKATSSPEHGKVNAPSGNMIEGATL-----RPSGDS-----PYLL 233  
87 IFENCKSR-KGSWCGTL-----103  
234 IGQETLTQGNQNSGQIPQCKVLVFCDDLPVNAEHQVKGVEQKGGPPQGTETVYT 293  
104 --DFFVVGFCYCAEGR--AGWYGG--DCMR-----CGQVLR--APKG 137  
294 CSGNVFLMGFTMLTKNPPGSGSGSPSCVKAADREVDGDSKAVPLDVGSPVNIHCAG 353  
138 QILLES-----YPLAHCEWTHA---KPGVIT-----Q 163  
354 CSLTAGTWGTAIYHELSSVCRALIHACKLPNSGAVVNVNNGPYSDPLGSLNGIKSEE 413  
164 LRFVWLSLEFDYM-----CQDYVEYVD-----GDRNDGIIKRYVCGN--ERPAP 206  
414 LKSLARSRFPDVSSSTGRSGCCPMPGFEVEBNCVYTTSKORAMERAGCVCTNMAARLAV 473  
207 IQS--IGSSLHVLFFHSDG-SKNPFDFF-----AIYEITAGSSSPCF 245  
474 LDKDLIPSLFETLAKGGLTTTWTGLHLDAEKPFVWELMRSNVLDNLTLPMASSBPG 533  
246 HDGTCV-LDKAGS---YKCACTAGYTCQRCENLLEBN---CSDPGSPVNGYQKITGP 297  
534 NETNVCVYDIDLDQLOPVWKTYSCEPQSSFPACMMDDSDNKKAKCDPGLPENGHTLHGQS 593  
298 GLINRHAHKITGVVSPFCNNSVYVLSGNKRTCOQNGESGKOPICR--ACREPKISLV 355  
594 --IDGFVY--GSSIVYSCVHLVYLSGLETVTCTTNGTSAPRPKICIKVITCONPVPVSYG 649  
356 RRRVLPVMOVSRERPLHOLYSAFSGKQLO--SAPTKKPLLPFGD-----LP 400  
650 SVEIKP---PKRTNISRVGSPFLALPRLPLRLABAARPPRPSPRSQSPSTVDLASKVLP 706  
401 MGYOHLHTQLOECISPPYRRIIGSSRRFCLRTGKMSGRAPSCIPICGIENITAP-----455  
707 EGHVYVGRATVYTCESRYELLGSGQRCDSSNGMNSGAPASCI P VCGRSDSPSPFIWNG 766  
456 -KTQGLRMPQWQAIYRRTSGVHDSLHGAMFLVCSGLNVNERTVVAHAHCTLDGKXTM 514  
767 NSTEIGQPMQWGISRWLA-----DHNMFLOCGGSLNLEKWTIVTAHACVYSATAEI 819

QY 515 IKPADLKVTLGKRYRDRDDDEKTIQSLQISATILHPNYPILLDADIDAIKLDKARIST 574  
DB 820 IDSOFKTYIGKRYRDRSDRDVDYQVREALEIHVNPYDGNLNFIALIQLTPTVLT 879  
QY 575 RVQPICLAASRDISTPQESH-----TVAGNVVLADVSPGPKNDLRSVGVSVDSL 628  
DB 880 RVQPICLPT--DITL---REHLKEGLAVVTGNG---LNNENTYSMICOAVLPVVAAS 930  
QY 629 LCEOHEDHGIPIVSTDNMECASMEPTAPSDICTAETGTGIAAVSPGRASPEPRMHLML 688  
DB 931 TCEGVYHEADLPPLTVENMECAVYK-KGRYDACSBSGG--PLVFADDSRTERRWLEGI 987  
QY 689 VSNVSYDKTSGH-RLSTAFVLPFKMIER 717  
DB 988 VSNVSYDKTSGH-KRANQYGFTRVNFSLMIRQ 1017

RESULT 3  
154763  
Ra-reactive factor (EC 3.4.21.-) 1 precursor - human  
N:Alternate names: mannose binding protein-associated serine proteinase 1 (MASP-1)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 09-Jul-2004  
C:Accession: 154763; JN0883  
R:Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.  
Int. Immunol. 6, 665-669, 1994  
A:Title: Molecular characterization of a novel serine protease involved in activation of  
A:Reference number: 154763; MUID:94289349; PMID:8018603  
A:Accession: 154763  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-699 <SAT>  
A:Cross-references: UNIPROT:P48740; GB:D28593; NID:G790963; PIDN:BA05928.1; PID:G471128  
R:Takeuchi, F.; Takayama, Y.; Hattori, H.; Kawakami, M.  
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993  
A:Title: A new member of the C1s family of complement proteins found in a bactericidal f  
A:Reference number: JN0883; MUID:94059062; PMID:8240317  
A:Accession: JN0883  
A:Molecule type: mRNA  
A:Residues: 1-234, 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>  
A:Cross-references: DDBJ:D1752; NID:G439712; PIDN:BA04477.1; PID:G439713  
A:Experimental source: liver  
C:Comment: This is a serum bactericidal factor that activates complement C4 and C2 compo  
C:Genetics:  
A:Gene: GDB:MASP1; GDB:CRANF; CRANF1; PRSS5; MASP  
A:Cross-references: GDB:361104; GDB:330954; OMIM:600521  
A:Map position: 3q27-3q28  
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol  
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-448, 449-699/Product: Ra-reactive factor #status predicted <MAT>  
F:19-135/Domain: C1r/C1s repeat homology <C1R1>  
F:143-181/Domain: EGF homology <EGF>  
F:185-294/Domain: C1r/C1s repeat homology <C1R2>  
F:301-362/Domain: complement factor H repeat homology <FH1>  
F:367-432/Domain: complement factor H repeat homology <FH2>  
F:449-691/Domain: trypsin homology <TRY>  
F:49-178, 407/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:73-91, 143-157, 153-166, 168-181, 185-212, 242-260, 301-349, 329-362, 367-414, 397-432, 436-572,  
F:155/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted  
F:448-449/Cleavage site: Arg-Ile (autolytic) #status predicted  
F:490, 552, 646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;  
Best Local Similarity 24.9%; Pred. No. 1.4e-24;  
Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

QY 69 CRNEENCDSCLTHPGCTIFENCKSCRNNGWGTLDLPVYKGFYCAECRAGWY-----CGD 124  
DB 143 CKHEDEBELSDGH-----CHN-----YIGGYCS-CRFGYLIHTDNT 180  
QY 125 C-MRCGVLPAPKQIILL-----ESYPLAHCEWTHAKRGFVQLRFLVLSLEFDYM-- 176

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Db      181 CRVCSNLTQKRGVITSPDFNPYKSSCLTITLSECFMVLNLFEDI---FDIQDH 237
Qy      177 ----COYDVEVRDNDGDIIRKVCNERPAPISIGSLAHVLFSDSKNDFGFAI 232
Db      238 PEVPCPDYIKIKKPG---KVLGPFCEKAPETISQSHSVLILFISDLSAENKGRRL- 292
Qy      233 YEETACSSPFCFHDGTCVLIDKAGSYKACLAGYTGQRCENLLEERNCSDPGFVNGYOK 292
Db      293 -----SYRAA-----GNECEPL-----QP--PVH----- 309
Qy      293 ITGGGLINGRHAIGIVVSFF-----CINSL-VLSGNEKR-----TCQNGESGCKQ 339
Db      310 -----GRIEBSQAKY-----FFKQVLVSCPTGYKVLKDVNEMDTFOIECKIKGTWANKI 359
Qy      340 PIC-IKACREBKISDLVRRRLPMQVQSRPTPLHQLVSAFQKSLQKLSAPTKKALPFGD 398
Db      360 PTCGIYDCRNP-----GR 372
Qy      399 LPMGYQHLMT-----OLQYECISPFYRLGSSR--PTCLRTGKMS-----GRA-PSC 442
Db      373 LKHGLIFSTRNNLTYSKSEIKVSCGEPYKMLNNTGITYCSAQGVMMKVLGRLPTC 432
Qy      443 IPICG-----KENTTAPKTQGLRMPQOATIRRTSGVHDSLHKAMFLVCSGA 492
Db      433 LPVCGLPKFKRKLMAIFN-GRPAQKGT-FWIML-----SHLNGQPF--CGGS 478
Qy      493 LVNERTVVAACHV---TDIGKVT-----MIKTADLVVVLGKPYRDDRDREKTIQSQIS 544
Db      479 LGGSSWTVTAHCHQSLDPPDLRLSDLSLSPDFKILIGKMR--LRDENEQHLGVK 536
Qy      545 AILHPNVDILLDADIAILKLDKARISTRVQPCICAAASRDLSFSQE-SHITVAGMNV 603
Db      537 HTLHPDYDNTFENDVALVELLESPLVNAFVPICLPEBQ-----QEGAMVIVSGMK 591
Qy      604 LADVRSQGNQDITRSGVSVSDSLCEQHEHGIPIVSYTDNNFCASWEPTAPSDICTA 663
Db      592 QFLORFP-----ETLMEIETPIVDHSTQKAYAP--LKKKATRDWICAG-EKEGGKACAG 644
Qy      664 ETGSIANVSFGRASPFRMHLMLGVMSYDKTCSHRLSTAFVLPFKMIR 717
Db      645 DSGGPMVTLNRERG---QWLVGTVMGDDCGKDRYK-VYSYIHNNKMIQR 693

RESULT 4
C1HNRB
Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
C1Species: Homo sapiens (man)
C1Date: 15-Nov-1984 #sequence revision 30-Jun-1991 #text change 09-Jul-2004
C1Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
R1Leysus, S.P.; Kurachi, K.; Sakataessen, K.S.; Davie, E.W.
Biochemistry 25, 4855-4863, 1986
A1Title: Nucleotide sequence of the cDNA coding for human complement C1r.
A1Reference number: A24170; MUID:87026566; PMID:3021205
A1Accession type: mRNA
A1Residues: 1-705 <LEV>
A1Cross-references: UNIPROT:P00736; GB:M14058; NID:G179643; PIDN:AAA51851.1; PID:G179644
R1Journet, A.; Tobi, M.
Biochem. J. 240, 783-787, 1986
A1Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
A1Reference number: A29768; MUID:87156625; PMID:3030286
A1Accession: A29768
A1Molecule type: mRNA
A1Residues: 1-151; 'L', 153-705 <JOU>
A1Cross-references: GB:X04701; NID:G29538; PIDN:CAA28407.1; PID:G29539
R1Arlaud, G.J.; Williams, A.C.; Gagnon, J.
Biochem. J. 241, 711-720, 1987
A1Title: Complete amino acid sequence of the A chain of human complement-clasical pathw
A1Reference number: A29769; MUID:87241246; PMID:3036070
A1Accession: A29769
A1Molecule type: protein
A1Residues: 18-166; 'X', 168-463 <ARL>

```

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A1Note: 152-Leu was also found
R1Arlaud, G.J.; van Dorselelaer, A.; Bell, A.; Mancini, M.; Aude, C.; Gagnon, J.
FEBS Lett. 222, 129-134, 1987
A1Title: Identification of erythro-beta-hydroxyasparagine in the BGF-like domain of humar
A1Reference number: S02422; MUID:88005128; PMID:2820791
A1Accession: S02422
A1Molecule type: protein
A1Residues: 152-186 <AR3>
R1Arlaud, G.J.; Gagnon, J.
Biochemistry 22, 1758-1764, 1983
A1Title: Complete amino acid sequence of the catalytic chain of human complement subcomp
A1Reference number: A00916; MUID:83204762; PMID:6303394
A1Accession: A00916
A1Molecule type: protein
A1Residues: 464-705 <AR2>
R1Nielsen, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
A1Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH-;
A1Reference number: A37820; MUID:90354439; PMID:2387866
A1Accession: A37820
A1Molecule type: protein
A1Residues: 18-26; 'L', 153-160; 'X', 252-255 <TH1>
R1Pelloux, S.; Nielsen, N.M.; Hudry-Clergeon, G.; Petillot, Y.; Fillhol, O.; Arlaud, G.J.
FEBS Lett. 386, 15-20, 1996
A1Title: Identification of a cryptic protein kinase C2 phosphorylation site in human con
A1Reference number: S68830; MUID:96221263; PMID:8635594
A1Accession: S68830
A1Molecule type: protein
A1Residues: 133-137; 187-211; 610-613 <PEL>
A1Experimental source: Plasma
A1Comment: C1r is a dimer of identical chains, each of which is activated by cleavage int
C1Chain: while fragment gamma remains disulfide-bonded to the B chain to form C1r II.
C1Comment: This protein is a serine protease that combines with C1q and C1s to form C1, t
n, activate C2 and C4.
C1Genetics:
A1Gene: GDB:C1R
A1Cross-references: GDB:119729; OMIM:216950
A1Map position: 12p13-12p13
C1Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homolo
C1Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; duf
F1-1-17/Domain: signal sequence #status predicted <SIG>
F1-1-138/Domain: C1r/C1s repeat homology <C1R1>
F1-146/3/Product: complement C1r chain A #status experimental <ACH>
F1-146-189/Domain: BGF homology <BGF>
F1-183-302/Domain: C1r/C1s repeat homology <C1R2>
F1-297-463/Product: C1r gamma fragment #status experimental <GFR>
F1-309-471/Domain: complement factor H repeat homology <FH1>
F1-376-447/Domain: complement factor H repeat homology <FH2>
F1-464-705/Product: complement C1r chain B #status experimental <BCH>
F1-464-697/Domain: trypsin homology <TRY>
F1-71-89; 146-165; 161-174; 176-189; 193-220; 250-268; 309-358; 338-371; 376-429; 406-447; 451-577;
F1-125; 221; 514; 581/Binding site: carbohydrate (Asn) (covalent) #status experimental
F1-167/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F1-206/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status experimental
F1-463-464/Cleavage site: Arg-Ile (autolytic) #status experimental
F1-502; 557; 654/Active site: His, Asp, Ser #status predicted

Query Match 10.2%; Score 403.5; DB 1; Length 705;
Best local similarity 22.9%; Pred. No. 2,5e-19;
Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;

Qy      44 ECCEYQIEC-----VC-----PKREVGTIFCC-----RNEBEC 77
Db      69 EGCFYDYVKSADKSLGRFCGLGSPGNPGRKKEFGSGNRMLLTFHTDFSENEN--G 126
Qy      78 SCIIHQCTIF--ENCKSCRNQSGWGTLD-----DFYVKGFCACRAGM----- 120
Db      127 TIMFYGFLAYVAQVLDDEKASNSKSGEEDPQCGHLCHNIVGYFCS-CRGEYLED 165
Qy      121 ---YGGDCMRCQGVLRAPKQOI-LLE---SYPLNACHWTTHAKPGFVQLRFVMSLEF 173
Db      186 RHSCQABC--SSRLYTEASGYISLSEYPRSYPPDLRCNYSIRVERGLTLHLKLE--PF 240

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Qy 174 D-----YMCQDYVEVADGDNRDGQIIKRVCGNERPAPISGSSLHLVLFHSDGSKNFD 227
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 241 DIDDHQVHCPCYDQIQI-----YANGKNIGFCGKGRPRDLDTSNAYDLFFTEDESQDSR 296
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 228 GFHAITY-EETIACSSSPCFHNGTCVLDKAGSYKACACLAGYGCQCEMLERNKNSDQGR 286
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 297 GWMKRYTEIIEIKCPQPKTLDEFITIIOMLPQYQ---FRDYPIATCK-----339
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 287 VNGYQKTIQSGPGLINGRAKIGTVVSPFCNNSVYLSGNEKRTCCOONSGMSKQIPIC-1KA 345
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 340 -QGIQLLEGNOVL-----HSFT-----AVCDDGTMHAMRCIKID 375
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 346 CREPKISDLYRRVRLPMQVQRETPRLHQLYSAFSSKQKQSAPTKKPALPFGDI-----PM 401
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 376 CGQGR-----NLPMGDFRYTTTM 393
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 402 GYQHLHTOLOYECISPPFR---RLGSSNR-----TCLRTGKWSG---RAPSCIPICGK 448
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 394 GVNTYKAIQYCHPEPPYKMQTRAGSRESEGVYTTCTAOGIMKNEQKEKIPRLCLPYCGK 453
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 449 IEN-----ITAPKTQGLRPMQALYRRTSQVHDSLHKGAMFLVCSGALVNERTVV 500
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 454 PVNVEQKRIITGGOKAKMSPMQV---FTNIHG---RG-----GGALLGDKRIL 498
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 501 VAAHCVTDLGKVTMIKTADLKVLGKFRYRDDREKTIQSLQ-----ISAILHPNY-- 552
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 499 TAAATLYPKEHBAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSVHPDYRQ 548
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 553 -DPIILDADIALIKLDKARISTRVQPTICLAASRLSTSPQESH-ITYAGNNVLAD---- 606
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 549 DESYNFEDIALILENSVTLGPNLPLICLP--DNDTFYDLGLMGVYSGGVSEKIAH 605
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 607 ----VRSQFNDKTLRSQVSVDSLLCEQHEHDGIPVSVTDNMFCASMEPTAPSDICT 662
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 606 DLRFRLP-----VANPQACENMLRGNKRDVFSQNFPCAG-HPSLKQDAGQ 651
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 663 AETGGIAAVSPFGRAPEPRMHLMLGVSMSYDKTCSHRLSTAFTKVLPEFKWIRRNK 720
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 652 GDSCGVFAVRDPN-----TDRWVATGIVSMGIG--CS-RGYFYFTVLVYVMIKKEME 702
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

## RESULT 5

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A:59271
A:reactive factor (EC 3.4.21.-) 2 precursor - human
N:Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
C:Species: Homo sapiens (man)
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: A59271
R:Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaible, W.J.; Laursen, S.B.; Poulsen, K.
Nature 386, 506-510, 1997
A:Title: A second serine protease associated with mannan-binding lectin that activates c
A:Reference number: A59271; MUID:97242412; PMID:9087411
A:Accession: A59271
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-686 <JEN>
A:Cross-references: UNIPROT:000187; GB:Y09926; NID:g4007626; PIDN:CAA71059.1; PID:g40076
A:Experimental source: tissue liver
A>Note: submitted to Genbank, December 1996
A>Note: parts of this sequence, including the amino end of the mature protein, were dete
C:Genetics:
A:Gene: GDB:MASP2
A:Cross-references: GDB:6071500
A:Map position: 1p36.2-1p36.3
C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homol
C:Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine P
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-444/445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F:19-134/Domain: C1r/C1s repeat homology <C1R1>
F:142-180/Domain: EGF homology <EGF>
F:184-293/Domain: C1r/C1s repeat homology <C1R2>
F:300-361/Domain: complement factor H repeat homology <FH1>

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F:366-430/Domain: complement factor H repeat homology <FH2>
F:445-679/Domain: trypsin homology <TRY>
F:72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-552,;
F:158/Modified site: erythro-beta-hydroxyasparagine (asn) #status predicted
F:444-445/Cleavage site: Arg-11e (autolytic) #status predicted
F:483,532,633/Active site: His, Asp, Ser #status predicted

```

```

Query Match 10.2%; Score 400.5; DB 1; Length 686;
Best Local Similarity 22.7%; Pred. No. 3,9e-19;
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

```

```

Qy 128 CGQVLR--APK-----GOILLESYP-----LNAHCENTHAKGPFVQLRPMLSLEFDY 175
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 11 CGSVATPLGFKMPEVPFGRILASPFQGEVYANDERRKNTLAPFGYRLKILFTFDELISH 70
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 176 MCOYDYVEVADGDNRDGQIIKRVCGNE---RPAP-----IQSGSSLHLVLFHSDG--KN 225
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 71 LCEYDFYKLSG---AKVLATLCGSESTDEAPKQDTFYSIGSSLDITFRSDYSNEKP 126
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 226 FDGFHAITY-EETIACSSSP---CFHNGTCVLDKAGSYKACACLAGYTCQR---CENL 274
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 127 FTGFEAFYAEDIDECVAPGEAPTCDH--CHNHGGEFYCGCRAGYVLAHRNKRITCSAL 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 275 -----LEE-----277
      |||
Db 184 CSGQVFTQSGEUSPEYPPRPYKLSCTYSISLEBSVILDFVESFDVETHEPTLCY 243
      |||
Qy 278 -----RNCSDP 283
      |||
Db 244 DFLKIQIDREHNGPFGCKTLPHRIETKSNVTITFTVDESQDHTGMIHTSTAHACRYP 303
      |||
Qy 284 GGPVNGYQKTIQSGPGLINGRAK-IGTVVSPFCNNSY-VLSG---NEKRTQONGEW 335
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 304 MAPNNGH-----VSPQAKYILKDSFSIFCEYELQGLPKLSTFPAVQKXGSW 354
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 336 SGKQPIC-1KACREPKISDLYRRVRLPMQVQRETPRLHQLYSAFSSKQKQSAPTKKPAL 394
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 355 DRPMFACSIYDCGP--DDLPSGRV-----EYITGE-----383
      |||
Qy 395 PFGDLPNGYOHHTLOYECISPPY--RLGSSNRRTCLRTGKWSG---RAPSCIPICGK 448
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 384 -----GVTTYKAVIQSCBEFFPYTMKAVDKVCADGFWTSKSEKSLPVECPYCGL 436
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 449 IENITAPKTQGLR---MPQALYRRTSQVHDSLHKGAMFLVCSGALVNERTVVA 502
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 437 SARTTGRIRYGGQKAKPDPWQVLLIGTIT-----AAGLLLYDNWVILTA 481
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 503 AHCVTDLGKVTMIKTADLKVLGKFRYRDDREKTIQSLQ-----ISAILHPNY-DP 554
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 482 AHAYVE---QKIDASALDIRMG-----TLKRLSBHYTQAMSEAVFIHGGYTHD 526
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 555 IILDADIALIKLDKARISTRVQPTICLAASRLSTSPQESHITVAGNNVLADVSPGFKN 614
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 527 AGFENDIALIKLNKKVINSNITPICPRKEABSFMKTDIGTASMG---LQRFGLA 582
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 615 DTLRSQVSVVDSLLCEQHEHDGIP-VSVTDNMFCASMEPTAPSDICTAETGGIAVSF 673
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 583 RNLVYVPIPIYDHQKCPAAVEKPEYPRGSYANMLCAGLE-SGSKDCRQSGG--ALVF 639
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 674 PGRASPEPRMHLMLGVSMSYDKTCSHRLSTAFTKVLPEFKWIE 716
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 640 --LDSETERMFVGIVSMGNCSEAGQGYVTVKIVNIYIPWIE 680
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

## RESULT 6

```

S05008
Complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S05008
R:Kinoshita, H.; Sakiyama, H.; Tokunaga, K.; Imajobi-Ohmi, S.; Hamada, Y.; Isono, K.; Sak
FEBS Lett. 250, 411-415, 1999
A:Title: Complete primary structure of a calcium-dependent serine proteinase capable of

```





Eur. J. Biochem. 156, 49-57, 1986  
 A>Title: Human complement component C1s. Partial sequence determination of the heavy chain  
 A:Reference number: A25396; MUID:86164350; PMID:3007145  
 A:Accession: A25396  
 A:Molecule type: Protein  
 A:Residues: 16-61;168-219;287-293; 'K', 295-334;384-445 <SPY>  
 R:Hees, D.; Schaller, U.; Rickli, E.B.  
 Biochemistry 30, 2827-2833, 1991  
 A>Title: Identification of the disulfide bonds of human complement C1s.  
 A:Reference number: A38407; MUID:91175725; PMID:2007122  
 A:Accession: A38407  
 A:Molecule type: Protein  
 A:Residues: 131-134, 'X', 136-146, 'X', 148-150;155, 'X', 157-162;166-170, 'X', 172-174, 'X', 176-177, 'X', 387-402, 'X', 404-408;416-424, 'X', 426-431;547-556;592-597;617, 'X', 619-627, 'X', 629-635  
 R:Thielens, N.M.; Audé, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.  
 J. Biol. Chem. 265, 14469-14475, 1990  
 A>Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH<sub>2</sub>-terminal domain of human complement C1s.  
 A:Reference number: A37820; MUID:90354439; PMID:2387866  
 A:Accession: B37820  
 A:Molecule type: Protein  
 A:Residues: 16-25; 'X', 203-207 <THI>  
 R:Thielens, N.M.; Van Dorsselaer, A.; Gagnon, J.; Arlaud, G.J.  
 Biochemistry 29, 3570-3578, 1990  
 A>Title: Chemical and functional characterization of a fragment of C1s containing the epitope for monoclonal antibody A32672.  
 A:Reference number: A32672; MUID:30283368; PMID:2141278  
 A:Accession: A32672  
 A:Content: annotation; erythro-beta-hydroxyasparagine site, content  
 A:Note: about half of the A chains contain erythro-beta-hydroxyasparagine  
 C:Comment: This protein is a serine protease that combines with C1q and C1r to form C1s and C1.  
 C:Comment: C1s is a dimer of identical chains, each of which is activated by cleavage in C1s.  
 A:Gene: GDB:C1S  
 A:Cross-reference: GDB:119730; OMIM:120580  
 A:Map position: 12p13-12p13  
 A:Intron: 291/1; 329/3; 356/1; 399/1; 424/1  
 A:Note: the 1st of introns may be incomplete  
 C:Superfamily: complement-activating serine proteases C1r/C1s/MASP; C1r/C1s repeat homology  
 C:Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; dimer  
 F:1-15/Domain: signal sequence #status predicted <SIG>  
 F:11-12/Domain: C1r/C1s repeat homology <C1R1>  
 F:16-68/Domain: complement subcomponent C1s #status experimental <MAT>  
 F:16-437/Product: complement subcomponent C1s chain A (heavy chain) #status experimental  
 F:135-171/Domain: EGF homology <EGF>  
 F:135-287/Domain: C1r/C1s repeat homology <C1R2>  
 F:294-354/Domain: complement factor H repeat homology <FH>  
 F:359-421/Domain: complement factor H repeat homology <FH>  
 F:438-688/Product: complement subcomponent C1s chain B (light chain) #status experimental  
 F:438-675/Domain: tryptophan homology <TRY>  
 F:65-83;135-147;143-156;158-171;175-202;234-251;294-341;321-354;359-403;386-421;425-549;174-406/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental  
 F:174-406/Binding site: carboxydrate (Asn) (covalent) #status experimental  
 F:437-438/Cleavage site: Arg-116 (complement subcomponent C1r) #status experimental  
 F:475-529;632/Active site: His, Asp, Ser #status predicted

Query Match 8.5%; Score 334; DB 1; Length 688;  
 Best Local Similarity 21.7%; Pred. No. 1,1e-11;  
 Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

QY 137 GQILL-----ESYPLNAHCWTIAKPGFVQLRFLVMSLEFDYVQDYVEARDGNDRG 192  
 DB 21 GEILSPYPOAYEVEKSWDIEPEGYIHLVFTTHDIEISEKCAVDSVOIISGDEEG 80  
 QY 193 QIKKVCNERRAP-----QSIGSLAVLFPSDS--KNDDGFAIY--BEITACS---S 241  
 DB 81 RLGGQSSNPNHSHFVIEFQVFNKLQVITFKSDPSNERETGFAAYVAVDINECTDVID 140  
 QY 242 SPGFHDTGVLDKXGKYKACLAGY----- 266  
 DB 141 VPCSHFCNFI---GGFCGPPRYFLHDDMKNGCVACSGDVFALGELASPRYKPRP 197  
 QY 267 TGORCENLL-----EERRCSD-----PGPVNGYOKIT 294  
 DB 198 ENSRCEYQIRLEKGFQVVVTLRRDFVEAADSAGNCLDSLVFVAGDRGPGYCGH----- 253

QY 295 GGPGLIN-----GRHAK-I 307  
 DB 254 GPGPLINIERKSNALDIIFQDTLGGKKWKLRYHGDPMPCKEDFPNSVWEPKAKYVF 313  
 QY 308 GTVSPFCNNY-VLSG-----NEKTCQNGEMSGK---QYICAKCEPKISDLVR 357  
 DB 314 RDVQVITCLDGFVEVERVATSFYSTQNGKMSNKLKCPV---DCGIF----- 362  
 QY 358 RVLPMQVSRETLHQVLSAFAFKQKQSPVTKP--ALPGDDPMVQHLHTOLOVEICIS 416  
 DB 363 -----ESTENKVEDPESTLFGSV-----IRYCEE 388  
 QY 417 PFY--RLGSSRRRTCLRTGKMSGRA-----PSCIPICGKIBNTAPKTQGLRPMWQAIY 469  
 DB 389 PYYVMGEGGEGHCAANGSVNVEYGLPELPKCPVPG-----VP-----REFPEEK-- 435  
 QY 470 RRTSGVHDSLHKGMFLV-----CSGALVNESTVVAAHCVTDLGKVTMIKTDKLV 524  
 DB 436 QRITGSDADIKNPPMQVFPEDNPWAGALINBYWVLTAAHVVEGNEPPTM-----YV 487  
 QY 525 GKRYRDDDRDEKTIQSLQISAILHPYDPLL-----DADIALIKLIXARISRVQ 577  
 DB 488 GSTSVQTSRLAKS-KMLTPRHVFTHPEWKLEVPBGRTNFDNDIALVRLKDPVMPGPTVS 546  
 QY 578 PICLAASRDISTFOESHITVAGMNVLAIVRSDFKND---TLRSGVSVVDSILCEQH 634  
 DB 547 PILTPGSSDYNMLDDGLGISGCG-----RTE--KRDAVRLKARLPAIPRKCEYK 599  
 QY 635 EDHGIPVS-----VTDNMCASMEPTAPSDICTAETGTGIAAVSPGRASPEPRHMLGL 688  
 DB 600 VER--PDADEAVYFPPNMICAGGE--KGMDSCKSGGAFVADP---NDKTKFYAAGL 652  
 QY 689 VSWSYDKTCSHRSTAFKTLPRKDWIERMK 720  
 DB 653 VSWG--PQCG--TYGLYTRVKNYVDMIMTKMQ 680

RESULT 10  
 A56318  
 enteropeptidase (EC 3.4.21.9) precursor [validated] - human  
 N:Alternate names: enterokinase  
 C:Species: Homo sapiens (man)  
 C>Date: 19-May-1995 #sequence\_revision 09-Aug-1996 #text\_change 09-Jul-2004  
 C:Accession: A56318; B43090  
 R:Kittamoto, Y.; Velle, R.A.; Donis-Keller, H.; Sadler, J.E.  
 Biochemistry 34, 4562-4568, 1995  
 A>Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic  
 A:Reference number: A56318; MUID:95234679; PMID:7718557  
 A:Accession: A56318  
 A:Molecule type: mRNA  
 A:Residues: 1-1019 <KIT>  
 A:Cross-references: UNIPROT:P98073; GB:U09860; NID:g746412; PIDN:AA050138.1; PID:g746413  
 R:Kittamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994  
 A>Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease composed  
 A:Reference number: A43090; MUID:94329561; PMID:8052624  
 A:Accession: B43090  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 749-1019 <KIT>  
 A:Cross-references: GB:U09860  
 C:Comment: The mechanism of association with the membrane of the intestinal brush border  
 (noted below) or with amino-terminal myristoylation of the heavy chain.  
 A:Gene: GDB:PRS37  
 A:Cross-reference: GDB:384083; OMIM:226200  
 A:Map position: 21q21-21q21  
 C:Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)  
 ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve  
 ducts.  
 C:Function: cleaves activation peptide from trypsinogen to produce active trypsin  
 A:Description: cleaves activation peptide from trypsinogen to produce active trypsin







JX0210  
 protein C (activated) (BC 3.4.21.69) precursor - mouse  
 N/Alternate names: vitamin K-dependent serine proteinase  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: JX0210  
 J/Ida, N.; Sato, M.; Teujiura, A.; Iwase, R.; Hashimoto-Gotoh, T.  
 R. Biochem. 111, 491-495, 1992  
 A/Title: Isolation and characterization of a mouse protein C cDNA.  
 A/Reference number: JX0210; MUID:92316897; PMID:1618739  
 A/Accession: JX0210  
 A/Molecule type: mRNA  
 A/Residues: 1-461 <TAD>  
 A/Cross-references: UNIPROT:P33587; GB:D10445; NID:G220385; PIDN:BA01235.1; PID:G220386  
 A/Experimental source: liver  
 C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re  
 B.  
 C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxylu  
 F/1-33/Domain: signal sequence #status predicted <SIG>  
 F/27-85/Domain: Gla domain homology <Gla>  
 F/34-41/Domain: propeptide #status predicted <PRO>  
 F/42-186,199-461/Product: protein C #status predicted <PRC>  
 F/42-186/Domain: light chain #status predicted <PLC>  
 F/91-130/Domain: EGF homology <EG1>  
 F/139-461/Domain: heavy chain #status predicted <PCH>  
 F/139-461/Domain: activation peptide #status predicted <ACT>  
 F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>  
 F/212-445/Domain: trypsin homology <TRY>  
 F/47,48,55,57,60,61,66,67,70,76/Modified site: gamma-carboxylglutamic acid (Glu) #status  
 F/112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F/121-130,139-150,146-159,161-174,182-319,238-254,373-387,398-426/Disulfide bonds: #stat  
 F/214,290,355/Binding site: carbohydrate (Aen) (covalent) #status predicted  
 F/253,299,402/Active site: His, Asp, Ser #status predicted  
 Query Match 8.1%; Score 320; DB 1; Length 461;  
 Best Local Similarity 23.9%; Pred. No. 6e-14;  
 Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;  
 152 WT-----HAKPGF-----VIQLRFVMSLEFDYVCOYDVEVDGDRDGOITKRV 198  
 14 WGISSTPAHDPDPVPSSEHAAQVLRVRANSFLE-----EMRPG-SLERECMEEI 62  
 199 CGNERPAPI-OSIGSSHLVLFHSGSNPDSFAHYEITACSSPCFHOCTCLDXAGS 257  
 63 CDEBAOEIRFQWVDTLAFWI-----KYPDDQCSAPPLDHCDCPCGGETCI-DGIGS 116  
 258 YKCACTAGYTGQRCENLLEERNCSDPGAPVNGYOKITGSPGL-----INGRAKIGTVV 311  
 117 FSCSCDGMGEKPCQQLRPDC-----RVNNGGLHVCLEESNRCA----- 160  
 312 SFPCNNSYVLSGNEK-----TCQNGEWGSKOPICAKREPKISDLVRRRLPMOV 364  
 161 ---CAPVEIADDMRCKSTVNFPCGKGRWIEK-----KRIIL----- 196  
 365 QSRPTPLHQLYSAFNSQKQASAPTKKRALPBGDLPMGYQHLYTQLQYECISPTRYLGS 424  
 197 -KRRTD-----EDELPPD----- 210  
 425 SRRRTCLRTGKMGSRAPICPIGKIENITAPKTQGLRMPQAAIYRRTSGVNDLSKGA 484  
 211 -----RIVNGTLTK-QG-DSPQAILL-----DSKKK-- 235  
 485 WFLVCSGALVNTVVAAHCVTDLGKVTMTKADLKVILGKFRDDEKTIQSLQIS 544  
 236 --LACGVLHTSVTLTAHCEVETKLT-----VRLGEY--DLRRDMHELDIDIK 283  
 545 AIIHNPVDPILLADAIILKLDKARISTRVPICL-----AASRDISTSGEHIIVAG 600  
 284 EILVHPVNTSSNDIALILKAPATLSKIVPICPNNGLAQOELLQAGQETVVI--G 341  
 601 MNVLADVRSPGKNDTL-----RSGVSVSVSLCEEQHEDHGIPVSVTDMNFC 649

Db 342 WGYQSRIRKDRNRKFFILTFIRIPLVARNECEVKNV-----VSENMLC 387  
 Qy 650 ASMEPTAPSDICFAETGAAVAFPPGRASPEPMHLMGLVSWGYDTCSHRLSTA-PTKV 708  
 Db 388 AGIITGNT-RDACGDSGGPMVVFPRG-----TWFLVGLVSKG--EGCGHTNNYGIYTKV 438  
 Qy 709 LPRKDWI 715  
 Db 439 GSVLKNWI 445  
 RESULT 13  
 A43090  
 enteropeptidase (BC 3.4.21.9) precursor [validated] - bovine  
 N/Alternate names: enterokinase  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: A43090; A48874; A61436  
 R/Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994  
 A/Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo  
 A/Reference number: A43090; MUID:94329561; PMID:8052624  
 A/Accession: A43090  
 A/Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A/Residues: 1-1035 <KIT>  
 A/Molecule type: mRNA  
 A/Cross-references: UNIPROT:P98072; GB:U09859; NID:G746410; PIDN:AA040026.1; PID:G746411  
 A/Experimental source: small intestine  
 R/Lavalle, E.R.; Rememulla, A.; Racie, L.A.; DiBlaasio, E.A.; Ferenz, C.; Grant, K.L.; J  
 J. Biol. Chem. 268, 23311-23317, 1993  
 A/Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of bc  
 A/Reference number: A48874; MUID:94043122; PMID:8226855  
 A/Accession: A48874  
 A/Molecule type: mRNA  
 A/Residues: 801-1035 <LAV>  
 A/Cross-references: GB:D19663; NID:G416131; PIDN:AA16035.1; PID:G416132  
 A/Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.  
 A/Reference number: A61436; MUID:92189715; PMID:1799406  
 A/Accession: A61436  
 A/Molecule type: Protein  
 A/Residues: 801-807, 'Y', 809-827 <LIG>  
 C/Comment: The mechanism of association with the membrane of the intestinal brush border  
 C/Keywords: glycoprotein; hydrolysis; intestine; serine proteinase; transmembrane protein.  
 C/Comment: Conversion from membrane-bound to soluble forms may involve further processing  
 C/Complex: mature enteropeptidase is variously reported to contain two (heavy and light)  
 1:ide linked  
 C/Function: cleaves propeptide from trypsinogen to produce active trypsin  
 A/Pathway: intestinal digestive hydrolyase cascade  
 C/Superfamily: enteropeptidase; Ctr/Cis repeat homology; LDL receptor ligand-binding rep  
 C/Keywords: glycoprotein; hydrolysis; intestine; serine proteinase; transmembrane protein.  
 F/22-38/Domain: transmembrane #status predicted <TM>  
 F/52-117/Product: enteropeptidase mini chain #status predicted <MC>  
 F/118-800/Product: enteropeptidase heavy chain #status predicted <HC>  
 F/199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F/358-520/Domain: Ctr/Cis repeat homology <CTR>  
 F/542-647/Domain: LDL receptor ligand-binding repeat homology <LDL1>  
 F/659-693/Domain: scavenger receptor cysteine-rich domain homology <SRCR>  
 F/801-1035/Product: enteropeptidase light chain #status predicted <LC>  
 F/801-1030/Domain: trypsin homology <TRY>  
 F/116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Binding  
 F/788-912,926-842,926-993,957-972,983-1011/Disulfide bonds: #status predicted  
 F/841,892,987/Active site: His, Asp, Ser #status predicted  
 Query Match 8.0%; Score 317.5; DB 1; Length 1035;  
 Best Local Similarity 24.6%; Pred. No. 2.1e-13;  
 Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;



A/Cross-references: UNIPROT:Q9JUT7; DDBJ:AB049189

A/Experimental source: strain Male, 7-week-old

R/Satom, S.; Yamasaki, Y.; Tsuzuki, S.; Hitomi, Y.; Iwanaga, T.; Fushiki, T.

Biochem. Biophys. Res. Commun. 287, 995-1002, 2001

A/Title: A role for membrane-type serine protease (MT-SPL) in intestinal epithelial turn

A/Reference number: JC7775; PMID:11573963

A/Contents: Small intestine

A/Accession: JC7775

A/Molecule type: mRNA

A/Accession: 1-855 <SAT>

A/Cross-references: DDBJ:AB037898

C/Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease

of specific proteins or peptides on the brushborder membranes. It also participates in

lial migration and/or cell loss.

C/Genetics:

A/Genes: mt-spl

A/Map position: basolateral cell surface

C/Superfamily: membrane-bound arginine-specific serine proteinase

C/Keywords: protein digestion

Query Match 7.9%; Score 313; DB 2; Length 855;

Best Local Similarity 21.4%; Pred. No. 3.4e-13;

Matches 151; Conservative 78; Mismatches 227; Indels 250; Gaps 33;

82 HPG--CTIFENCKSCRNKSGWGLDLPYKGFYCAECRAGWYGDCKRCQVLRAPKQI 139

324 HPGFATFFQLPKM---SSCGGLSE--AQGFSSP---YYPG----- 358

140 LLESLPLNACEWTIHAKEGVVQLRFLVMSLEFDY---CQDYVEVRDGNRQGI 195

359 ---HYPNINCTWNIKVPNNNNVAKRFELFVLDPNIPVSGCTKDYVEING----- 406

196 KRVGNERPAPIOSLSLHLFHSDSKXNDFGHAYEETACSSSPC-----FHDGTC 250

407 EKFCGERSQFVSSNSKITVHFSDHSYTDGFLAEY--LSYSDNDCPQMFCKTGRC 464

251 VL-----DKAGSYKACIAGY---TGRCENTL-----ERNCS 281

465 IRKDLRCGMADCPDGERHRCNATHQFCKQFCKPLFWCDSVNDGSDSDESGS 524

282 DPGSPVNGYQKITGGPGLINGRAKIGTVSFFCNSIVL---SGNEKRTCOQNGMSG 337

525 CPAG-----SFKCSNGKCLPQSQQCNGKDCGSDSDEAS 558

338 KQPICAKCREPKISDLVRRVRLPMQVSRETPHLQLYSAFQKXQLQSAPTKKPALPG 397

559 CDVNAVAVSC----- 567

398 DLPWGYOHLHTQYECISPFYRLGSSRRCTLRGKMSGRAPSCIPICGKIENITAKT 457

568 -----TKYTYRC-----QNGCLINKN-----PBC---DGKDCSDGSDSDE 599

458 Q---GLR-----WPMQAIYRTSGVHDSLHKGAMFLVCSGALVN 495

600 KNCDCGLRSFTQARVVGTVNADGEWPMQVSLHALGQ-----H-----LCGASLIS 647

496 ERTVVAACHCTDGLKTYMTIAD---LKVVLGKFRDDBDEKTIQSLQISAILIHPNY 552

648 PDWLVAACHFQD---ETIFKYSHTWTAFGL--LDPQSKRSASAGVQEHKIKRIITPSF 703

553 DPILLDDIATLKLKLDKARISTRVOPICLASRDLSFQESHITVAGMNVLADVRSPGF 612

704 NDFPFDDIALLELEKPAEYISTVVRPICLPDNTHTVPAGKA--IWTGWM---GHTKEGGT 758

613 KNDTLRSGVSVVDLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDICTAETGG-IAAV 671

759 GALLIQGEIRIVINQTCBEL---LPQITPRMMCVGF--LSGGVDSQCGSDSGPLSSV 812

672 SFPGRASBPFRWMLMGLVMSYDKTCSHRLST-AFTKVLPRKDWIE 716

813 EKDGRI-----FQAGVWSG--EGCAQRNKPQVYTRIPVYRDWIK 850

Search completed: July 12, 2005, 17:10:04

Job time : 55 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 12, 2005, 17:08:16 ; Search time 173 Seconds

(without alignments)  
2131.197 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945  
Sequence: 1 MEIGCWTLQTLFLQLLLIS.....LSTAFKVLFPKDMIRNMK 720

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

1: uniprot\_03:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	3945	100.0	2 O6UXH9	O6uxh9 homo sapien
2	3936	99.8	2 O6N062	O6n062 homo sapien
3	3921.5	99.4	2 O96JW2	O96jw2 homo sapien
4	3612	91.6	2 O8BU25	O8bu25 m mus muscu
5	3612	91.6	2 O8K2B8	O8k2b8 mus musculu
6	2823	71.6	2 O6DIV5	O6div5 xenopus tro
7	2059	52.2	2 O71RE9	O71re9 homo sapien
8	949	24.1	2 O9Y432	O9y432 homo sapien
9	678	17.2	2 O8T981	O8t981 tachypleus
10	672	17.0	1 LFC_TACTR	Lfc_tactr
11	665	16.9	1 LFC_CARRO	Lfc_carro
12	665	15.4	2 O26423	O26423 carcinosc
13	608.5	15.4	2 O868H7	O868h7 branchiost
14	604	15.3	2 O868H5	O868h5 branchiost
15	597	15.1	2 O868H6	O868h6 branchiost
16	576.5	14.6	2 O868H4	O868h4 branchiost
17	507.5	12.9	2 O6GPF9	O6gpf9 xenopus lae
18	490.5	12.4	2 O6U1O8	O6u1o8 gallus gall
19	489.5	12.4	2 O6PUJ1	O6puj1 xenopus lae
20	483	12.2	2 O9JIS9	O9jis9 rattus norv
21	482.5	12.2	2 O8CHN8	O8chn8 rattus norv
22	482	12.2	2 O8AXR1	O8axr1 xenopus lae
23	478	12.1	1 CRAR_HUMAN	CRAR_HUMAN
24	475	12.0	1 CRAR_MOUSE	CRAR_MOUSE
25	468	11.9	2 O8GFS4	O8gfs4 mus musculu
26	467	11.8	2 O8CGA3	O8cga3 rattus norv
27	466	11.8	2 O8AXR0	O8axr0 xenopus lae
28	459	11.6	2 O8CD27	O8cd27 mus musculu
29	457	11.6	2 O9PVY2	O9pyv2 triakis ecy
30	452	11.5	2 O920S0	O920s0 mus musculu
31	448	11.4	2 O9PVY3	O9pyv3 cyprinus ca

32	447	11.3	2 O6Q1O9	O6q1o9 gallus gall
33	436.5	11.1	2 O7ET70	O7et70 lampetra ja
34	428	10.8	1 C1R_MOUSE	C1r_MOUSE
35	424	10.7	2 O9JTS8	O9jts8 rattus norv
36	421.5	10.7	2 O9PVY4	O9pyv4 xenopus lae
37	420	10.6	2 O9QX84	O9qx84 rattus norv
38	417	10.6	2 O91MP0	O91mp0 mus musculu
39	416.5	10.6	2 O8CFG9	O8cfg9 mus musculu
40	412	10.4	2 O923J8	O923j8 mus musculu
41	403.5	10.2	1 C1R_HUMAN	C1R_HUMAN
42	401.5	10.2	2 O8CHP7	O8chp7 cavia porce
43	401.5	10.2	2 O81ND8	O81nd8 halocynthia
44	400.5	10.2	2 O01654	O01654 halocynthia
45	400.5	10.2	2 O9DGC2	O9dgc2 cyprinus ca
46	398.5	10.1	2 O7ZT69	O7zt69 lampetra ja
47	395	10.0	2 O8CRG8	O8crg8 mus musculu
48	384	9.7	2 O01655	O01655 halocynthia
49	382.5	9.7	2 O01655	O01655 lampetra ja
50	382	9.7	2 O8AW90	O8aw90 lampetra ja
51	381	9.7	2 O9PS25	O9ps25 sus scrofa
52	380.5	9.6	2 O69DK8	O69dk8 sus scrofa
53	378.5	9.6	1 CASP_MESAU	CASP_MESAU
54	376	9.5	2 O9JTB3	O9jtb3 rattus norv
55	372.5	9.4	2 O81AD7	O81ad7 halocynthia
56	371.5	9.4	2 O9QX90	O9qx90 rattus norv
57	370	9.4	2 O8CG14	O8cg14 mus musculu
58	369	9.4	2 O8BTC4	O8btc4 mus musculu
59	368	9.3	2 O9DGC1	O9dgc1 cyprinus ca
60	366	9.3	2 O9DGC0	O9dgc0 cyprinus ca
61	364	9.2	2 O8CH28	O8ch28 mus musculu
62	364	9.2	2 O8VBV4	O8vbv4 mus musculu
63	357	9.0	2 O6DUJ6	O6duj6 cyprinus ca
64	354	9.0	2 O91674	O91674 xenopus lae
65	342	8.7	2 O8R099	O8r099 mus musculu
66	340.5	8.6	2 O70542	O70542 rattus norv
67	340.5	8.6	2 O6PET1	O6pet1 rattus norv
68	339.5	8.6	2 O70W31	O70w31 oncorhynch
69	335	8.5	2 O7PY92	O7py92 anopheles g
70	335	8.5	2 O69BL0	O69bl0 manduca sex
71	334	8.5	2 O8AYE4	O8aye4 brachydanio
72	334	8.5	2 C1S_HUMAN	C1S_HUMAN
73	331.5	8.4	1 ENTK_HUMAN	ENTK_HUMAN
74	330.5	8.4	1 ENTK_PIG	ENTK_PIG
75	329.5	8.4	1 CSM1_HUMAN	CSM1_HUMAN
76	329	8.3	1 CSM1_MOUSE	CSM1_MOUSE
77	328	8.3	1 ST14_HUMAN	ST14_HUMAN
78	318	8.1	1 CSM2_HUMAN	CSM2_HUMAN
79	317.5	8.0	1 ENTK_BOVIN	ENTK_BOVIN
80	316.5	8.0	1 PRTC_MOUSE	PRTC_MOUSE
81	315	8.0	1 FA7_RABIT	FA7_RABIT
82	314.5	8.0	1 FA7_CHICK	FA7_CHICK
83	314	8.0	1 ST14_MOUSE	ST14_MOUSE
84	313	7.9	2 O9JUI7	O9jui7
85	311	7.9	2 O9JUI7	O9jui7
86	310.5	7.9	2 O7T3B6	O7t3b6 brachydanio
87	310.5	7.9	2 O7T3B6	O7t3b6 brachydanio
88	309.5	7.8	2 O6PF94	O6pf94 mus musculu
89	309.5	7.8	2 TMS6_MOUSE	TMS6_MOUSE
90	305	7.7	1 PRTC_CANFA	PRTC_CANFA
91	304	7.7	1 ENTK_MOUSE	ENTK_MOUSE
92	302.5	7.7	1 FA7_MOUSE	FA7_MOUSE
93	301.5	7.6	2 O8JHD0	O8jhd0 brachydanio
94	300.5	7.6	2 O6ITD0	O6itd0 pseudonaja
95	299.5	7.6	2 O6ITD9	O6itd9 pseudonaja
96	299	7.6	2 O80YN4	O80yn4 rattus norv
97	298.5	7.6	2 O90YK1	O90yk1 brachydanio
98	298.5	7.6	2 O6P7I9	O6p7i9 xenopus lae
99	297.5	7.5	2 O9BU99	O9bu99 homo sapien
100	297.5	7.5	2 O8CAN9	O8can9 mus musculu
101	297	7.5	1 PRTC_PIG	PRTC_PIG
102	296	7.5	1 PRTC_RABIT	PRTC_RABIT
103	295.5	7.5	2 O8CIR9	O8cir9 mus musculu
104	295.5	7.5	2 O804X2	O804x2 fugu rubrip

105	295	7.5	425	2	Q804X7	Q804X7 gallus gall	178	263	6.7	653	2	Q8VCS4	Q8VCS4 mus musculus
106	294	7.5	461	2	Q68FY8	Q68FY8 rattus norv	179	262.5	6.7	300	2	Q81P94	Q81P94 aurelia aur
107	293.5	7.4	407	1	FA7_BOVIN	P22457 bos taurus	180	262.5	6.7	461	1	FA9_HUMAN	P00740 homo sapien
108	293	7.4	430	2	Q804X0	Q804X0 figu rubrip	181	262.5	6.7	461	1	FA9_PANTH	Q95nd7 pan troglod
109	292	7.4	461	1	PRTC_RAT	P31394 rattus norv	182	262.5	6.7	1042	1	CORI_HUMAN	Q95G55 homo sapien
110	291.5	7.4	390	2	Q69DJ3	Q69DJ3 sus scrofa	183	262	6.6	477	1	URRT_DESRO	P15638 desmodus ro
111	291	7.4	376	1	FA10_TROCA	P81428 tropidechis	184	261.5	6.6	284	2	Q8AXQ8	Q8AXQ8 xenopus lae
112	291	7.4	475	1	Q804W9	Q804W9 figu rubrip	185	261.5	6.6	442	1	UROK_PIG	P04155 sus scrofa
113	289.5	7.3	466	2	Q6SAP5	Q6SAP5 felis silve	186	261.5	6.6	561	1	Q7QDTP9	Q7QDTP9 anopheles g
114	288.5	7.3	802	2	Q6UXD8	Q6UXD8 homo sapien	187	261	6.6	431	1	UROK_HUMAN	P00749 homo sapien
115	287.5	7.3	811	1	TMS6_HUMAN	Q81u80 homo sapien	188	260.5	6.6	433	1	UROK_BOVIN	Q95589 bos taurus
116	285.5	7.2	300	2	Q7P2D2	Q7P2D2 anopheles g	189	260.5	6.6	264	2	Q9EQZ8	Q9EQZ8 rattus norv
117	285.5	7.2	452	1	FA9_CANFA	P18540 canis famli	190	260.5	6.6	456	2	Q7TT43	Q7TT43 mus musculus
118	285	7.2	504	2	Q6PGW7	Q6PGW7 brachydanio	191	260.5	6.6	452	2	Q6PAG2	Q6PAG2 xenopus lae
119	284	7.2	432	2	Q6GNA2	Q6GNA2 xenopus lae	192	259	6.6	245	2	CTRB_GADMO	P80646 gadus morhu
120	284	7.2	974	2	Q9OWD8	Q9OWD8 bufo japoni	193	259	6.6	416	1	FA9_BOVIN	P00741 bos taurus
121	283.5	7.2	482	1	FA10_RAT	Q63207 rattus norv	194	259	6.6	474	2	Q8JHC8	Q8JHC8 brachydanio
122	283.5	7.2	589	2	Q6PJA5	Q6PJA5 homo sapien	195	259	6.6	581	2	Q9XZM7	Q9XZM7 strongyloce
123	283	7.2	376	1	FA10_HOPST	P83370 hoplocephal	196	258.5	6.6	683	2	Q8MRH5	Q8MRH5 drosophila
124	282.5	7.2	320	2	Q8CIR7	Q8CIR7 rattus norv	197	258.5	6.6	786	1	STUB_DROME	Q05319 drosophila
125	282	7.1	456	1	PRTC_BOVIN	Q95md9 ornithorhyn	198	258.5	6.6	787	2	Q9VEY6	Q9VEY6 gadus morhu
126	282	7.1	469	2	Q9GMD9	Q9GMD9 ornithorhyn	199	258	6.5	263	2	Q9PWQ6	P16227 papio cynoc
127	282	7.1	1466	2	Q6GJX4	Q6GJX4 brachydanio	200	258	6.5	433	1	UROK_PAPCY	P16227 papio cynoc
128	281.5	7.1	476	2	Q6GJX4	Q6GJX4 xenopus lae	201	258	6.5	545	2	Q7OKS0	Q7OKS0 anopheles g
129	281.5	7.1	558	2	Q6L7I1	Q6L7I1 rattus norv	202	258	6.5	612	2	Q804W7	Q804W7 figu rubrip
130	281	7.1	481	1	FA10_MOUSE	Q88947 mus musculu	203	257.5	6.5	1004	2	P79953	P79953 xenopus lae
131	281	7.1	492	1	FA10_BOVIN	P00743 bos taurus	204	257	6.5	568	2	Q7Q8L2	Q7Q8L2 anopheles g
132	280.5	7.1	264	1	CTRL_HUMAN	P40313 homo sapien	205	256.5	6.5	264	2	Q9DDP8	Q9DDP8 mus musculus
133	280.5	7.1	269	2	Q8IUMO	Q8IUMO homo sapien	206	256.5	6.5	264	2	Q9EROS	Q9EROS mus musculus
134	280	7.1	562	1	TPA_HUMAN	P00750 homo sapien	207	255.5	6.5	268	2	Q642S8	Q642S8 xenopus tro
135	278.5	7.1	466	1	FA7_HUMAN	P08709 homo sapien	208	255.5	6.5	763	2	Q31430	Q31430 lampetra ja
136	278.5	7.1	824	1	Q6ICC2	Q6ICC2 homo sapien	209	255	6.5	325	2	Q15944	Q15944 sarcophaga
137	278	7.0	408	2	Q804X5	Q804X5 drosophila	210	255	6.5	845	2	Q6GRS4	Q6GRS4 xenopus lae
138	278	7.0	433	2	Q804X5	Q804X5 gallus gall	211	255	6.5	315	2	Q7TT44	Q7TT44 mus musculus
139	278	7.0	488	1	FA10_HUMAN	P00742 homo sapien	212	254.5	6.5	374	2	Q7OCC5	Q7OCC5 anopheles g
140	278	7.0	1113	1	CORI_MOUSE	Q93319 mus musculu	213	254.5	6.5	461	2	Q95ND6	Q95ND6 pan troglod
141	277	7.0	539	1	TPA_RAT	P18637 rattus norv	214	254	6.4	314	2	Q9VR15	Q9VR15 drosophila
142	276.5	7.0	655	1	HGFA_HUMAN	Q04756 homo sapien	215	254	6.4	617	1	THRB_RAT	P18232 rattus norv
143	276.5	7.0	679	2	Q96PQ8	Q96PQ8 homo sapien	216	253.5	6.4	487	2	Q9NZP8	Q9NZP8 homo sapien
144	276	7.0	559	2	Q6P7U0	Q6P7U0 mus musculu	217	253.5	6.4	618	2	Q6GNK4	Q6GNK4 xenopus lae
145	275.5	7.0	1134	2	Q7RTY7	Q7RTY7 homo sapien	218	253.5	6.4	628	2	Q9VER6	Q9VER6 drosophila
146	274.5	7.0	625	1	THRB_BOVIN	P00735 bos taurus	219	253	6.4	471	2	Q804X6	Q804X6 gallus gall
147	274.5	7.0	654	2	Q6ONF4	Q6ONF4 canis famli	220	253	6.4	616	2	Q97507	Q97507 sus scrofa
148	274.5	7.0	1235	2	Q659T9	Q659T9 clona intes	221	253	6.4	1070	2	P91972	P91972 aplysia cal
149	274.5	7.0	3670	1	CSM3_HUMAN	Q72407 homo sapien	222	252	6.4	260	2	Q6P2V9	Q6P2V9 xenopus tro
150	273.5	6.9	443	2	Q8JHC3	Q8JHC3 brachydanio	223	252	6.4	261	2	Q66HW9	Q66HW9 brachydanio
151	273.5	6.9	517	2	Q8KOD2	Q8KOD2 mus musculu	224	252	6.4	607	2	Q6DFJ5	Q6DFJ5 xenopus lae
152	273.5	6.9	566	1	TPA_BOVIN	Q28198 bos taurus	225	251.5	6.4	261	2	Q7PG94	Q7PG94 anopheles g
153	273	6.9	366	2	Q9QX85	Q9QX85 rattus norv	226	251	6.4	285	2	Q8CIP7	Q8CIP7 rattus norv
154	273	6.9	560	2	Q14520	Q14520 homo sapien	227	251	6.4	337	2	Q804W8	Q804W8 figu rubrip
155	273	6.9	2796	1	CSM3_MOUSE	Q80C79 mus musculu	228	250.5	6.3	347	1	HPT_RABIT	P19007 cycctolagus
156	272.5	6.9	321	2	Q6WZL2	Q6WZL2 homo sapien	229	250	6.3	306	1	BSS4_MOUSE	Q9ER10 mus musculu
157	271.5	6.9	244	1	KLKE_HUMAN	Q92876 homo sapien	230	250	6.3	562	2	Q8S0Z3	Q8S0Z3 sus scrofa
158	271.5	6.9	461	2	Q6IEE4	Q6IEE4 rattus norv	231	250	6.3	845	2	Q61Z06	Q61Z06 xenopus lae
159	271	6.9	433	2	Q8MHT7	Q8MHT7 cycctolagus	232	250	6.3	1379	2	Q9V4NE	Q9V4NE drosophila
160	271	6.9	433	2	Q8MHT7	Q8MHT7 cycctolagus	233	250	6.3	1397	2	Q7KQD9	Q7KQD9 drosophila
161	270	6.9	559	1	TPA_MOUSE	P11214 mus musculu	234	249.5	6.3	400	2	Q27081	Q27081 cycchyleus
162	270	6.9	477	1	URRT_DESRO	P98119 desmodus ro	235	249.5	6.3	875	1	NETR_HUMAN	P56710 homo sapien
163	270	6.8	490	1	FA10_RABIT	Q19045 cycctolagus	236	249	6.3	263	2	Q6GPI1	Q6GPI1 homo sapien
164	269	6.8	261	2	Q6DHDB	Q6DHDB brachydanio	237	249	6.3	263	2	Q9CRJ5	Q9CRJ5 m mus muscu
165	269	6.8	643	2	Q97506	Q97506 sus scrofa	238	248.5	6.3	459	1	FA9_MOUSE	P16234 mus musculu
166	269	6.8	833	2	Q96442	Q96442 strongyloce	239	248.5	6.3	645	2	Q7PWE4	Q7PWE4 anopheles g
167	267.5	6.8	268	2	Q6GQEB9	Q6GQEB9 xenopus lae	240	248.5	6.3	1135	2	Q7QI37	Q7QI37 anopheles g
168	267	6.8	339	2	Q9QX91	Q9QX91 rattus norv	241	248	6.3	259	2	Q6AZC2	Q6AZC2 brachydanio
169	267	6.8	455	2	Q7SY86	Q7SY86 xenopus lae	242	248	6.3	261	2	Q9W7Q4	Q9W7Q4 paratichthy
170	267	6.8	868	2	Q9Y1V3	Q9Y1V3 polyanthroca	243	248	6.3	263	1	CTRB_HUMAN	P17538 homo sapien
171	266	6.7	352	2	Q7KVM3	Q7KVM3 drosophila	244	248	6.3	340	2	Q800I7	Q800I7 meleagris g
172	265.5	6.7	250	2	Q9V514	Q9V514 drosophila	245	248	6.3	638	1	KAL_HUMAN	P03952 homo sapien
173	264.5	6.7	431	1	URTB_DESRO	P98121 desmodus ro	246	248	6.3	764	1	CFAB_PANTH	Q86440 pan troglod
174	264.5	6.7	618	1	THRB_MOUSE	P19221 mus musculu	247	248	6.3	775	2	Q6P550	Q6P550 mus musculu
175	264	6.7	653	1	HGFA_MOUSE	Q97098 mus musculu	248	248	6.3	991	2	Q6N2M2	Q6N2M2 mus musculu
176	263.5	6.7	263	2	Q7SX97	Q7SX97 brachydanio	249	247.5	6.3	307	2	Q7TMK0	Q7TMK0 mus musculu
177	263	6.7	270	2	Q7QI44	Q7QI44 anopheles g	250	247.5	6.3	311	2	Q9W2C2	Q9W2C2 drosophila

251	247.5	6.3	991	1	BMP1_MOUSE	P98063	mus musculus	324	237.5	6.0	415	2	Q7PY21	Q7PY21	anopheles g
252	247	6.3	235	2	Q28731	Q28731	oryctolagus	325	237.5	6.0	735	2	O57381	O57381	xenopus lae
253	247	6.3	270	2	Q7PKE7	Q7PKE7	anopheles g	326	237.5	6.0	735	2	O66K13	O66K13	xenopus lae
254	247	6.3	275	1	TRYT_CANFA	P15944	canis famli	327	237.5	6.0	810	1	PLMN_ERIEU	Q29485	eritaceus e
255	247	6.3	354	2	Q917V4	Q917V4	drosoephila	328	237	6.0	237	2	O91515	O91515	fugu rubrip
256	247	6.3	366	2	Q81924	Q81924	domlyx mori	329	237	6.0	263	1	CTRB_RAT	P07338	rattus norv
257	247	6.3	764	1	CFAB_HUMAN	P00751	homo sapien	330	237	6.0	263	2	O6PES4	O6PES4	xenopus lae
258	247	6.3	966	1	BMP1_HUMAN	P13497	homo sapien	331	236.5	6.0	251	2	Q7QW2	Q7QW2	anopheles g
259	246.5	6.2	235	2	Q90387	Q90387	cynops pyr	332	236.5	6.0	274	1	MCTE_RAT	P50343	rattus norv
260	246.5	6.2	264	2	Q9D960	Q9D960	mus musculu	333	236.5	6.0	707	1	BMP1_XENLA	P98070	xenopus lae
261	246.5	6.2	297	2	Q88781	Q88781	rattus ratt	334	236.5	6.0	751	2	O99JCB	Q99JCB	rattus norv
262	246.5	6.2	323	2	Q96Q64	Q96Q64	homo sapien	335	236	6.0	1013	2	O62381	O62381	mus musculu
263	246.5	6.2	347	1	HPT_ATEGE	P50417	ateles geof	336	236	6.0	239	2	Q7Q057	Q7Q057	anopheles g
264	246.5	6.2	622	1	THRB_HUMAN	P00734	homo sapien	337	235.5	6.0	812	1	PLMN_MOUSE	P20918	mus musculu
265	246.5	6.2	622	2	Q727B3	Q727B3	homo sapien	338	235.5	6.0	260	2	Q9W7Q3	Q9W7Q3	paralichthy
266	246	6.2	263	2	Q7PKB6	Q7PKB6	anopheles g	339	235.5	6.0	369	2	O6AXZ6	O6AXZ6	rattus norv
267	246	6.2	263	2	Q9D8X8	Q9D8X8	anopheles g	340	235.5	6.0	453	2	O812A6	O812A6	mus musculu
268	246	6.2	764	1	CFAB_GORGO	Q864V9	gorilla gor	341	235	6.0	270	1	TRYT_MERUN	P50342	meriones un
269	246	6.2	812	1	PLMN_BOVIN	P06868	bos taurus	342	235	6.0	336	2	Q7RTY5	Q7RTY5	homo sapien
270	245.5	6.2	265	2	Q804G1	Q804G1	brachydantio	343	235	6.0	345	2	Q28800	Q28800	pan troglod
271	245.5	6.2	369	2	Q7OKL1	Q7OKL1	anopheles g	344	235	6.0	524	2	Q7SXH8	Q7SXH8	brachydantio
272	245.5	6.2	467	2	Q967X8	Q967X8	panilius a	345	235	6.0	812	1	PLMN_RAT	O01177	rattus norv
273	245	6.2	248	2	Q7PKB8	Q7PKB8	anopheles g	346	235	6.0	1420	1	APOA_MACMU	P14417	macaca mula
274	245	6.2	263	2	Q6GNF7	Q6GNF7	xenopus lae	347	234.5	5.9	395	2	O9BZM1	Q9BZM1	homo sapien
275	245	6.2	638	2	Q8R0P5	Q8R0P5	mus musculu	348	234.5	5.9	453	1	TMS3_MOUSE	O6NP02	mus musculu
276	245	6.2	639	1	BMPH_STRPU	P98069	strongyloce	349	234.5	5.9	489	2	Q7Q432	Q7Q432	anopheles g
277	244.5	6.2	608	2	Q9PTW7	Q9PTW7	strophio ca	350	234.5	5.9	624	2	O9DATT3	Q9DATT3	mus musculu
278	244	6.2	263	2	Q9DC66	Q9DC66	mus musculu	351	234.5	5.9	575	2	O81RB8	O81RB8	mus musculu
279	244	6.2	322	2	Q920S2	Q920S2	mus musculu	352	234	5.9	263	1	CTRA_GADMO	P47786	gadus morhu
280	244	6.2	638	1	KAL_MOUSE	P26262	mus musculu	353	233.5	5.9	263	1	CTRA_GADMO	O74251	brachydantio
281	243.5	6.2	245	2	Q7PJQ0	Q7PJQ0	anopheles g	354	233.5	5.9	267	2	Q7S2S1	Q7S2S1	epitretus
282	243.5	6.2	285	2	O8CG42	O8CG42	rattus norv	355	233.5	5.9	420	2	Q90504	Q90504	epitretus
283	243.5	6.2	435	1	SNAX_PROME	P50049	dirosophila	356	233	5.9	273	2	O9XSM1	O9XSM1	ovis aries
284	243.5	6.2	764	1	CFAB_PONPY	Q864V1	pongo pygma	357	233	5.9	445	2	O8CJ17	O8CJ17	rattus norv
285	243	6.2	273	1	TRYT_SKEP	Q9XAM2	ovis aries	358	232.5	5.9	936	2	O81FX2	O81FX2	crasostrea
286	243	6.2	282	2	Q9D4I3	Q9D4I3	mus musculu	359	232.5	5.9	1013	2	O43897	Q43897	homo sapien
287	243	6.2	442	2	Q804X1	Q804X1	fugu rubrip	360	232.5	5.9	1013	2	O43897	Q43897	homo sapien
288	242.5	6.1	564	2	O8MKR1	O8MKR1	oryctolagus	361	232	5.9	283	2	Q7Q0S6	Q7Q0S6	anopheles g
289	242.5	6.1	574	2	O86R18	O86R18	ilyanassa o	362	232	5.9	416	1	HEPS_RAT	P14272	rattus norv
290	242.5	6.1	691	2	O57658	O57658	gallus gall	363	232	5.9	638	1	KAL_RAT	Q29461	bos taurus
291	242.5	6.1	1019	2	O57382	O57382	xenopus lae	364	231.5	5.9	269	2	EL2_BOVIN	Q91039	gadus morhu
292	242	6.1	247	2	Q7PKB9	Q7PKB9	anopheles g	365	231.5	5.9	270	2	O91039	Q91039	gadus morhu
293	241.5	6.1	279	2	Q99MS4	Q99MS4	mus musculu	366	231.5	5.9	371	2	O8CT16	O8CT16	rattus norv
294	241.5	6.1	314	2	Q7QLC2	Q7QLC2	anopheles g	367	231.5	5.9	483	2	O8T8X4	O8T8X4	drosoephila
295	241.5	6.1	416	2	O86T26	O86T26	homo sapien	368	231.5	5.9	483	2	O9VK10	O9VK10	anopheles g
296	241	6.1	306	2	Q7Q058	Q7Q058	anopheles g	369	231.5	5.9	624	2	O9SMK7	O9SMK7	oryctolagus
297	241	6.1	346	1	HPT_MESAU	Q51086	mesocricetu	370	231.5	5.9	666	2	O6VPUB	O6VPUB	drosoephila
298	241	6.1	818	2	O6PBA6	O6PBA6	brachydantio	371	231	5.9	242	2	O93266	Q93266	pseudopleur
299	241	6.1	1415	2	O8MJ16	O8MJ16	bos taurus	372	231	5.9	1008	2	Q93266	Q93266	pseudopleur
300	240.5	6.1	238	2	Q9W7Q6	Q9W7Q6	paralichthy	373	231	5.9	1012	2	O9W7M6	Q9W7M6	mus musculu
301	240.5	6.1	422	2	O8WVCI	Q8WVCI	homo sapien	374	230.5	5.8	295	2	O69E28	O69E28	homo sapien
302	240.5	6.1	441	2	Q7QKX8	Q7QKX8	anopheles g	375	230.5	5.8	244	2	O8QW3	O8QW3	anguilla ja
303	240	6.1	242	2	Q92099	Q92099	paranotoche	376	230	5.8	265	2	O9VVT3	O9VVT3	drosoephila
304	240	6.1	1059	2	Q72411	Q72411	homo sapien	377	230	5.8	318	2	Q7RTY9	Q7RTY9	homo sapien
305	239.5	6.1	240	2	Q98TH0	Q98TH0	engraulis j	378	230	5.8	372	2	O9YIK6	O9YIK6	anopheles g
306	239.5	6.1	406	1	HPT_HUMAN	P00738	homo sapien	379	230	5.8	607	2	O91001	O91001	gallus gall
307	239.5	6.1	1015	2	Q9Y6L7	Q9Y6L7	homo sapien	380	230	5.8	329	1	HPT_CANFA	P19006	canis famli
308	239.5	6.1	1078	2	Q9U000	Q9U000	homo sapien	381	229.5	5.8	374	2	Q9VUG2	Q9VUG2	drosoephila
309	239.5	6.1	3567	2	Q9ES77	Q9ES77	bos taurus	382	229.5	5.8	624	1	FAIL_MOUSE	Q9BK47	luidia foli
310	239	6.1	245	1	CTRA_BOVIN	Q7PZ03	anopheles g	383	229	5.8	267	2	O9BK47	Q9BK47	luidia foli
311	239	6.1	314	2	Q7PZ03	Q7PZ03	anopheles g	384	229	5.8	274	2	O924N9	Q924N9	mus musculu
312	239	6.1	436	1	HEPS_MOUSE	Q55453	mus musculu	385	229	5.8	722	2	O6NUP5	O6NUP5	xenopus lae
313	239	6.1	456	2	Q7QC30	Q7QC30	anopheles g	386	229	5.8	733	2	O9VTK9	O9VTK9	drosoephila
314	239	6.1	977	2	Q91925	Q91925	xenopus lae	387	229	5.8	845	2	O9DGR1	O9DGR1	xenopus lae
315	238.5	6.0	268	2	O46151	O46151	pacifastacu	388	229	5.8	347	2	O63927	O63927	mus sp. hap
316	238.5	6.0	578	2	O6Q017	O6Q017	bos taurus	389	228.5	5.8	352	2	O6UMB4	O6UMB4	gadus morhu
317	238	6.0	237	1	TRYP_ASTFL	P00765	atactus flu	390	228.5	5.8	513	2	O7PKB9	O7PKB9	anopheles g
318	238	6.0	263	1	CTR2_CANFA	P04813	canis famli	391	228.5	5.8	600	2	O17490	O17490	anopheles g
319	238	6.0	275	1	TRYT_PIG	Q9N241	bis scrofa	392	228.5	5.8	600	2	O7PV58	O7PV58	anopheles g
320	238	6.0	375	1	PCE_FACTR	P21902	tachyples	393	228.5	5.8	1084	2	Q9BP40	Q9BP40	halocynthia
321	238	6.0	435	2	O9NFY2	Q9NFY2	anopheles lae	394	228.5	5.8	2516	2	Q7TQ52	Q7TQ52	mus musculu
322	238	6.0	767	2	Q9DGR2	Q9DGR2	xenopus lae	395	228.5	5.8	2526	2	Q7TQ51	Q7TQ51	mus musculu
323	237.5	6.0	286	2	Q7QAX5	Q7QAX5	anopheles g	396	228.5	5.8					

397	228.5	5.8	2531	1	NTC1_MOUSE	Q01705	mus musculus	470	223	5.7	529	2	Q7Q239	Q7Q239	anopheles g
398	228.5	5.8	2531	2	QBK428	QBK428	mus musculus	471	222.5	5.6	411	2	Q9VUF0	Q9VUF0	drosophila
399	228.5	5.8	2531	2	Q7T050	Q7T050	mus musculus	472	222.5	5.6	417	2	HEPS_HUMAN	HEPS_HUMAN	homo sapien
400	228	5.8	3687	2	QW332	QW332	drosophila	473	222.5	5.6	434	1	UROK_CHICK	UROK_CHICK	gallus gall
401	227.5	5.8	227.5	2	Q91004	Q91004	gus musculus	474	222.5	5.6	455	1	TMS5_MOUSE	TMS5_MOUSE	mus musculus
402	227.5	5.8	242	1	TRV1_SALSA	P35031	salmo salar	475	222.5	5.6	790	1	PLMN_PIG	PLMN_PIG	sus scrofa
403	227.5	5.8	251	1	KUK2_HUMAN	Q9P093	homo sapien	476	222.5	5.6	954	2	Q75UQ6	Q75UQ6	acheaxneae
404	227.5	5.8	251	1	QB089	QB089	homo sapien	477	222	5.6	267	2	Q9V942	Q9V942	drosophila
405	227.5	5.8	349	2	Q28802	Q28802	pan troglod	478	222	5.6	269	1	EL2_PIG	Q921N4	sus scrofa
406	227.5	5.8	385	2	Q28659	Q28659	homo sapien	479	222	5.6	273	2	Q921N4	Q921N4	mus musculus
407	227.5	5.8	418	2	Q61E15	Q61E15	rattus norv	480	222	5.6	275	1	TRV2_HUMAN	P20231	homo sapien
408	227.5	5.8	714	2	Q7PWES	Q7PWES	rattus norv	481	222	5.6	275	1	TRV2_HUMAN	P20231	homo sapien
409	227	5.8	242	2	Q6R179	Q6R179	tautogolabr	482	222	5.6	275	2	Q6RTM8	Q6RTM8	homo sapien
410	227	5.8	263	2	Q7YS64	Q7YS64	xeopus lae	483	222	5.6	276	2	Q6RTM8	Q6RTM8	homo sapien
411	227	5.8	275	2	Q7YS62	Q7YS62	xeopus lae	484	222	5.6	282	2	Q6NZY1	Q6NZY1	homo sapien
412	227	5.8	324	1	TEST_MOUSE	Q9J1H7	mus musculus	485	222	5.6	422	1	DESI_HUMAN	Q9J1S2	homo sapien
413	227	5.8	336	2	Q80YD8	Q80YD8	mus musculus	486	222	5.6	423	2	Q6UWJ1	Q6UWJ1	homo sapien
414	227	5.8	417	2	Q8BZ10	Q8BZ10	mus musculus	487	222	5.6	561	2	Q7PN97	Q7PN97	anopheles g
415	227	5.8	488	2	Q9TYH4	Q9TYH4	schistosoma	488	222	5.6	860	2	Q7QAH1	Q7QAH1	anopheles g
416	227	5.8	1464	2	Q23995	Q23995	drosophila	489	221.5	5.6	453	2	Q803Z4	Q803Z4	brachydanio
417	227	5.8	1464	2	Q24132	Q24132	drosophila	490	221.5	5.6	2531	1	Q6ZMC3	Q6ZMC3	homo sapien
418	227	5.8	1464	2	Q9VC47	Q9VC47	drosophila	491	221.5	5.6	2531	1	NTC1_RAT	Q9TU53	rattus norv
419	226.5	5.7	238	1	TRV3_SALSA	P35033	salmo salar	492	221.5	5.6	3620	2	Q9TU53	Q9TU53	canis famil
420	226.5	5.7	257	2	Q8BZ04	Q8BZ04	mus musculus	493	221	5.6	227	2	Q7PHB4	Q7PHB4	anopheles g
421	226.5	5.7	371	2	Q8MS52	Q8MS52	drosophila	494	221	5.6	221	1	TRV2_SALSA	P35032	salmo salar
422	226.5	5.7	761	1	NETR_MOUSE	Q8MS62	mus musculus	495	221	5.6	258	2	Q97399	Q97399	phaedon coc
423	226.5	5.7	855	2	Q7Z410	Q7Z410	homo sapien	496	221	5.6	268	1	CLCR_RAT	P55091	rattus norv
424	226.5	5.7	1429	1	ATRN_HUMAN	Q75882	homo sapien	497	221	5.6	273	1	MCT7_RAT	P27435	rattus norv
425	226	5.7	394	1	URTG_DESRO	P49150	desmodus ro	498	221	5.6	273	2	Q6PEW8	Q6PEW8	rattus norv
426	226	5.7	432	2	Q6UX37	Q6UX37	homo sapien	499	221	5.6	314	2	Q6RUT2	Q6RUT2	mus musculus
427	226	5.7	437	1	TMS4_HUMAN	Q6UX37	homo sapien	500	221	5.6	974	2	Q6RUT2	Q6RUT2	drosophila
428	226	5.7	490	2	Q6P7D7	Q6P7D7	rattus norv	501	221	5.6	1234	2	Q7P1Q7	Q7P1Q7	anopheles g
429	226	5.7	625	1	FAL1_HUMAN	P03951	homo sapien	502	221	5.6	1322	2	Q7PNR7	Q7PNR7	anopheles g
430	225.5	5.7	312	2	Q7M755	Q7M755	mus musculus	503	220.5	5.6	242	2	Q80VS4	Q80VS4	mus musculus
431	225.5	5.7	347	1	HPT_PIG	Q8AP87	sus scrofa	504	220.5	5.6	250	2	Q8CGR5	Q8CGR5	anopheles g
432	225.5	5.7	418	2	Q8S5K2	Q8S5K2	drosophila	505	220.5	5.6	272	2	Q7Q9W5	Q7Q9W5	anopheles g
433	225.5	5.7	418	2	Q9VA87	Q9VA87	drosophila	506	220.5	5.6	277	2	Q80WM7	Q80WM7	mus musculus
434	225.5	5.7	429	2	Q8AVB0	Q8AVB0	brachydanio	507	220.5	5.6	360	2	Q17489	Q17489	anopheles g
435	225.5	5.7	445	2	Q7Q956	Q7Q956	anopheles g	508	220.5	5.6	360	2	Q7PEV7	Q7PEV7	anopheles g
436	225.5	5.7	457	1	TMS5_HUMAN	Q9J363	homo sapien	509	220.5	5.6	468	2	Q9U0G3	Q9U0G3	pacifastacu
437	225	5.7	243	2	Q7PY20	Q7PY20	anopheles g	510	220.5	5.6	506	2	Q7PR64	Q7PR64	anopheles g
438	225	5.7	328	2	Q80Z40	Q80Z40	rattus norv	511	220.5	5.6	808	2	Q7YU36	Q7YU36	drosophila
439	225	5.7	387	2	Q9XY57	Q9XY57	ctenocephal	512	220.5	5.6	1067	1	TLD_DROME	P25723	drosophila
440	225	5.7	393	2	Q6RX66	Q6RX66	armigeres s	513	220	5.6	260	2	Q9W7P9	Q9W7P9	paralichthy
441	225	5.7	432	2	Q7QKL4	Q7QKL4	anopheles g	514	220	5.6	261	2	Q962G7	Q962G7	culex pipie
442	225	5.7	455	2	Q8CDD0	Q8CDD0	mus musculus	515	220	5.6	275	1	TRB1_HUMAN	Q5661	homo sapien
443	225	5.7	490	2	Q920K3	Q920K3	rattus norv	516	220	5.6	275	2	Q6B051	Q6B051	homo sapien
444	225	5.7	490	2	Q7TN04	Q7TN04	mus musculus	517	220	5.6	331	2	Q8RIA6	Q8RIA6	mus musculus
445	225	5.7	615	1	FAL2_HUMAN	P00748	homo sapien	518	220	5.6	331	2	Q80X17	Q80X17	mus musculus
446	224.5	5.7	246	2	Q88301	Q88301	mus musculus	519	220	5.6	568	2	Q7Q064	Q7Q064	anopheles g
447	224.5	5.7	251	2	Q54854	Q54854	rattus norv	520	219.5	5.6	244	1	TRV2_XENTIA	P70059	xeopus lae
448	224.5	5.7	253	2	Q91Y82	Q91Y82	mus musculus	521	219.5	5.6	248	2	Q7QAX4	Q7QAX4	anopheles g
449	224.5	5.7	271	1	EL2_RAT	P00774	rattus norv	522	219.5	5.6	248	2	Q7SZT1	Q7SZT1	xeopus lae
450	224.5	5.7	274	1	TRV1_ANOGA	P35035	anopheles g	523	219.5	5.6	255	2	Q6NUI2	Q6NUI2	galleria lae
451	224.5	5.7	1022	1	HPT_MOUSE	Q61646	mus musculus	524	219.5	5.6	271	1	EL2_MOUSE	P52208	mus musculus
452	224.5	5.7	1427	2	TLD_BRARE	Q57460	brachydanio	525	219.5	5.6	347	1	HPT_MOUSE	Q60574	mus caroli
453	224.5	5.7	1427	2	Q8AV18	Q8AV18	mesocricetu	526	219.5	5.6	761	1	CPAB_MOUSE	P04166	mus musculus
454	224	5.7	242	2	Q7TIR8	Q8AV11	oncorhynch	527	219.5	5.6	1378	2	Q6BH72	Q6BH72	mus musculus
455	224	5.7	245	2	Q7TIR8	Q7TIR8	pangaeus h	528	219.5	5.6	1444	2	Q6A051	Q6A051	mus musculus
456	224	5.7	245	2	CTRB_BOVIN	P00767	bos taurus	529	219.5	5.6	276	2	Q7QAM5	Q7QAM5	anopheles g
457	224	5.7	248	2	O16126	O16126	boltenia vi	530	219	5.6	318	2	Q80UR4	Q80UR4	mus musculus
458	224	5.7	261	1	KUK2_HORSE	Q6J321	equus cabal	531	219	5.6	343	1	PS58_HUMAN	Q6651	homo sapien
459	224	5.7	490	1	TMS2_MOUSE	Q9J198	mus musculus	532	219	5.6	365	2	Q97366	Q97366	holocricitia
460	224	5.7	1174	2	Q9VYR4	Q9VYR4	drosophila	533	219	5.6	374	2	Q81862	Q81862	dermacentor
461	224	5.7	262	2	Q9PSV8	Q9PSV8	anopheles g	534	218.5	5.5	375	2	Q817W8	Q817W8	dermacentor
462	223.5	5.7	234	2	Q90244	Q90244	actipenser c	535	218.5	5.5	435	1	TMS4_MOUSE	Q9VC45	mus musculus
463	223.5	5.7	366	1	Q9W7Q0	Q9W7Q0	paralichthy	536	218.5	5.5	787	2	Q6S1G0	Q6S1G0	naja kaouch
464	223.5	5.7	348	1	HPT_HUMAN	P00739	homo sapien	537	218.5	5.5	1007	2	Q8UJ28	Q8UJ28	xeopus lae
465	223.5	5.7	1242	1	JAG1_BRARE	Q9Y57	brachydanio	538	218.5	5.5	1379	2	Q6T256	Q6T256	homo sapien
466	223.5	5.7	1629	2	Q9V513	Q9V513	drosophila	539	218.5	5.5	232	2	Q7PG16	Q7PG16	anopheles g
467	223.5	5.7	1674	2	Q8SY35	Q8SY35	drosophila	540	218	5.5	242	2	Q7SX90	Q7SX90	brachydanio
468	223	5.7	242	2	Q9W7Q7	Q9W7Q7	paralichthy	541	218	5.5	271	2	Q54213	Q54213	streptomyce
469	223	5.7	454	1	TMS3_HUMAN	P57727	homo sapien	542	218	5.5	271	2	Q54213	Q54213	streptomyce

















DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSH1; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 720 AA; 80198 MW; DC98B8C7241289D3 CRC64;

Query Match 100.0%; Score 3945; DB 2; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-287;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 MELGCMTQLGLTFPLQLLLISSLPREYVINEACPGAEMNIMCRCECEYDQIECVCPKRE 60
DB 1 MELGCMTQLGLTFPLQLLLISSLPREYVINEACPGAEMNIMCRCECEYDQIECVCPKRE 60
OY 61 VVGTTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFYCAECRAGW 120
DB 61 VVGTTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFYCAECRAGW 120
OY 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
DB 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
OY 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
DB 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
OY 181 YVEVRDGNRQGOILKRVCGNERPAPIQSISSSLHLVLFHSDGSKNFDGFHAIYEITRACS 240
DB 181 YVEVRDGNRQGOILKRVCGNERPAPIQSISSSLHLVLFHSDGSKNFDGFHAIYEITRACS 240
OY 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
OY 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
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DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRRVL 360
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DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRRVL 360
OY 361 PMOVSRRTPLHQLYSAAFSKOKLOSAPTKKPPALPFGLDPMGYOHLHTQLOYECSIPFYR 420
DB 361 PMOVSRRTPLHQLYSAAFSKOKLOSAPTKKPPALPFGLDPMGYOHLHTQLOYECSIPFYR 420
OY 421 RLGSSRRRTCLRTGKMGSRAPSCIPICGKIENITAKTGGLRMPQALYRRSTSGVHDSGL 480
DB 421 RLGSSRRRTCLRTGKMGSRAPSCIPICGKIENITAKTGGLRMPQALYRRSTSGVHDSGL 480
OY 481 HKGANFLVCSGALNERTVVAACHCVTLGKTYMKTADLVYLGKFRDDDBDEKTIQS 540
DB 481 HKGANFLVCSGALNERTVVAACHCVTLGKTYMKTADLVYLGKFRDDDBDEKTIQS 540
OY 541 LOISAIILHPNDPILLDADIAILKLDKARISTVOPICLAASRDLSTFQESHITVAG 600
DB 541 LOISAIILHPNDPILLDADIAILKLDKARISTVOPICLAASRDLSTFQESHITVAG 600
OY 601 MNVLADVSPGFKNDTLRSQVSVVDLLCEQHEDHGI PVSVTDNMECASMEPTAPSDI 660
DB 601 MNVLADVSPGFKNDTLRSQVSVVDLLCEQHEDHGI PVSVTDNMECASMEPTAPSDI 660
OY 661 CTAEFGGIAAASFPGASPEPRMHLMLGVSMYDKTCSHRUSTATTKVLFPKDIERMNK 720
DB 661 CTAEFGGIAAASFPGASPEPRMHLMLGVSMYDKTCSHRUSTATTKVLFPKDIERMNK 720
OY 661 CTAEFGGIAAASFPGASPEPRMHLMLGVSMYDKTCSHRUSTATTKVLFPKDIERMNK 720
DB 661 CTAEFGGIAAASFPGASPEPRMHLMLGVSMYDKTCSHRUSTATTKVLFPKDIERMNK 720

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RESULT 2

Q6N062 PRELIMINARY; PRT; 720 AA.  
 AC Q6N062;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp668N24154.  
 GN Name=DKFZp668N24154;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteria; Primates; Catarrhini; Hominoidea; Homo.  
 NC NCB1\_taxonomy=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon endothel;  
 RG The German CDNA Consortium;  
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Pobo G., Han M., Wiemann S.;  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 DR EMBL; BX640676; CAE5808.1; -.  
 DR HSSP; P00734; 1BB0.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_Like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sush1\_SCF\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sush1; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00179; EGF\_Ca; 1.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSH1; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR EGF-like domain; Hydrolase; Hypothetical protein; Protease;  
 KW Serine protease.  
 SQ SEQUENCE 720 AA; 80196 MW; E98A9F9948EE777D CRC64;

Query Match 99.8%; Score 3936; DB 2; Length 720;  
 Best Local Similarity 99.7%; Pred. No. 7.5e-287;  
 Matches 718; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MELGCMTQLGLTFPLQLLLISSLPREYVINEACPGAEMNIMCRCECEYDQIECVCPKRE 60
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OY 61 VVGTTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFYCAECRAGW 120
DB 61 VVGTTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFYCAECRAGW 120
OY 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
DB 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
OY 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
DB 121 YGDCMRCGOYLRAKQQLLESYPLNAHCMTIHAKEGFTQLRFVWLSLEFPMQCYD 180
OY 181 YVEVRDGNRQGOILKRVCGNERPAPIQSISSSLHLVLFHSDGSKNFDGFHAIYEITRACS 240
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DB 241 SSPCFHDTGCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGLI 300
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DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGESGKOPICIRACREPKISDLVRRRVL 360
OY 361 PMOVSRRTPLHQLYSAAFSKOKLOSAPTKKPPALPFGLDPMGYOHLHTQLOYECSIPFYR 420
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 Db 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWPQOAIYRTSGVHDGSL 480  
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 Db 481 HKGAMFLVCSGALVNEFTVVAACVTDLGKVTMIKTADLKVILGKRYRDDDEKTIQS 540  
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 Db 541 LQTSATILHNPYDILLADIALIKLIDKARISRRVPCILASRDISTFQESHITVAG 600  
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 Db 601 MNTLVADVRSFGPKNDTLRSGVSVSDSLCEQEHEDGIPVSYTDNMFCASWEPTAPSDI 660  
 Qy 661 CTAAETGIIAIVSPGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFYVLPFKWIERNMK 720  
 Db 661 CTAAETGIIAIVSPGRASPEPRMHLMLGLVSWSYDKTCSHRLSTAFYVLPFKWIERNMK 720  
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 Q96JW2 PRELIMINARY; PRT; 737 AA.  
 AC Q96JW2; 096JW2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ14935.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX PubMed=14702039; DOI=10.1038/ng1285;  
 RA Oca T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Ite R.,  
 RA Makametu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Obeyseshi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi K., Kanda K., Yokoi T., Puruya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Niinomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Horita T., Kusano J.,  
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Nishibashi K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Nishikawa K., Matsunawa H., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Higashigaki H., Watanabe T., Sugiyama A., Takemoto M., Kakakami B.,  
 RA Hishigaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Taashiro H., Tanigami A., Fujiyama T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hideo M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Ohtsuri R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsunuma K., Nakajima T., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizumura K., Suganuma J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
 RT "Complete sequencing and characterization of 21,243 full-length human  
 cDNAs";  
 RT Nac. Genet. 36:40-45(2004).  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 DR EMBL, AK027841; BAB55404.1; -.

DR HSP, P00736; 1GPZ.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Set\_Cys.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00084; EGF; 1.  
 DR Pfam; PF00084; Sushi\_1.  
 DR Pfam; PF00084; Sushi\_1.  
 DR Pfam; PF00084; Sushi\_1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00020; TRYPSIN; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; Sushi; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW EGF-like domain; Hydrolase; Protease; Serine protease.  
 SQ SEQUENCE 737 AA; 81952 MW; 4f51689c5eb32b44 CRC64;

Query Match 99.4%; Score 3921.5; DB 2; Length 737;  
 Best Local Similarity 97.6%; Pred. No. 9,5e-286;  
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Qy 1 MELGCTWQGLTFLQLLISSLPREYTVINEACPGAEMNIMCECEYDQIECVCPGKRE 60  
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 Qy 121 YGSDCKRCGCVLAPAPGQILLESYPLNAHCEWTIHAKEGVIQRLVYMLSLFEDYMCQYD 180  
 Db 121 YGSDCKRCGCVLAPAPGQILLESYPLNAHCEWTIHAKEGVIQRLVYMLSLFEDYMCQYD 180  
 Qy 181 YVEVRDGDNRDQIIRKVCGERPADIQISGSLHVLPHSDGSKNFDGPHAIYEEITACS 240  
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 Qy 241 SSGCFHDGTVLADKASYSKACLAGYTGQRCENL-----LEERRNSDP 283  
 Db 241 SSGCFHDGTVLADKAPYKACLAGYTGQRCENLLEERRNSDP 300  
 Qy 284 GGPVNGYOKITGGPGILINGHAKIGTVSPFCNSYVLSGNEKRTCOQNGSGKQPICI 343  
 Db 301 GGPVNGYOKITGGPGILINGHAKIGTVSPFCNSYVLSGNEKRTCOQNGSGKQPICI 360  
 Qy 344 KACREPKISDLYRRVLPQVQSRETPLHQLVSAFSSKQKQAPTKKPLPFSDLPNGY 403  
 Db 361 KACREPKISDLYRRVLPQVQSRETPLHQLVSAFSSKQKQAPTKKPLPFSDLPNGY 420  
 Qy 404 QHHTLOLQVHCISPPFRRLASSRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWP 463  
 Db 421 QHHTLOLQVHCISPPFRRLASSRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWP 480  
 Qy 464 MQAATRRTSQGVDSLHKGAMFLVCSGALVNEFTVVAACVTDLGKVTMIKTADLKVY 523  
 Db 481 MQAATRRTSQGVDSLHKGAMFLVCSGALVNEFTVVAACVTDLGKVTMIKTADLKVY 540  
 Qy 524 LKGYRDDDEKTIQSLSAIIILHNPYDILLADIALIKLIDKARISRRVPCILAS 583

Db 541 LGRFYRDDDDREKTIQSIQISAIILHPNYDPIILDADIALIKLADKARISTRVOPICLAA 600  
Qy 584 SRDLSTFSQESHITVAGNNVLADYRSPGKNDTLRSGVSVVSDILCEQHEHDGIPVSV 643  
Db 601 SRDLSTFSQESHITVAGNNVLADYRSPGKNDTLRSGVSVVSDILCEQHEHDGIPVSV 660  
Qy 644 TDNNFCAWEPPTASDITCTATGCIAAVSFPGRASPEPRHMLMGLVNSYKTCSSHLSLT 703  
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Qy 704 AFTKVLPEPKDWIERNMK 720  
Db 721 AFTKVLPEPKDWIERNMK 737  
RESULT 4  
Q8BU25 PRELIMINARY; PRT; 720 AA.  
AC Q8BU25  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone: E43002G05 product: hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and Serine proteases, trypsin family domain containing protein, full insert sequence.  
OS Name=E43002G05Rik;  
GN Mus musculus (Mouse);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Mech. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RA The FANTOM Consortium;  
RT "The RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama J., Nishi K., Kitsuina T., Teshiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama S., Nishino T., Harada A., Yamamoto S., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NOD; TISSUE=Thymus;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ono M., Ohnato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomari A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to peptidase family 11.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
DR EMBL: AK088017; BAC40098.1; -.  
DR HSP: P00736; 1GPZ.  
DR MGD: MGI:2445082; E43002G05Rik.  
DR CO: CO:005615; Extracellular space; TAS.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR006209; EGF-like.  
DR InterPro: IPR06210; IEGF.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR InterPro: IPR000436; Sushi\_SCR\_CCP.  
DR Pfam: PF00431; CUB; 1.  
DR Pfam: PF00008; EGF; 1.  
DR Pfam: PF00084; Sushi; 1.  
DR Pfam: PF00089; Trypsin; 1.  
DR PRINTS: PR00722; CHYMOTRYPsin.  
DR SMART: SM00042; CUB; 1.  
DR SMART: SM00181; EGF; 2.  
DR SMART: SM00020; TRYP\_SPC; 1.  
DR PROSITE: PS01180; CUB; 1.  
DR PROSITE: PS00022; EGF\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS00026; EGF\_3; 1.  
DR PROSITE: PS00923; SUSHI; 2.  
DR PROSITE: PS02240; TRYPsin DOM; 1.  
KW EGF-like domain; Hydrolase; Hypothetical protein; Protease;  
KW Serine protease.  
SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;  
Query Match 91.6%; Score 3612; DB 2; Length 720;  
Best Local Similarity 90.1%; Pred. No. 1,6e-262;  
Matches 649; Conservative 33; Mismatches 38; Indels 0; Gaps 0;  
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Db 1 MELDRWAQLGLVFLQILLISSLPREYTVINACPGAEWNTMCRBCGYDIECVCPKRE 60  
Qy 61 VVGTTTCCRNENECSCILHRCCTIFENCKSCRNSMGCTLDDFVYKGFYCAECRAGW 120  
Db 61 VVGTTTCCRNENECSCILHRCCTIFENCKSCRNSMGCTLDDFVYKGFYCAECRAGW 120  
Qy 121 YGDCMRCGQVLRAPKQIILLESYPLNACGEMTTHAKRGVFIOLRFYMLSLDPYMCQYD 180  
Db 121 YGDCMRCGQVLRAPKQIILLESYPLNACGEMTTHAKRGVFIOLRFYMLSLDPYMCQYD 180  
Qy 181 YVEVRDNDNDDGQIRKVCNERNRPAPQISIGSSILHVLFHSDDGSKNPDGFPAIYBEITACS 240  
Db 181 YVEVRDNDNDDSPTRKFCNERNRPAPIRSTGSSILHVLFHSDDGSKNPDGFPAIYBEITACS 240  
Qy 241 SSPCFHDGTCVLDKAGSYKCAICLAGTYGRCENLLEBRNCSDPGPGVNGYQKITGSGFLI 300

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Db 241 SSBPFHGTCLDITGSKACLAGYTGRCENLLEBRNCSDLGPGVNGYKKTTEGGGL 300
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Db 301 NEHHVIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL 360
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Db 481 HKGAMFLVCGALVNERTVVAHCVTLGKATITKADLKVYLGRFYRDDDEKTIOS 540
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Db 541 LQISAILHNPYDPIILDADIAILKLDKARISTRVOPICLAARDLSTSFOSHTVAG 600
Qy 601 WNLADYRSPGKNDTLRSGVSVVDSLLCEBOHEDHGIPVSVDNNFCSAWEFTAPSDI 660
Db 601 WNLADYRSPGKNDTLRSGVSVVDSLLCEBOHEDHGIPVSVDNNFCSAWEFTAPSDI 660
Qy 661 CTATGTGIAVSPGRASPEPRMILMGVMSVYKTSHTLSTFTVLPFKMIERNMK 720
Db 661 CTATGTGIAVSPGRASPEPRMILMGVMSVYKTSHTLSTFTVLPFKMIERNMK 720

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## RESULT 5

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ID Q8K2B8 PRELIMINARY; PRT; 720 AA.
AC Q8K2B8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Regeneration associated muscle protease.
GN Name=B430002605Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kraemer R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhac N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
RA Datschenko L., Marziana K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleto M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguolino N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skelton U., Smallin D.E., Scherch A., Schein J.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RC Strauberg R.;

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RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RA Strauberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031841; AA31841.1; -
DR EMBL; BC057685; AA57685.1; -
DR HSP; P00736; 1GPZ.
DR MGI; MGI:2445082; B430002605Rik.
DR GO; GO:0005615; Cytoplasmic space; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; Sushi; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PSS0026; EGF_3; 1.
DR PROSITE; PSS0923; Sushi; 2.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
DR Hydrolase; Protease; Serine protease.
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;

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Query Match 91.6%; Score 3612; DB 2; Length 720;

Best Local Similarity 90.1%; Pred. No. 1.6e-262; Index 0; Gaps 0;

Matches 649; Conservative 33; Mismatches 38; Indels 0;

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Qy 1 MEIGCWTOGLTFLQILLISLPREYVINEACPGAEWIMCRECEYDIEGVCPKRE 60
Db 1 MELDRNAQLGLVFLQILLISLPREYVINEACPGAEWIMCRECEYDIEGVCPKRE 60
Qy 61 VVGITPPCCNENEDCSCIHPGCTIFENCKSCRNGSGTGLDDFYVKGFCYACRCAGW 120
Db 61 VVGITPPCCNENEDCSCIHPGCTIFENCKSCRNGSGTGLDDFYVKGFCYACRCAGW 120
Qy 121 YGSDCRRCGVAPAPGQILLSEYPLNAGEWTHAKPGVIOLRPMLSLEFDYMCQYD 180
Db 121 YGSDCRRCGVAPAPGQILLSEYPLNAGEWTHAKPGVIOLRPMLSLEFDYMCQYD 180
Qy 181 YVEVRDNDNDGQIIKRVCGNERPAPIOSIGSSLAHYLFHSDGSKNPGFAIYEETPACS 240
Db 181 YVEVRDNDNDGQIIKRVCGNERPAPIOSIGSSLAHYLFHSDGSKNPGFAIYEETPACS 240
Qy 241 SSBPFHGTCLDITGSKACLAGYTGRCENLLEBRNCSDLGPGVNGYKKTTEGGGL 300
Db 241 SSBPFHGTCLDITGSKACLAGYTGRCENLLEBRNCSDLGPGVNGYKKTTEGGGL 300
Qy 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL 360
Db 301 NGRHAKIGTVSPFCNNSYVLSGNEKRTCOONGEMSGKOPICIKACREPKISDLVRRVL 360
Qy 361 PMOVSHETPLHOLYSAFSGKOLQSAPTKKPALPGDLPNGYOHHTLOLQYECISPFYR 420
Db 361 PMOVSHETPLHOLYSAFSGKOLQSAPTKKPALPGDLPNGYOHHTLOLQYECISPFYR 420
Qy 421 RLGSSRRTCRLRTGKMSGRABSCIPICGKIENITAPKTQGLRMPQQAIIYRTSGVHDGSL 480
Db 421 RLGSSRRTCRLRTGKMSGRABSCIPICGKIENITAPKTQGLRMPQQAIIYRTSGVHDGSL 480
Qy 481 HKGAMFLVCGALVNERTVVAHCVTLGKATITKADLKVYLGRFYRDDDEKTIOS 540
Db 481 HKGAMFLVCGALVNERTVVAHCVTLGKATITKADLKVYLGRFYRDDDEKTIOS 540

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QY 541 LQISAIIILHPYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITVAG 600  
DQ 541 LRVSAIIILHPYDPIILDADIAIKLIDKARISTRVOPICLATRSTDSFQESHITVAG 600  
QY 601 MNVLADVRSPGKNDTLRSRGVSVVSDSLCEQEHEDHGIPVSYDNMFCAKSWETAPSDI 660  
DQ 601 MNVLADVRSPGKNDTLHYGNVAVVDPMLCEQEHEDHGIPVSYDNMFCAKSWETAPSDI 660  
QY 661 CTAETGGAIVASFPGRASPEPRMHLMGVSVSYDKTCSHRLSTAFTKVLPEKDWIERNMK 720  
DQ 661 CTAETGGAIVASFPGRASPEPRMHLVGVSVSYDKTCSHRLSTAFTKVLPEKDWIERNMK 720  
RESULT 6  
Q6DIVS PRELIMINARY; PRT; 722 AA.  
AC Q6DIVS.  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DE MGC89196 protein.  
GN Name=MGC89196.  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_TaxID=8364;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Alauser R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
Dietzeno L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.O., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
Kryzhanovskiy M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,  
Jones S.J., Maitra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RA Klein S., Gerhardt D.S.,  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
EMBL: BC075430: AAH75430.1  
DR GO: GO:0005509; F:calcium ion binding; IEA.  
DR GO: GO:0004295; F:trypsin activity; IEA.  
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR000859; CUB.  
DR InterPro: IPR000742; EGF\_2.  
DR InterPro: IPR001881; EGF\_Ca.  
DR InterPro: IPR006209; EGF\_like.  
DR InterPro: IPR006210; IEGF.  
DR InterPro: IPR001254; Peptidase\_S1.  
DR InterPro: IPR009003; Pept\_Ser\_Cys.  
DR InterPro: IPR000436; Sushi\_SCR\_CCP.  
DR Pfam: PF00431; CUB; 1.  
DR Pfam: PF00008; EGF; 1.  
DR Pfam: PF00084; Sushi; 2.  
DR Pfam: PF00089; Trypsin; 1.

DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00160; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS50923; SUSHI; 2.  
DR PROSITE; PS50240; TRYPsin\_DOM; 1.  
KW EGF-like domain; Hydrolyase; Protease; Serine protease.  
KW KEGG domain; Hydrolyase; Protease; Serine protease.  
SQ SEQUENCE 722 AA; 80366 MW; F17356320601AB82 CRC64;

Query Match 71.6%; Score 2823; DB 2; Length 722;  
Best Local Similarity 66.9%; Pred. No. 2, 9e-203;  
Matches 483; Conservative 110; Mismatches 127; Indels 2; Gaps 1;

QY 1 MEIGCWTLQGLTFLQULLISLP--REYTYINACRGAENIMCRCECEYDQIECVGRPK 58  
DQ 1 MALIVMSLVVASIHLGLTAAPRSKTYVINENCPGAENIMCRDCEYDQVECAAPDG 60  
QY 59 REYVGYTIPCCRBENECDSCLHPGCTIPENCKSCRGSMGGTLDPFYVKGFCACERA 118  
DQ 61 NQKVGITIPCCRBENECDSCLHPGCTIPENCKSCRGSMGGTLDPFYIKGYSCECRM 120  
QY 119 GWYGDGCMRGGOYLRAPKQIILLESYPNANCEWTIHAKEGFIYQLRFVNLSEFDYMCQ 178  
DQ 121 GWYGDGCMRGGOYLRAPKQIILLESYPNANCEWTIHAKEGFIYQLRFVNLSEFDYMCQ 180  
QY 179 YDYEVVDGNGNRQGIITKRCGNERPAPISQSSILHLVPHSGSKNPFDPHAYEITA 238  
DQ 181 YDYEVVDGNGNRQGIITKRCGNERPAPISQSSILHLVPHSGSKNPFDPHAYEITA 240  
QY 239 CSSSPCHDGTCTLDKXKAYKACLAGYTGRCENLLEERNCSDPGPNVNGYQKIGTAPG 298  
DQ 241 CSSPCHDGTCTLDKXKAYKACLAGYTGRCENLLEERNCSDPGPNVNGYQKIGTAPG 300  
QY 299 LINGRHAKITGVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICAKCREPKISDLVRR 358  
DQ 301 LSLANHKVGFPIHFCNNSYVLSGNERACLOQAQSGKQPVCIKCKEKPVALDVROK 360  
QY 359 VLPNQVOSRETPHLQLYSAAPSKOKLOSAPTKKRALPFGDLPNGYOHILHQLQYECISPF 418  
DQ 361 VLPNQVOSRETPHLQLYSAAPSKOKLOSAPTKKRALPFGDLPNGYOHILHQLQYECISPF 420  
QY 419 YRRLGSSRRITCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDG 478  
DQ 421 YRRLGSSRRITCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDG 480  
QY 479 SLHKGAFLVCSGALVNERTVVVAACVTDLGRVTMIKTADLKVVLGKFFRDDDRDEKTI 538  
DQ 481 SLHKGAFLVCSGALVNERTVVVAACVTDLGRVTMIKTADLKVVLGKFFRDDDRDEKTI 540  
QY 539 QSLQISAIIILHPYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITV 598  
DQ 541 QSLQISAIIILHPYDPIILDADIAIKLIDKARISTRVOPICLAASRDLSFQESHITV 600  
QY 599 AGMVLADVRSPGKNDTLRSRGVSVVSDSLCEQEHEDHGIPVSYDNMFCAKSWETAPSD 658  
DQ 601 AGMVLADVRSPGKNDTLHYGNVAVVDPMLCEQEHEDHGIPVSYDNMFCAKSWETAPSD 660  
QY 659 DICTAETGGAIVASFPGRASPEPRMHLMGVSVSYDKTCSHRLSTAFTKVLPEKDWIERN 718  
DQ 661 DICTAETGGAIVASFPGRASPEPRMHLVGVSVSYDKTCSHRLSTAFTKVLPEKDWIERN 720  
QY 719 MK 720  
DQ 721 MK 722

RESULT 7  
Q7IRE9

ID Q71R89 PRELIMINARY; PRT; 417 AA.  
 AC Q71R89;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,  
 RA Wan D.F., Gu J.R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL: AF370386; AAQ1524.1; -.  
 DR HSSP: P00734; 1B80.  
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0004295; F:trypsin activity; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Interpro: IPR001254; Peptidase\_S1.  
 DR Interpro: IPR001314; Peptidase\_S1A.  
 DR Interpro: IPR000436; Pept\_Ser\_Cys.  
 DR PRINTS: PR00722; CHYMOTRYPSIN.  
 DR SMART: SM00020; TRYPSIN\_1.  
 DR PROSITE: PSS0923; SUBST\_1.  
 DR PROSITE: PSS0240; TRYPSIN\_DOM\_1.  
 DR Hydrolase; Protease; Serine protease.  
 KW SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.2%; Score 2059; DB 2; Length 417;  
 Best Local Similarity 95.6%; Pred. No. 3.5e-146;  
 Matches 389; Conservative 1; Mismatches 17; Indels 0; Gaps 0;  
 QY 314 FCNNSVYLGNKERTCOQNGEMSGKOPICIKACREPKISDLVRRRLVPMQVSHETPLHQ 373  
 DB 11 FVTTPTMLVAMRKELASRMERMSKOPICIKACREPKISDLVRRRLVPMQVSHETPLHQ 70  
 QY 374 LYSAAFSKQKQKQSAFTKPKPALPFGLDPMGYOHHTQLOVEICISPFYRLGSSRRRTCLRTG 433  
 DB 71 LYSAAFSKQKQKQSAFTKPKPALPFGLDPMGYOHHTQLOVEICISPFYRLGSSRRRTCLRTG 130  
 QY 434 KMGGRASCTPICKIKENITAPKTQGLRWPMQAAIYRTSGVNHGSLHKGMFLVCGAL 493  
 DB 131 KMGGRASCTPICKIKENITAPKTQGLRWPMQAAIYRTSGVNHGSLHKGMFLVCGAL 190  
 QY 494 VNERTVVAHAHCVTDLGRVMIKTADLKVVLGKRYRDDDDDEKTIQSLQISATILHPNYD 553  
 DB 191 VNERTVVAHAHCVTDLGRVMIKTADLKVVLGKRYRDDDDDEKTIQSLQISATILHPNYD 250  
 QY 554 PILLDADIALIKLDKARISTRVOPICLAASRDISTSFOSHSITVAGMNLADVRSPGPK 613  
 DB 251 PILLDADIALIKLDKARISTRVOPICLAASRDISTSFOSHSITVAGMNLADVRSPGPK 310  
 QY 614 NDTLRSGVSVVDSLLCEQHEHGHGIVASTDNNFCASWEPTASDICTAETGIAAVSF 673  
 DB 311 NDTLRSGVSVVDSLLCEQHEHGHGIVASTDNNFCASWEPTASDICTAETGIAAVSF 370  
 QY 674 PGRASPEPRMHLMLGWSYDKTCSHRLSTAFATVLPFKMIERNMK 720  
 DB 371 PGRASPEPRMHLMLGWSYDKTCSHRLSTAFATVLPFKMIERNMK 417

RESULT 8  
 ID Q9Y432 PRELIMINARY; PRT; 181 AA.  
 AC Q9Y432;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Hypothetical protein DKFZp586H2123 (Fragment).  
 GN Name=DKFZp586H2123;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Ansgore W., Mirkner U., Mewes H.W., Gaassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL050214; CAB43317.1; -.  
 DR PIR: T08805; T08805.  
 DR HSSP: P00736; 1MD7.  
 DR MEROPS: S01.998; -.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0004295; F:trypsin activity; IEA.  
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR Interpro: IPR001254; Peptidase\_S1.  
 DR Interpro: IPR000903; Pept\_Ser\_Cys.  
 DR Pfam: PF00089; Trypsin\_1.  
 DR SMART: SM00020; TRYPSIN\_1.  
 DR PROSITE: PSS0240; TRYPSIN\_DOM\_1.  
 DR Hydrolase; Hypothetical protein; Protease; Serine protease.  
 KW NON TER  
 SQ SEQUENCE 181 AA; 19962 MW; ABC793BB682D439 CRC64;

Query Match 24.1%; Score 949; DB 2; Length 181;  
 Best Local Similarity 99.4%; Pred. No. 2.9e-63;  
 Matches 180; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 540 SLQISATILHPNDPILLDADIALIKLDKARISTRVOPICLAASRDISTSFOSHSITVA 599  
 DB 1 SLQISATILHPNDPILLDADIALIKLDKARISTRVOPICLAASRDISTSFOSHSITVA 60  
 QY 600 GNVVLADVRSPGPKNDTLRSGVSVVDSLLCEQHEHGHGIVASTDNNFCASWEPTASD 659  
 DB 61 GNVVLADVRSPGPKNDTLRSGVSVVDSLLCEQHEHGHGIVASTDNNFCASWEPTASD 120  
 QY 660 ICTAETGIAAASFPGASPEPRMHLMLGWSYDKTCSHRLSTAFATVLPFKMIERNM 719  
 DB 121 ICTAETGIAAASFPGASPEPRMHLMLGWSYDKTCSHRLSTAFATVLPFKMIERNM 180  
 QY 720 K 720  
 DB 181 K 181

RESULT 9  
 ID Q8T9S1 PRELIMINARY; PRT; 1019 AA.  
 AC Q8T9S1;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Factor C precursor.  
 OS Tachypleus tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Metostomata; Xiphosura;  
 OC Limulidae; Tachypleus.  
 NC NCB1\_TaxID=6853;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21955715; PubMed=11958140;  
 RA Wang D., Liu J., Chen L., Wang L., Yang G., Wu X., Zhang W.;  
 RT Cloning and expression of Tachypleus tridentatus factor C.;  
 RL Acta Biochim. Biophys. Sin. 34:77-82(2002).  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL: AF467804; AAL75577.1; -.  
 DR HSSP: P00745; 1FDP.  
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO: GO:0008233; F:peptidase activity; IEA.  
 DR GO: GO:0005529; F:sugar binding; IEA.  
 DR GO: GO:0004295; F:trypsin activity; IEA.

DR GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR00742; EGF\_2.  
 DR InterPro; IPR006209; EGF\_1like.  
 DR InterPro; IPR006210; EGF.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR004043; LCC1.  
 DR InterPro; IPR01304; Lectin\_C.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF03815; LCC1; 1.  
 DR Pfam; PF00059; Lectin\_C; 1.  
 DR Pfam; PF00084; Sush1; 3.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 5.  
 DR SMART; SM00034; CLECT; 1.  
 DR SMART; SM00181; EGF; 1.  
 DR SMART; SM00603; LCC1; 1.  
 DR SMART; SM00020; Tryp\_SPC; 1.  
 DR PROSITE; PS50041; C\_TYPE\_LECTIN\_2; 1.  
 DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS00290; Ig\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS50820; LCC1; 1.  
 DR PROSITE; PS50923; SUSH1; 5.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 DR HydroLase; Protease; Serine protease; Signal.  
 K1 SIGNAL 1 25 Potential.  
 FT SEQUENCE 1019 AA; 112248 MW; 88E51730AE595993 CRC64;  
 Query Match 17.2%; Score 678; DB 2; Length 1019;  
 Beet Local Similarity 25.6%; Pred. No. 5.5e-42;  
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAENINM-----CECECEYDQIE---CVCPEKREYVGYTIPCCRNNEECDSCLIHPGCT 86  
 DB 184 PNGQMSPPKPCIECAKAVSSPEHCKVTAIPSGNMIEGATL-----RSCDS-----PHYL 233  
 QY 87 IFENCKSGR-NGSWGTL----- 103  
 DB 234 IGEFTLTGCGNGQSGQIPCKKLVFCPDLDPVNHAEHQVIGYEQKYGPQGTSEVYTT 293  
 QY 104 --DDFYVNGFYCAEGR--AGWYGG--DCMR-----CGVLR--APKG 137  
 DB 294 CSGNVFLMGFNTLKCNDGWSGSGPSCVAVADREVDCKSAVDFLDVGEPVRIHCPAG 353  
 QY 138 QILLES-----YPLNAHCERTIHA---KPGFVI----- 163  
 DB 354 CSLTAGTWGTATYIHELSSVCRAIHAQKLRNSGGAHVANNPISDFLSGLDNGIKSEE 413  
 QY 164 LRFVWLSTLEPYM-----COYDYVEVD-----GDNRDGQIIKRVCGN--ERPAP 206  
 DB 414 LKSLARSPRPDYVSSSTAGRSQCPDGPMEVEENCYVTSKORAMERAGVCTNMAARLAV 473  
 QY 207 IQS--IGSSHLVLFHSDG--SKPFGFH-----AIYEBETACSSSCF 245  
 DB 474 LDKDVIPLSLTEALNGKGLTTWTGLRLDAEKPEWELMDRSNVVLDNLTFWASGEPG 533  
 QY 246 HDGTCV-LDKXGS-----YKCACLAGYGORCENLLEBN---CSDPGVNVGYQKITGP 297  
 DB 534 NETNVCVYLDIDQOLPVMKTRSCFPSSFPACMMLSDNRKAKCDDPGSLGNHATIHQS 593  
 QY 298 GLINGRHAKIGTVVSFCNNSVYLSGNEKRTCOQNGESGKQPICIK--ACREPKISDLV 355  
 DB 594 --IDGFVA--GSSINYSCEVLAHLSGTETVCTTGTSAPKPRCTIKVITQNPVPSYG 649  
 QY 356 RRRVLPVQSGRETFPLHQLYSAPSKQYLQ--SAPTKKPLPFED-----LP 400

DB 650 SVEIKP----PSRINSISRVSGPFLRLPLPLARAKPPPKRRSSQPSITVDLASKVKLP 706  
 QY 401 MGQYHLHTOLOYECISPPFYRRRLGSSRRRTCLRTGKSGRABSCIPICGKIENITAP----- 455  
 DB 707 EGHYVSGRAIYTCESRYELLGSGRRCCSNMWSGPRAPSCIPVCGRSDSPSFTIMWG 766  
 QY 456 -KTQGLRMPWQAAIYRTSGVHDGSLHKGWFLVCSGALVNERTVVAACHVYDLGKVTM 514  
 DB 767 NSTEIQWPMQAGISWLA-----DHNWFLQCGSLNEXKWIYVAACHVYSATAEI 819  
 QY 515 IKTADLKVVNGKFEYRDDDEKTIQSLQISAILHPHYDPIILDADIAIKLDKARIST 574  
 DB 820 IDPSQFKIYIGKYYRDRSDRDYQVREALEIHVNPYDGNLNFQIALQLKTPVLT 879  
 QY 575 RVQPICLASRDISTFQESH-----TVAGNVNLADVSPGPKNDTLASGVSVYDSL 628  
 DB 880 RVQPICLPT--DIYT--REHLKEGLAVVTGMC---LNNENTYSEMIQAVALPVVAAS 930  
 QY 629 LCEQEHEDHGIPIVSYDNMNCASWEPTAPSDICTAETGILAAVSPGRASPEPRHLMGL 688  
 DB 931 TCEEGYKEADLPVTYENNECAGYK-KGRYDACSQSGG--PLVAFDSDRTERRWLEGI 987  
 QY 689 VSWSYDKTCSH-RLSTAFTKVLPEKWIER 717  
 DB 988 VSWSGSGCGCKANQYGGFTVNVFLSWIRQ 1017

RESULT 10  
 LFC\_TACTR  
 ID LFC\_TACTR STANDARD; PRT; 1019 AA.  
 AC P28175;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).  
 OS Tachypleus tridentatus (Japanese horseshoe crab).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;  
 OC Limulidae; Tachypleus.  
 OX NCBI\_TaxID=6853;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.  
 RX MEDLINE=91177916; PubMed=2007602;  
 RA Muta T., Miyata T., Misumi Y., Tokunaga F., Nakamura T., Toh Y.,  
 RA Ikehara Y., Iwanaga S.;  
 RT "Limulus factor C. An endotoxin-sensitive serine protease zymogen with  
 RT a mosaic structure of complement-like, epidermal growth factor-like,  
 RT and lectin-like domains.";  
 RL J. Biol. Chem. 266:6554-6561(1991).  
 CC -1- FUNCTION: This enzyme is closely associated with an endotoxin-  
 CC sensitive hemolymph coagulation system which may play important  
 CC roles in both hemostasis and host defense mechanisms. Its active  
 CC form catalyzes the activation of factor B.  
 CC -1- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and  
 CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form  
 CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic  
 CC substrates.  
 CC -1- ENZYME REGULATION: Activated by Gram-negative bacterial  
 CC lipopolysaccharides and chymotrypsin.  
 CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by  
 CC a disulfide bond.  
 CC -1- SUBCELLULAR LOCATION: Secreted in hemolymph.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=long;  
 CC IsoId=P28175-1; Sequence=Displayed;  
 CC Name=short;  
 CC IsoId=P28175-2; Sequence=VSP\_005413, VSP\_005414;  
 CC -1- SIMILARITY: Belongs to the peptidase S1 family.  
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.  
 CC -1- SIMILARITY: Contains 1 LCC1-like domain.  
 CC -1- SIMILARITY: Contains 1 LCC1 domain.  
 CC -1- SIMILARITY: Contains 5 Sush1 (CCP/SCR) domains.  
 CC -----

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CC or send an email to [license@isb-ebc.ch](mailto:license@isb-ebc.ch)).  
CC -----  
DR EMBL; D90271; BAA14315.1; -;  
DR EMBL; D90272; BAA14316.1; -;  
DR PIR; A38738; A38738.  
DR HSSP; P00746; 1FDP.  
DR MEROPS; S01.219; -;  
DR Interpro; IPR000742; EGF\_2.  
DR Interpro; IPR006209; EGF-like.  
DR Interpro; IPR006210; IEGF.  
DR Interpro; IPR004043; LCCL.  
DR Interpro; IPR001304; Lectin\_C.  
DR Interpro; IPR001254; Peptidase\_S1.  
DR Interpro; IPR001314; Peptidase\_S1A.  
DR Interpro; IPR009003; Pept\_Ser\_Cys.  
DR Interpro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF003815; LCCL; 1.  
DR Pfam; PF000059; Lectin\_C; 1.  
DR Pfam; PF00084; Sushi; 5.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 5.  
DR SMART; SM00034; CLECT; 1.  
DR SMART; SM00181; EGF; 1.  
DR SMART; SM00603; LCCL; 1.  
DR SMART; SM00020; TRYSP; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
DR PROSITE; PS00041; C-TYPE LECTIN\_2; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; FALSE\_NEG.  
DR PROSITE; PS00026; EGF\_3; 1.  
DR PROSITE; PS00923; SUSHT; 5.  
DR PROSITE; PS00240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; 1.  
DR PROSITE; PS00133; TRYPSIN\_SER; 1.  
KW Alternative splicing; Cell adhesion; Direct protein sequencing;  
KW EGF-like domain; Glycoprotein; Hemolymph clotting; Hydrolase; Lectin;  
KW Repeat; Serine protease; Signal; Sushi.  
FT SIGNAL 1 25  
FT CHAIN 26 1019 Limulus clotting factor C.  
FT CHAIN 26 690 Limulus clotting factor C heavy chain.  
FT CHAIN 691 1019 Limulus clotting factor C light chain.  
FT CHAIN 691 762 Limulus clotting factor C chain A.  
FT CHAIN 763 1019 Limulus clotting factor C chain B.  
FT DOMAIN 102 137 EGF-like.  
FT DOMAIN 140 197 Sushi 1.  
FT DOMAIN 198 256 Sushi 2.  
FT DOMAIN 258 323 Sushi 3.  
FT DOMAIN 325 421 LCCL.  
FT DOMAIN 436 568 C-type lectin.  
FT DOMAIN 574 636 Sushi 4.  
FT DOMAIN 689 750 Sushi 5.  
FT DOMAIN 763 1019 Serine protease.  
FT ACT\_SITE 809 865 Charge relay system (By similarity).  
FT ACT\_SITE 865 865 Charge relay system (By similarity).  
FT ACT\_SITE 866 966 Charge relay system (By similarity).  
FT BINDING 960 960 Substrate (By similarity).  
FT DOMAIN 643 689 Pro-rich.  
FT DISULFID 106 118 By similarity.  
FT DISULFID 112 125 By similarity.  
FT DISULFID 127 136 By similarity.  
FT DISULFID 436 447 By similarity.  
FT DISULFID 464 564 By similarity.  
FT DISULFID 538 556 By similarity.  
FT DISULFID 794 810 By similarity.  
FT DISULFID 932 951 By similarity.

FT DISULFID 962 996 By similarity.  
FT CARBOHYD 523 523 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 534 534 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 624 624 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 740 740 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 767 767 N-linked (GlcNAc...) (potential).  
FT CARBOHYD 912 912 N-linked (GlcNAc...) (potential).  
FT VARSPPLIC 492 498 LTTTWIG -> TNNVAT (in isoform Short).  
FT VARSPPLIC 499 1019 /FTId=VSP\_005413.  
FT VARSPPLIC 1019 1019 Missing (in isoform Short).  
FT SEQUENCE 1019 AA; 112346 MW; 58C2864C6715289B CRC64;  
SQ  
Query Match 17.0%; Score 672; DB 1; Length 1019;  
Best Local Similarity 25.6%; Pred. No. 1,6e-41;  
Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;  
QY 34 PGLAEWNIM---CRECEVDQIE---CVCGRKEVVGITPPCCRNENEDSCLIHFCT 86  
DB 184 PNCQWSFPPEKCIKRECAKVSPEHGKVNAPSGNMIEGATL-----RFSQDS---FYVL 233  
QY 87 IFENCKSCR-NGSMGGLT-----  
DB 234 IGGETLTCGGNGWMSQIIPQCKTLVPCPDIDPVNHAHOVKIGVEQKYGQPGTEVYTT 293  
QY 104 --DDFYKGFYCAECR--AGMYG--DCNR-----CGQVLR--APKG 137  
DB 294 CSGNYFLMGFTLTKCNPDSMSSGQSPSCVAVADREDCSKAVDFLDVGEPRHINCPAG 353  
QY 138 QILLES-----YPLNAHCENTHA---KQFYI-----Q 163  
DB 354 CSLTAGTVMGTALYHELSSVCRAAIIHAGKLPNSGCAVHVNNNGPYSDFLGSLNGIKSEE 413  
QY 164 LRVTMLSLERDVM-----QOYDVEVRD-----GNRQGIILKRVGCGN--RRAP 206  
DB 414 LKSLARSFRPDYVSSSTAGSGCPDGEFEVENECVYVTSKORAMERAOQVCTMAALAV 473  
QY 207 IQG--IGSSLHVFHSDG--SKNFDGFH-----AIYERITACSSSPCF 245  
DB 474 LDKDLIPSSLTETLRKGLTITWIGLHRLDAEKPFVWELMDRNVYLVNDLTFWASGEPG 533  
QY 246 HDQTCV-LDRKAGS---YKCAAGYTGQRCENLEERN---CSDPGPNVGXOKITGCP 297  
DB 534 NETNCGVYLDIRDQLQPVWTKTSCFQSPSFCQMDLSDRNKAKCDDPLENGHATLHGQS 593  
QY 298 GLNGRHAKTIGTVSPFCNNSTYLSGNEKRTCOQNGEMSGKQPICIK--ACREPKISDV 355  
DB 594 --IDGFYA--GSSIRYSCVTLHVLSTGETVCTTNGTWSAPKPRCIKVITCQNPVPSYG 649  
QY 356 RRRVLPVQVSGRETPHQLVSAFASKQKQ---SAPTKKPALPFGD-----LP 400  
DB 650 SVRIKP---PSRNNISIRVSGSPFLRLPLRLPLARAKPPKRRSSQPSIVDLASKKLP 706  
QY 401 MGYOHLHTLOVEICISPFYRRLGSSRRTCRLRTGKWSGRAPSCIPICQKENTITAP----- 455  
DB 707 EGHYRVSRAIYTCESRYVELLGSQGRCDNSQNMWSPRASCIPVGRSDSPSPFIWNG 766  
QY 456 -KTQGLRMPQQAIIYRTSGVHDGSLHKAMFLVCSGALVNERTVVAACVTDLGKVTM 514  
DB 767 NSTEIGQMPWQAQISRWLA-----DHNNMFLOCGGSLNEXKVIYVAACVTVASATARI 819  
QY 515 IKNADLKVLVQKPYRDDDRDEKTIQSLQISAILHPHYDPLILDADIDAIKLDKARIST 574  
DB 820 IDPSQKITVIGKTYRDSRDDDYVQREALEHVNEDGNNLFDALQLKTPVTLLT 879  
QY 575 RVQPICLAARDLSTFQESH-----TVAGNNVLADVRSPPGKNDTLRSGVSVSDSL 628  
DB 880 RVQPICLPT--DITT---REHLKEGLAVVTGNG-----LNENNTYSEMIGQAVLPVVAAS 930  
QY 629 LCEQSHDHGCIPIVSVTDNNFCASWEPTAPSDITTAETGIAAIVSPGRASPEPRHLMGL 668  
DB 931 TCEGVEKADLPVLTVENMFCAGYK--KGRYDACGDSGG--PLVFADDSRTERRRWVLEGI 967

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QY      689 VSMWYDKTCSH-RLSTAFKYLPPKMIER 717
Db      988 VSMGSPGCGKANGYGFTKVNVLWIRQ 1017

RESULT 11
LFC_CARRO STANDARD; PRT; 1019 AA.
ID LFC_CARRO
AC 026422;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Limulus clotting factor C precursor (EC 3.4.21.84) (PC).
OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
   Limulidae; Carinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95268506; PubMed=7538401;
RA Ding J.L., Navas M.A. III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
   Singapore horseshoe crab, Carinoscorpius rotundicauda.";
RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).
CC -1- FUNCTION: This enzyme is closely associated with an endotoxin-
   sensitive hemolymph coagulation system which may play important
   roles in both hemostasis and host defense mechanisms. Its active
   form catalyzes the activation of factor B.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
   124-Ile-Ile-125 bonds in Limulus clotting factor B to form
   activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
   substrates.
CC -1- ENZYME REGULATION: Activated by Gram-negative bacterial
   lipopolysaccharides and chymotrypsin (by similarity).
CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
   a disulfide bond (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted in hemolymph.
CC -1- SIMILARITY: Belongs to the peptidase S1 family.
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 LCCU domain.
CC -1- SIMILARITY: Contains 5 Sushi (CCP/SCR) domains.
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CC -----
DR EMBL; S77063; AAB34361.1; -.
DR HSSP; P00746; IEDP.
DR MEROPS; S01.219; -.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR004043; LCCU.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001354; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF03815; LCCU; 1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 5.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00033; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00603; LCCU; 1.

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DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS50820; LCCU; 1.
DR PROSITE; PS50923; SUSHI; 5.
DR PROSITE; PS50240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
KW Cell adhesion; EGF-like domain; Glycoprotein; Hemolymph clotting;
   Hydrolyase; Lectin; Repeat; Serine protease; Signal; Sushi.
FT SIGNAL 1 25
FT CHAIN 26 1019
FT CHAIN 26 690
FT CHAIN 691 1019
FT CHAIN 691 762
FT CHAIN 763 1019
FT DOMAIN 102 137
FT DOMAIN 140 197
FT DOMAIN 140 198
FT DOMAIN 198 256
FT DOMAIN 258 323
FT DOMAIN 325 421
FT DOMAIN 436 568
FT DOMAIN 574 636
FT DOMAIN 689 750
FT DOMAIN 763 1019
FT ACT_SITE 809 809
FT ACT_SITE 865 865
FT ACT_SITE 966 966
FT BINDING 960 960
FT DOMAIN 643 689
FT DISULFID 106 118
FT DISULFID 112 125
FT DISULFID 127 136
FT DISULFID 436 447
FT DISULFID 464 564
FT DISULFID 538 556
FT DISULFID 794 810
FT DISULFID 932 951
FT DISULFID 962 996
FT CARBOHYD 523 523
FT CARBOHYD 534 534
FT CARBOHYD 624 624
FT CARBOHYD 740 740
FT CARBOHYD 767 767
FT CARBOHYD 912 912
SQ SEQUENCE 1019 AA; 112429 MW; 918A1ED8B17B6C3 CRC64;

Query Match 16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 5.2e-41;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNTMCRBCGCEYDIECYCEGKRE-----VGYTTPCCRNENEDSCLIH 82
Db 184 PNGQWNSNFPKRCIR-----ECAMVSSPEHGKVNALSGMIRGATL-----RFSCDS----- 229
QY 83 PGCTIFENCKSCR-NGSMWGTL-----
Db 230 PYVILIGQETLTCQNGMNGNGIIPCKKLVPCPDLDPVNHAEHKVIGVEQKYGFPQGT 289
QY 104 -----DDFYVKGFYCAECR--AGWYG--DKMR-----CGQVLR-- 133
Db 290 VTYTCSGNVFLMGSFDTLKCNPDGWSGSGSVAVADREVDCSKAVDFLDVGEPEVRIH 349
QY 134 APKQILLSE-----YPLNAHCEWTYHA-----KSGFYI----- 162
Db 350 CPAGCSLTAGTVMGTALYHEISVCRAAIHAGKLPNSGAVHVVNNGPYSPFLGSDINGI 409
QY 163 ---OLRFVNLSEFDY-----GQYDVEYRD-----GDRPDQIILKVGCGN--E 202
Db 410 KSEELKSLARFRFDVYRSSTAGSKGCPDGGFEVDENCYVYTSKQRAWERAGQSVCTINMA 469

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QY 203 RPAPIGS--IGSSLHVLPHSDG-SKNPDGFH-----AIYEITACSS 241
DB 470 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLRDAEKPIWELMDRSNVVNLNLTFWAS 529
QY 242 SPCHDGTCLV---DKAGS-YKACACLAGYGCQCEULEBERN---CSDPGGVNGYQKI 293
DB 530 GEPGENETNCVYMDIQDQLQSVWTKKSCFQPSFACMMDLSDRNKAKDDPDLSENGATL 589
QY 294 TGGPGLNGRHAIGTIVVSPFCNNSVYLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 590 HGGS--IDGYYA--GSSIRSCVHLHLSGTETVCTTNGTWSAPKRCIKVITCQNPV 645
QY 352 SDLVRRRVLPWQVSRETPHLQLYSAFSSKQKQ---SAPTKPALPFGD----- 398
DB 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAKPPKRRSSQPSVTLASK 702
QY 399 --LPMGQHHTLOLOECISPFYRLGSSRRTCLRTGKSGRAPASCIPICGKENTAP- 455
DB 703 VKLPEGHYRVGSRAIYTCESRYVELLQSGRRCDNSNGMSGRPASCIPIVCGRSDSPSPF 762
QY 456 ----KTQGLRMPQAAIYRTSGVHDGSLHKAMFLVCSGALVNBRTVVAAHCVTDLG 510
DB 763 IMNGNSTEIGQWPMQAGISRWLA-----DHNNMFLQCGSSLNEMKWTYTAACVYSA 815
QY 511 KVTWIKTADLVKLVGKPYRDDRDDEKTIQSLQISAILHPVYDILADADIAIKLIDKA 570
DB 816 TAEIIDNPFMYGKYYRDSRDDYQVREALEIHNPVYDGNLNFIDIALIQLKTPV 875
QY 571 RISTRVOPICLAARDLSTFSQESH-----TYAGNNVLADVSPGPKDTRLGVSIV 624
DB 876 TLATRVOPICLP---DIYTT--REHLKEGLAVVTGWC---LNENNTYSSTIQAAVLV 926
QY 625 VDSLCEGHEHDGIPVSYVDNMFCAWEPAPSDICTAETGIIAASFPGRASPEBRWH 684
DB 927 VAASTCEEGKEADLPITVENMFCAGYK-KGRYDACSQDSGG--PLVAFDSDSTERRW 983
QY 685 LMGVLSVYDKTCSH-RLSTAFTKVLPEFKWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGFYVFLSWIRQ 1017

RESULT 12
Q26423
ID 026423 PRELIMINARY; PRT; 1083 AA.
AC 026423;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Factor C.
GN Name:Factor C;
OS Carcinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Lmulidae; Carcinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95268506; Pubmed=7538401;
RA Ding J.L., Navas M.A. III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
RT Singapore horseshoe crab, Carcinoscorpius rotundicauda.";
RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).
CC -1- SIMILARITY: Belongs to peptidase family S1.
EMBL, F07064; AB034362.1; -.
DR HESP; P00746; 1FDP.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000743; BGP_2.
DR InterPro; IPR006209; BGP_1like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro; IPR004043; LCCL.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF03815; LCCL; 2.
DR Pfam; PF03059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 3.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS50041; C-TYPE_LECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00026; IG_MHC; 3; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50923; SUSHI; 5.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Hydrobase; Protease; Serine protease.
SQ SEQUENCE 1083 AA; 120227 MW; C82CC45ACF9CB7 CRC64;

```

```

Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No.5,6e-41;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNIMCECECYDDIECVCPKRE-----VGYTITPCCRNENECDSCLIH 82
DB 248 PNGQMSNFPKCLR---ECAMVSPBHKVNALSGDMIGAIL-----RFSQDS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 294 PYLLIGDETITCQNGQNGQIPIQCKNLVFCPDLDPVNAHKKYKIGVEQKGFPGQTE 353
QY 104 -----DDFYVKGFCYAEGR--AGWYGG--DCNR-----CGQVLR-- 133
DB 354 VITYCGSNYFLMGFDLTKCNPDGWSGSGPSQSVKVDREYDCDSKAVDFLDVGBEVRIH 413
QY 134 APRQILLES-----YPLNAHCWHTIA---KRGVYI----- 162
DB 414 CPAGCSLTAGTWTGTAIYHELSSVCRAIHAQKLPSNGGAVHVNNGPYDPLGSLDNGI 473
QY 163 ---QLRFVMLSLFEDYV-----CQDYVEVRD-----GDNRDGQIIRKVCN--E 202
DB 474 KSEELKSLASRFDFVSSSTAGKSGCPDGMFEVDENCVVYTSKQAMERAAQGVCTTMAA 533
QY 203 RPAPIGS--IGSSLHVLPHSDG-SKNPDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLRDAEKPIWELMDRSNVVNLNLTFWAS 593
QY 242 SPCHDGTCLV---DKAGS-YKACACLAGYGCQCEULEBERN---CSDPGGVNGYQKI 293
DB 594 GEPGENETNCVYMDIQDQLQSVWTKKSCFQPSFACMMDLSDRNKAKDDPDLSENGATL 653
QY 294 TGGPGLNGRHAIGTIVVSPFCNNSVYLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGGS--IDGYYA--GSSIRSCVHLHLSGTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 352 SDLVRRRVLPWQVSRETPHLQLYSAFSSKQKQ---SAPTKPALPFGD----- 398
DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAKPPKRRSSQPSVTLASK 766
QY 399 --LPMGQHHTLOLOECISPFYRLGSSRRTCLRTGKSGRAPASCIPICGKENTAP- 455
DB 767 VKLPEGHYRVGSRAIYTCESRYVELLQSGRRCDNSNGMSGRPASCIPIVCGRSDSPSPF 826
QY 456 ----KTQGLRMPQAAIYRTSGVHDGSLHKAMFLVCSGALVNBRTVVAAHCVTDLG 510

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Db      827  IMNGNSTEIGQWQAGISRWLA-----DHNMFLQCGGSLNEMKVIYAAHCVTYSA  879
Oy      511  KVTWIKTADLKVYKGFYRDDDDREKTIQSLQISAILHPYVDPLLDADIAILKLDKA  570
Db      880  TAEIIDPQGFMYGKTYRDRSDDDVQVVEALEIHVNPYDGNLFDALQLKTPV  939
Oy      571  RISTRVOPICLAASRDLSFQESH-----TVAGNVLADVRSPGKNDTLRSGVSV  624
Db      940  TLTRVOPICLPT--DITF---REHLKGTLLAVTGMG---LNENNTYSETIQOAVLPV  990
Oy      625  VDSLCEQHEDHGIPIVSVTNMFCASWEPTABSDICTAETGTGIAAVSFERASPEPRM  684
Db      991  VAASTCEGYKADLPVTVTNMFCAQYK-KGRYDACSDDSG--PLVFADDSKTERRW  1047
Oy      685  LMGVSMGYDKTCSH-RLSTAFTKVLPEKDWIER  717
Db      1048  LEGIVSMGSPSCGKANYGFTKVNVLMSIRQ  1081

```

## RESULT 13

0868H7 PRELIMINARY; PRT; 680 AA.

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AC      0868H7, PRELIMINARY; PRT; 680 AA.
DT      01-JUN-2003 (TREMBlrel. 24, Created)
DT      01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Mannose-binding lectin associated serine protease-1.
GN      Name=MASP-1;
OS      Branchiostoma belcheri (Amphioxus).
OC      Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OX      Branchiostoma.
RN      NCB1_TaxID=7741;
RP      SEQUENCE FROM N.A.
RC      TISSUE=Notochord;
RX      MEDLINE=22593353; PubMed=12707349;
RA      Endo Y., Nonaka M., Saita H., Kakimura Y., Matsushita M.,
RA      Matsushita M., Fujita T.;
RT      "Origin of mannose-binding lectin-associated serine protease (MASP)-1
RT      and MASP-3 involved in the lectin complement pathway traced back to
RT      the invertebrate, amphioxus";
RL      J. Immunol. 170:4701-4707(2003).
CC      -1- SIMILARITY: Belongs to peptidase family S1.
DR      EMBL; AB089267; BAC75886.1; -.
DR      HSSP; P00736; IAPQ.
DR      GO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0005509; F:calcium ion binding; IEA.
DR      GO; GO:0004263; F:chymotrypsin activity; IEA.
DR      GO; GO:0008233; F:peptidase activity; IEA.
DR      GO; GO:0005293; F:sugar binding; IEA.
DR      GO; GO:0004295; F:trypsin activity; IEA.
DR      GO; GO:0006956; P:complement activation; IEA.
DR      GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR      InterPro; IPR000152; Asx_hydroxyl_S.
DR      InterPro; IPR000859; CUB.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR001254; Peptidase_S1.
DR      InterPro; IPR001314; Peptidase_S1A.
DR      InterPro; IPR011361; Pept_S1_Comp_Acc.
DR      InterPro; IPR009003; Pept_ser_Cys.
DR      InterPro; IPR000436; Sushi_SCR_CCP.
DR      Pfam; PF00431; CUB; 2.
DR      Pfam; PF00089; EGF; 1.
DR      Pfam; PF00084; Sushi; 2.
DR      Pfam; PF00089; Trypsin; 1.
DR      PIRSF; PIRSF001155; C1r_C1s_MASP; 1.
DR      PRINTS; PR00722; CHYMOTRYPSIN.
DR      SMART; SM00033; CCP; 2.
DR      SMART; SM00043; CUB; 2.
DR      SMART; SM00179; EGF_CA; 1.
DR      SMART; SM00020; Tryp_Spc; 1.

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DR      PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR      PROSITE; PS01180; CUB; 2.
DR      PROSITE; PS01186; EGF_2; 1.
DR      PROSITE; PS01187; EGF_CA; 1.
DR      PROSITE; PS50923; SUSHI; 2.
DR      PROSITE; PS50240; TRYPSIN_DOM; 1.
DR      PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR      PROSITE; PS00135; TRYPSIN_SER; 1.
DR      EGF-like domain; Hydroxylase; Lectin; Protease; Serine protease.
SQ      SEQUENCE 680 AA; 75871 MW; 496985A9A4728318 CRC64;

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Query Match 15.4%; Score 608.5; DB 2; Length 680;  
 Best Local Similarity 26.3%; Pred. No. 5.5e-37;  
 Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;

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Oy      46  CEVDQIECV-----CPGKEV-----VGYT  65
Db      84  CEVDYVVMGDKLVGLFCGETDPTREKVGDRVIBSTGSLSEFKSDPSNVDRHGFV  143
Oy      66  IPCCRNENECDSCLHPGCTIFENCKSCNNGSGTLDIFYKGFACACRAG-WYGD  124
Db      144  VHYRVVDREDC--AVDNGGCHNF---CHN-----YISGYCS-CRAGYWTMKD  185
Oy      125  ---C-WRCG-QVLRAPIGQILLES---YPLNAHCWTHAKGFVQLRFVMSLEFPD-  174
Db      186  RETCKECCGQVLTQSLGTTSSPEYRLRYKVLDCDKIOVERGYVTIQF--DDFDV  242
Oy      175  ----YWCQDYVEVRDNDRDQIIKVCGNRPAPIQSIGSLHVLPHSDGSKNPDG  229
Db      243  EQHREVSCEPYDLKLVQAGDEKGP---YCGKTVPTITSTDHGMHVFPHSDGSKNKG  298
Oy      230  HAIYEITACSSBPCFHDGTCVLDAKAGYCACLAAGTGCRCENLEBRNCSDDGGVNG  289
Db      299  RAYTYFT-----TARPCAL-----SAP-----  315
Oy      290  YQKITGPGPLINGHAKIGTVSPFCNNSYVLSCNEKRTCOQNGESGKOPICAKREP  349
Db      316  ----AYGMESGNFYSQVRSFACGEYGLDQPDHRCVQADGSMGQVPTC-----  362
Oy      350  KISDLVRRRLVPMQVDSRETPRLHQLVSAFSSKOKLQAPTKKRALPGDLPNGYHLHQ  409
Db      363  ---ELVNGPLP-NISNGEIVDGNFS-----YADIAI-----  391
Oy      410  LQTECISPPFRRLGSSRRRLTRGKMSGRAPSCPTPGKIENTAPKTOGLR-----  463
Db      392  --YRC-DQFYEMAGEGTRFCBADGKMTGNBSPCKPTGCKEFTVTRGLVGGRPAMKAMP  448
Oy      464  WQAIYVRTSGVHDGSLHKAMFLVCSGALVNERTVVAAHCVTDLKVWIKTADLKV  523
Db      449  WMAHLHTPRGP-----FCGDTLGDQWVLTAAHCLVSPVTSPIILDSSFSVI  496
Oy      524  LGKF-YRDDRDREKTIQSLQISAILHPYVDPLLDADIAILKLDKARISTRVOPICLA  582
Db      497  LGKHAKDKOTBTGTV---QVAQIVHAPAFNFTFLADIALKLESAPRLNPIYTPICLL  553
Oy      583  ASRDLSF---QESHITVAGNVLADVRSPGKNDTLRSGVSVVDSLCEQHEDHGI  639
Db      554  SEERATATLVGREAATV--GMG---HSDQGFANSLREVFPLVTVSTCNKTYD----  603
Oy      640  PVSVTDNMFCAWEPPTABSDICTAETGTGIAAVSFERASPEPRNHLGLVMSYDKTCSH  699
Db      604  -FTVTSMDICGFG-EGGKDCRGDSGG--PLAFERTTA-EKVVQGEVVTWGMG--CGR  655
Oy      700  RLS-TAFTKVLPEKDWIERM  719
Db      656  KNKYGVTNVIQVLPWIDEVN  676

```

## RESULT 14

0868H5 PRELIMINARY; PRT; 680 AA.

ID 0868H5, PRELIMINARY; PRT; 680 AA.  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE Mannose-binding lectin associated serine protease-1.  
 GN Name=MASP1/3;  
 OS Branchiostoma belcheri (Amphioxus).  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 OC Branchiostoma.  
 NCBI\_TaxID=7741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2593355; PubMed=12707349;  
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsushita A., Takahashi M.,  
 RA Matsushita M., Fujita T.;  
 RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1  
 RT and MASP-3 involved in the lectin complement pathway traced back to  
 RT the invertebrate, amphioxus";  
 RL J. Immunol. 170:4701-4707(2003).  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB089507; BAC75888.1; -.  
 DR HSSP; P00736; IAPQ.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006956; P:complement activation; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Axx\_hydroxyl\_S.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR011361; Pept\_S1\_Comp\_Act.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 2.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sushi; 2.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PIRSF; PIRSF001155; Clr\_Cls\_MASP; 1.  
 DR PRINTS; PRO0722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 2.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00020; Tryp\_Sec; 1.  
 DR PROSITE; PS00010; Axx\_HYDROXYL; UNKNOWN\_1.  
 DR PROSITE; PS01180; CUB; 2.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS01187; EGF\_CA; 1.  
 DR PROSITE; PS50923; SUSHI; 2.  
 DR PROSITE; PS50240; TRYPsin\_DOM; 1.  
 DR PROSITE; PS00134; TRYPsin\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPsin\_SER; 1.  
 KM EGF-like domain; Hydroxylase; Lectin; Protease; Serine protease.  
 SQ SEQUENCE 680 AA; 75394 MW; 9837DF86B1C6766 CRC64;

Query Match 15.3%; Score 604; DB 2; Length 680;  
 Best Local Similarity 27.6%; Pred. No. 1.2e-36;  
 Matches 186; Conservative 80; Mismatches 229; Indels 178; Gaps 32;

QY 77 DSCLI-HPGCTIFENCSCKNGSGTLDDFYKGFCAECRAG-WTGGD---C-MRCG- 129  
 DB 152 DECAVDNKGGMHFN-----CHN-----YISGYCS-CRAGYWMKRETCFGCGR 195  
 QY 130 QVLRAPKGOILLBS-----YPLNAHCEWTIAKPGFVQLRPFVMSLEFD-----YMGQY 179  
 DB 196 QVLTQLSLGTSISSEPRPLRYLVDCDKIKQVEPRYVTLQF---DDPFDVQGEHVSQCPY 252  
 QY 180 DYVEVRDGDNRDGGIIRKVCGERPAPDIQSIGSLHVLFFSHDSGKNDFGFAIYEITAC 239  
 DB 253 DHLKIQAGDEKYGK---CCGKTVPPITSTIDHNMRFVFFSHDSGKNGFRATYFT---- 304

QY 240 SSSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGPVNGYOKITGGPGL 299  
 DB 305 -----TAPFCAL-----SAP-----AYGT 319  
 QY 300 INGRHAKIGTVSPFCNNSVLSGNEKRTQONGESGKQPI-C-ACRPPKISDLVRR 358  
 DB 320 MEGSNFTYSQKVSFACGEGYLLDPDHRVCOADGSGSVQPTCLVNVCGPP----- 370  
 QY 359 VLMQVQSRREPLHQLYSAFSPKQKQSAPTKKPAPFGDLPMGQHLHTQLQ-YECTSP 417  
 DB 371 -----PNTSNGEIEVDGNFSTADIATIRC-DQ 396  
 QY 418 FYRRLGSSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGR-----WPMQALYRR 471  
 DB 397 FYMAGEGRTFCFADGKMTNERSCKPTGCKPEFVTRGKLVGRPAMRGSPMAMJHRT 456  
 QY 472 TSGVHDGSLHKAMFLVCSGALNVERTVVAAACVTDLGKVTMIKTADLVYLGKF-YRD 530  
 DB 457 PRGP-----FCGGTLTGDDQWVLTAAHCLVSPVTSPIKDSFSEVILGKHVARD 504  
 QY 531 DDDDEKTIOSLOISATIIHENVPIILDDADITKLIDKARISTRVQPICLAASRDISTS 590  
 DB 505 KDTTEQTVQVAQTAA--HPAFNFTTSLADIALKLASPARLNPYITPICLSSEETAT 561  
 QY 591 F---QESHITVAGMNVLADVRSPGKNDLTRSGVSVDSILGCEQEDHGHIPVSVDNM 647  
 DB 562 LVREGRAVY--GNG-----HSDGFIANELREVPFLVDVNTGNKTYD-----FTYTSDM 610  
 QY 648 FCASWEPTAPSDICTAETGIIAIVSPGGRASPPRRHMLGLVMSYDKTCSHLS-TAFT 706  
 DB 611 ICAGFQ-EGGKXDCRGDSG--PLAFPERYA--EKWQGVVSMGNG--CGRKKYGVYT 663  
 QY 707 KVLPRKDMIERNM 719  
 DB 664 NVQLYLPWIDEM 676

RESULT 15  
 ID Q868H6 PRELIMINARY; PRT; 688 AA.  
 AC Q868H6;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
 DE Mannose-binding lectin associated serine protease-3.  
 GN Name=MASP-3;  
 OS Branchiostoma belcheri (Amphioxus).  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 OC Branchiostoma.  
 NCBI\_TaxID=7741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Notochord;  
 RX MEDLINE=22593355; PubMed=12707349;  
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsushita A., Takahashi M.,  
 RA Matsushita M., Fujita T.;  
 RT "Origin of mannose-binding lectin-associated serine protease (MASP)-1  
 RT and MASP-3 involved in the lectin complement pathway traced back to  
 RT the invertebrate, amphioxus";  
 RL J. Immunol. 170:4701-4707(2003).  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AB089268; BAC75887.1; -.  
 DR HSSP; P00760; IEXX.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006956; P:complement activation; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000152; Axx\_hydroxyl\_S.

DR InterPro; IPR000859; CUB.  
DR InterPro; IPR001881; EGF\_CA.  
DR InterPro; IPR006209; EGF\_Like.  
DR InterPro; IPR001254; Peptidase\_S1.  
DR InterPro; IPR001314; Peptidase\_S1A.  
DR InterPro; IPR001361; Pept\_S1\_Comp\_Act.  
DR InterPro; IPR009003; Pept\_Set\_Cys.  
DR InterPro; IPR000436; Subst\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 2.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Subst; 2.  
DR Pfam; PF00089; Trypsin; 1.  
DR PIRSF; PIRSF001155; C1r\_C1s\_MASP; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 2.  
DR SMART; SM00179; EGF\_CA; 1.  
DR SMART; SM00020; Tryp\_Spc; 1.  
DR PROSITE; PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
DR PROSITE; PS01180; CUB; 2.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS01187; EGF\_CA; 1.  
DR PROSITE; PS50923; SUSH1; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
DR EGF-like domain; Hydrolyase; Lectin; Protease; Serine protease.  
SQ SEQUENCE 688 AA; 76890 MW; 14B3AD8215BD4D15 CRC64;

Query Match 15.1%; Score 597; DB 2; Length 688;

Best Local Similarity 26.6%; Pred. No. 4.1e-36;  
Matches 197; Conservative 88; Mismatches 244; Indels 212; Gaps 36;

QY 46 CEYDQIECV-----CPGKREV-----VGYT 65  
DB 84 CEYDYVKYMEEDKLVGLFCGTEDTDEQVPGDRVIESGSLSEFKSDPSNADRHGFA 143  
QY 66 IPCCNENEEDSCLIHPGCTIFENCKSCRNGSWGTLDDFYVKGFYCAECRAG-WYGGD 124  
DB 144 VHYRVVDREDC-AVDNGSCHHF-----CHN-----YISGYCS-CRAGYWMKD 185  
QY 125 ---C-MRGG-QVLRAPKQIILLES---YPLAHCEWTIIHAKPGFVQLRFVMLSLERD- 174  
DB 186 RETCFPGCGQVLYTLSTISSPEYRLYPVLDGDMKIQVEPGYVTVLQF---DDDFV 242  
QY 175 ---YMCQYDVEVRDGNRDGQIIKRVCGNERPAPIQSIGSLHVLPHSDGSKNPDGF 229  
DB 243 EQHPEVSCPYDHLTKYKADKGP---YCGKTVPTITSTDHMHVFFHSDDSGENKGF 298  
QY 230 HAIYEITACSSSPCFHDGTCVLDAKASYKCACLAGYTGRCENILLEENCSDPGGPVNG 289  
DB 299 RAYVFT-----TARPEAL-----SAP----- 315  
QY 290 YQKITGPGGLNGRHAIGTVVSFFCNNSYVLSGNEKTCQONGEMSGKQPICIKACREP 349  
DB 316 ---AVGTWGSNFTYSQKVSFACGEGYILDGPHRVCOADSGWSGVQPTC----- 362  
QY 350 KISDLVRRRLPMQVQSRETPLHQLYSAFQKQLQSAPTKKPALFGDLPMGYOHLHTQ 409  
DB 363 ---ELVNGGPLP-NISNGEIVDGNFS-----YADIAI----- 391  
QY 410 LQYECISPFYRRLLGSSRRTCLRTGWSGRAPSCIPICGI-----ENIT--APKTQGLRW 462  
DB 392 --YRC-DQFYEMAGEGTRFCCEGKMTGNEPSCKPICGESSFPSSRDRIVGGPSKKG-AW 447  
QY 463 PMQAAIYRTSGVNHGSLHKAMFL---VCSGALVNERTVVAACHVTDLCKVTMIKTAD 519  
DB 448 PMQAAV-----IHQGAPRIKPCGCGALVDKMKILTAACV---GENDILPTGY 493  
QY 520 LKVVIGKPYRDDDEKTIQSLQISAILHPYVDPIILDADIAIKLIDKARISTRVQPI 579  
DB 494 FNVSLGLHKKEKPEDDNVVFP--EVERVIRHPMDKDNFSDIALLEKEVDLTDYIRPV 551

QY 580 CLAAS--RDLSSTFOESH-TVAGMNVLADVRSPGFKNDTLRSGVSVVSDSLCEQHED 636  
DB 552 CLQPSGRQSAQVQEGRAGVVTGKRTSWLF--GSEANTLQEVVFPVDOECVSAVEG 609  
QY 637 HGIPVSVTDNMFCASMEPTAPSDICTAETGIIAASFPGRASPEPRWHLMLGLVSWSYDKT 636  
DB 610 ---DYPTGMLCAGLR-IGKXSCDGDSCGPIILFDQPDPT-----RYVAGLVSWGEPS 661  
QY 697 CSH-RUSTAFTKVLPEKDWIE 716  
DB 662 CGRARKYGVARYENFVQWIK 682

Search completed: July 12, 2005, 17:13:18  
Job time : 199 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

## OM protein - protein search, using sw model

Run on: July 12, 2005, 17:08:11 ; Search time 43 Seconds  
(without alignments)  
1249.938 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945  
Sequence: 1 MELGCTQLGTLFLQLLLS.....LSTAFKVLPEKWIERNKK 720Scoring table: BLOSUM62  
Gapco 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/5B\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	665	16.9	1019	1	US-08-296-014A-4
3	665	16.9	1019	2	US-08-596-405-4
4	665	16.9	1019	2	US-08-877-620-4
5	665	16.9	1019	4	US-09-287-368-4
6	665	16.9	1019	4	US-09-626-795-4
7	665	16.9	1083	1	US-08-296-014A-2
8	665	16.9	1083	2	US-08-596-405-2
9	665	16.9	1083	2	US-08-877-620-2
10	665	16.9	1083	4	US-09-287-368-2
11	665	16.9	1083	4	US-09-626-795-2
12	482	12.0	699	4	US-09-949-016-6138
13	475	12.0	717	4	US-09-949-016-1182
14	399.5	10.1	691	4	US-09-949-016-7775
15	327	8.3	855	4	US-09-027-337-2
16	327	8.3	855	4	US-09-644-600-2
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33	310.5	7.9	419	5	PCT-US92-10243-1	Sequence 1, Appl1
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35	310.5	7.9	460	2	US-08-756-506-4	Sequence 4, Appl1
36	310.5	7.9	461	4	US-10-182-263-2	Sequence 2, Appl1
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80	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appl1
81	280	7.1	562	4	US-09-703-695A-4	Sequence 4, Appl1
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543	200.5	5.1	415	4	US-09-906-618-104	Sequence 104, App	616	192.5	4.9	225	2	US-08-557-146-12	Sequence 12, Appl
544	200.5	5.1	769	4	US-09-949-016-11019	Sequence 11019, A	617	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
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546	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	619	192.5	4.9	281	2	US-08-628-198-7	Sequence 7, Appl
547	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	620	192.5	4.9	281	5	US-09-201-038-7	Sequence 7, Appl
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551	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl	624	191.5	4.9	224	2	US-08-766-982-13	Sequence 13, Appl
552	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	625	191.5	4.9	224	3	US-08-944-483-36	Sequence 36, Appl
553	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	626	191.5	4.9	224	3	US-09-296-219-13	Sequence 13, Appl
554	199.5	5.1	2556	4	US-08-889-232-2	Sequence 2, Appl	627	191.5	4.9	225	2	US-09-027-137-5	Sequence 5, Appl
555	199.5	5.1	2556	4	US-09-121-457-2	Sequence 2, Appl	628	191.5	4.9	225	4	US-09-644-600-5	Sequence 5, Appl
556	199	5.0	249	4	US-09-949-016-8151	Sequence 8151, Ap	629	191.5	4.9	225	4	US-09-654-600A-5	Sequence 5, Appl
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564	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	637	191	4.8	254	4	US-09-679-426-525	Sequence 525, App
565	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	638	191	4.8	254	4	US-09-759-143-525	Sequence 525, App
566	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	639	191	4.8	254	4	US-09-651-236-525	Sequence 525, App
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573	198.5	5.0	223	4	US-09-601-318-2	Sequence 2, Appl	646	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
574	198.5	5.0	229	3	US-09-120-582-2	Sequence 2, Appl	647	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
575	198.5	5.0	232	2	US-08-978-404B-45	Sequence 46, Appl	648	189	4.8	220	4	US-09-679-426-327	Sequence 327, App
576	198.5	5.0	849	4	US-09-949-016-10271	Sequence 10271, A	649	189	4.8	220	4	US-09-759-143-327	Sequence 327, App
577	198	5.0	242	3	US-08-944-483-57	Sequence 57, Appl	650	189	4.8	220	4	US-09-651-236-327	Sequence 327, App
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579	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl	652	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl
580	197.5	5.0	222	1	US-08-266-407A-46	Sequence 46, Appl	653	189	4.8	225	2	US-09-644-600-4	Sequence 4, Appl
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586	196.5	5.0	300	1	US-08-448-937A-51	Sequence 1, Appl	659	189	4.8	233	2	US-09-154-344-2	Sequence 2, Appl
587	196.5	5.0	2523	4	US-08-185-432-18	Sequence 18, Appl	660	189	4.8	253	3	US-08-930-188-2	Sequence 2, Appl
588	196.5	5.0	2523	4	US-08-889-232-3	Sequence 3, Appl	661	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
589	196.5	5.0	2523	4	US-09-121-457-3	Sequence 3, Appl	662	189	4.8	253	4	US-09-764-762-3	Sequence 3, Appl
590	195.5	5.0	232	3	US-08-944-483-55	Sequence 45, Appl	663	189	4.8	233	5	PCT-US96-04294-2	Sequence 2, Appl
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592	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	665	189	4.8	312	4	US-09-023-942A-4	Sequence 4, Appl
593	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	666	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
594	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	667	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
595	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	668	189	4.8	449	4	US-09-679-426-617	Sequence 617, App
596	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	669	189	4.8	449	4	US-09-759-143-617	Sequence 617, App
597	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	670	189	4.8	449	4	US-09-651-236-617	Sequence 617, App
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603	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	676	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
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607	195.5	5.0	2471	4	US-09-121-457-1	Sequence 1, Appl	680	188	4.8	254	4	US-09-651-236-523	Sequence 523, App
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610	194.5	4.9	415	4	US-09-802-633-2	Sequence 2, Appl	683	188	4.8	253	3	US-08-807-151-5	Sequence 5, Appl
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686	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appli	759	181.5	4.6	259	1	US-08-467-156A-8	Sequence 8, Appli
687	188	4.8	333	4	US-08-991-761A-8	Sequence 8, Appli	760	181.5	4.6	259	2	US-08-628-198-8	Sequence 8, Appli
688	187.5	4.8	224	3	US-08-944-483-35	Sequence 35, Appli	761	181.5	4.6	299	3	US-09-201-038-8	Sequence 8, Appli
689	187.5	4.8	242	3	US-08-944-483-29	Sequence 29, Appli	762	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appli
690	187.5	4.8	255	3	US-08-906-769-83	Sequence 83, Appli	763	181	4.6	336	4	US-09-800-729-86	Sequence 648, Ap
691	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appli	764	180	4.6	254	4	US-09-949-016-6948	Sequence 648, Ap
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694	187.5	4.8	255	3	US-09-012-431-93	Sequence 83, Appli	767	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App
695	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appli	768	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App
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698	186	4.7	110	4	US-09-341-461-28	Sequence 28, Appli	771	179.5	4.6	205	4	US-09-232-149A-176	Sequence 176, App
699	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appli	772	179.5	4.6	205	4	US-09-159-812-176	Sequence 176, App
700	186	4.7	230	2	US-08-266-407A-47	Sequence 47, Appli	773	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App
701	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appli	774	179.5	4.6	205	4	US-09-685-166A-176	Sequence 176, App
702	186	4.7	230	2	US-08-766-982-12	Sequence 12, Appli	775	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App
703	186	4.7	230	3	US-08-944-483-53	Sequence 53, Appli	776	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App
704	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appli	777	179.5	4.6	205	4	US-09-679-426-176	Sequence 176, App
705	186	4.7	232	2	US-08-897-340-31	Sequence 31, Appli	778	179.5	4.6	205	4	US-09-759-143-176	Sequence 176, App
706	186	4.7	232	3	US-09-252-329-31	Sequence 31, Appli	779	179.5	4.6	205	4	US-09-651-236-176	Sequence 176, App
707	186	4.7	326	3	US-09-411-977-3	Sequence 3, Appli	780	179.5	4.6	259	6	5223425-2	Patent No. 5223425
708	186	4.7	326	4	US-10-057-951-3	Sequence 3, Appli	781	179.5	4.6	259	6	5223425-2	Patent No. 5223425
709	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appli	782	179.5	4.6	728	4	US-08-981-192-2	Sequence 2, Appli
710	185.5	4.7	261	3	US-08-163-919A-2	Sequence 2, Appli	783	179.5	4.6	788	4	US-09-908-322-2	Sequence 2, Appli
711	185.5	4.7	261	4	US-08-462-515-2	Sequence 2, Appli	784	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appli
712	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appli	785	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appli
713	185.5	4.7	306	4	US-09-386-642-53	Sequence 53, Appli	786	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appli
714	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appli	787	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appli
715	185.5	4.7	711	1	US-08-334-177-2	Sequence 8, Appli	788	179	4.5	233	3	US-09-578-103-4	Sequence 4, Appli
716	185.5	4.7	711	1	US-08-666-082B-1	Sequence 2, Appli	789	179	4.5	334	3	US-09-032-215-22	Sequence 22, Appli
717	185.5	4.7	711	5	PCT-US95-13630-2	Sequence 5, Appli	790	178.5	4.5	250	3	US-08-944-483-68	Sequence 68, Appli
718	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appli	791	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appli
719	185	4.7	247	1	US-08-944-483-49	Sequence 49, Appli	792	178.5	4.5	401	2	US-08-839-008-5	Sequence 5, Appli
720	185	4.7	258	1	US-08-744-023-3	Sequence 3, Appli	793	178.5	4.5	468	2	US-08-839-008-7	Sequence 7, Appli
721	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appli	794	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appli
722	185	4.7	258	3	US-09-261-767-3	Sequence 3, Appli	795	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appli
723	184	4.7	314	4	US-09-023-942A-6	Sequence 6, Appli	796	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appli
724	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appli	797	178.5	4.5	933	3	US-08-936-135-6	Sequence 6, Appli
725	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appli	798	178.5	4.5	933	3	US-09-439-711C-6	Sequence 6, Appli
726	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	799	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appli
727	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	800	177.5	4.5	248	2	US-09-213-970-3	Sequence 3, Appli
728	184	4.7	314	4	US-09-902-775A-257	Sequence 257, App	801	177.5	4.5	1964	3	US-09-467-997-1	Sequence 1, Appli
729	184	4.7	314	4	US-09-903-603A-257	Sequence 257, App	802	177	4.5	102	3	US-09-314-135-7	Sequence 7, Appli
730	184	4.7	314	4	US-09-904-920A-257	Sequence 257, App	803	177	4.5	110	4	US-09-270-767-45768	Sequence 45768, A
731	184	4.7	314	4	US-09-909-064-257	Sequence 257, App	804	177	4.5	223	4	US-08-278-091-11	Sequence 11, Appli
732	184	4.7	314	4	US-09-905-381A-257	Sequence 257, App	805	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appli
733	184	4.7	314	4	US-09-906-618-257	Sequence 257, App	806	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appli
734	184	4.7	314	4	US-08-766-982-2	Sequence 2, Appli	807	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appli
735	183.5	4.7	711	2	US-09-296-219-2	Sequence 2, Appli	808	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appli
736	183.5	4.7	711	4	US-09-600-991-20	Sequence 20, Appli	809	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appli
737	183.5	4.7	711	4	US-09-601-040A-12	Sequence 12, Appli	810	177	4.5	240	2	US-08-615-271-11	Sequence 11, Appli
738	183.5	4.7	711	4	US-09-949-016-6981	Sequence 6981, Ap	811	177	4.5	240	2	US-09-074-660-11	Sequence 11, Appli
739	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appli	812	177	4.5	240	3	US-09-074-659-11	Sequence 11, Appli
740	183.5	4.7	722	4	US-10-177-661-6	Sequence 6, Appli	813	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appli
741	183.5	4.7	722	4	US-09-023-942A-8	Sequence 8, Appli	814	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appli
742	183.5	4.7	722	4	US-08-252-493C-9	Sequence 9, Appli	815	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appli
743	182.5	4.6	258	4	US-09-276-197-9	Sequence 9, Appli	816	177	4.5	729	3	5378464-2	Patent No. 5378464
744	182.5	4.6	484	2	US-08-872-855-4	Sequence 4, Appli	817	177	4.5	830	6	5378464-2	Patent No. 5378464
745	182.5	4.6	720	3	US-09-734-675-2	Sequence 2, Appli	818	177	4.5	232	1	US-08-990-301A-4	Sequence 4, Appli
746	182.5	4.6	405	3	US-08-872-855-7	Sequence 7, Appli	819	177	4.5	232	1	US-08-936-135-12	Sequence 22, Appli
747	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appli	820	177	4.5	901	3	US-09-439-711C-22	Sequence 22, Appli
748	182	4.6	1055	4	US-09-855-722-2	Sequence 2, Appli	821	176.5	4.5	901	3	US-08-936-135-24	Sequence 24, Appli
749	182	4.6	1055	4	US-08-400-159-8	Sequence 8, Appli	822	176.5	4.5	906	4	US-08-936-135-8	Sequence 8, Appli
750	182	4.6	1055	4	US-09-855-722-3	Sequence 3, Appli	823	176.5	4.5	909	3	US-08-936-135-10	Sequence 10, Appli
751	182	4.6	1212	4	US-09-214-278-5	Sequence 5, Appli	824	176.5	4.5	909	4	US-09-439-711C-8	Sequence 8, Appli
752	182	4.6	1212	4	US-08-611-729A-8	Sequence 8, Appli	825	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appli
753	182	4.6	1238	3	US-09-195-524-8	Sequence 8, Appli	826	176.5	4.5				
754	182	4.6	1238	3			827	176.5	4.5				
755	182	4.6	1257	4			828	176.5	4.5				
756	182	4.6	1257	4			829	176.5	4.5				
757	182	4.6	1257	4			830	176.5	4.5				

831	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl	904	170	4.3	213	3	US-08-906-769-149	Sequence 149, App
832	176.5	4.5	925	4	US-09-116-473-2	Sequence 2, Appl	905	170	4.3	213	3	US-08-906-616-149	Sequence 149, App
833	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl	906	170	4.3	213	3	US-08-639-075A-149	Sequence 149, App
834	176.5	4.5	926	4	US-09-439-711C-14	Sequence 14, Appl	907	170	4.3	213	3	US-09-012-431-149	Sequence 149, App
835	176.5	4.5	926	3	US-08-936-135-16	Sequence 16, Appl	908	170	4.3	213	3	US-09-012-692-149	Sequence 149, App
836	176.5	4.5	931	4	US-09-439-711C-16	Sequence 16, Appl	909	170	4.3	213	3	US-08-906-613-149	Sequence 149, App
837	176	4.5	233	3	US-09-004-731-27	Sequence 27, Appl	910	170	4.3	717	4	US-09-601-040A-8	Sequence 8, Appl
838	176	4.5	233	3	US-08-749-699-27	Sequence 27, Appl	911	170	4.3	729	4	US-09-601-040A-4	Sequence 4, Appl
839	176	4.5	233	3	US-09-004-729-27	Sequence 27, Appl	912	170	4.3	1148	4	US-08-882-046-4	Sequence 4, Appl
840	176	4.5	242	3	US-08-944-483-58	Sequence 58, Appl	913	170	4.3	1148	4	US-09-566-047-4	Sequence 4, Appl
841	176	4.5	266	3	US-09-004-731-24	Sequence 24, Appl	914	169	4.3	95	3	US-09-374-135-8	Sequence 8, Appl
842	176	4.5	266	3	US-08-749-699-24	Sequence 24, Appl	915	169	4.3	110	4	US-09-341-461-25	Sequence 25, Appl
843	176	4.5	266	4	US-09-004-729-24	Sequence 24, Appl	916	169	4.3	237	5	US-08-096-946-11	Sequence 11, Appl
844	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl	917	169	4.3	237	5	PCT-US94-07329-11	Sequence 11, Appl
845	175	4.4	112	4	US-09-438-046-21	Sequence 21, Appl	918	169	4.3	237	5	PCT-US95-06157-1	Sequence 11, Appl
846	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl	919	169	4.3	375	4	US-09-755-100A-11	Sequence 11, Appl
847	175	4.4	909	4	US-09-439-711C-18	Sequence 18, Appl	920	168.5	4.3	222	6	5223425-6	Patent No. 5223425
848	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl	921	168.5	4.3	222	6	5223425-6	Patent No. 5223425
849	175	4.4	926	4	US-09-439-711C-20	Sequence 20, Appl	922	168.5	4.3	333	4	US-09-142-027A-12	Sequence 12, Appl
850	175	4.4	931	4	US-09-583-638-4	Sequence 4, Appl	923	168	4.3	245	3	US-08-906-769-121	Sequence 12, App
851	174	4.4	265	2	US-08-177-109A-57	Sequence 57, Appl	924	168	4.3	245	3	US-08-906-616-121	Sequence 121, App
852	174	4.4	265	2	US-08-687-706-57	Sequence 57, Appl	925	168	4.3	245	3	US-08-639-075A-121	Sequence 121, App
853	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl	926	168	4.3	245	3	US-09-012-431-121	Sequence 121, App
854	174	4.4	286	2	US-08-628-198-9	Sequence 9, Appl	927	168	4.3	245	3	US-09-012-692-121	Sequence 121, App
855	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl	928	168	4.3	245	3	US-08-906-613-121	Sequence 121, App
856	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl	929	167.5	4.2	261	1	US-08-744-026-5	Sequence 5, Appl
857	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, App	930	167.5	4.2	261	2	US-09-102-732-5	Sequence 5, Appl
858	173.5	4.4	294	4	US-10-067-422-12	Sequence 12, Appl	931	167.5	4.2	261	3	US-09-083-521-6	Sequence 6, Appl
859	173.5	4.4	414	4	US-09-270-767-16426	Sequence 46426, A	932	167.5	4.2	261	3	US-09-261-767-5	Sequence 5, Appl
860	173.5	4.4	717	3	US-08-872-855-9	Sequence 9, Appl	933	167.5	4.2	261	4	US-09-413-049-1	Sequence 1, Appl
861	173	4.4	211	4	US-09-220-731-25	Sequence 25, Appl	934	167.5	4.2	261	4	US-09-907-402-1	Sequence 10, Appl
862	173	4.4	211	3	US-09-242-999-20	Sequence 20, Appl	935	167.5	4.2	261	4	US-09-618-259-10	Sequence 4, Appl
863	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl	936	167.5	4.2	262	1	US-08-744-026-4	Sequence 4, Appl
864	172.5	4.4	449	2	US-08-839-008-2	Sequence 2, Appl	937	167.5	4.2	262	2	US-09-102-732-4	Sequence 4, Appl
865	172.5	4.4	449	4	US-09-919-497-89	Sequence 89, Appl	938	167.5	4.2	262	3	US-09-261-767-4	Sequence 4, Appl
866	172.5	4.4	458	4	US-09-949-016-7238	Sequence 7238, Ap	939	167.5	4.2	933	4	US-09-583-638-2	Sequence 2, Appl
867	172.5	4.4	1248	3	US-08-882-046-6	Sequence 6, Appl	940	167	4.2	103	3	US-09-374-135-5	Sequence 5, Appl
868	172.5	4.4	1248	4	US-09-566-047-6	Sequence 6, Appl	941	166.5	4.2	520	3	US-09-068-740A-3	Sequence 3, Appl
869	172.5	4.4	250	4	US-09-270-767-33709	Sequence 33709, A	942	166.5	4.2	702	3	US-09-068-740A-4	Sequence 4, Appl
870	172	4.4	357	4	US-09-270-767-43564	Sequence 43564, A	943	166.5	4.2	723	3	US-09-068-740A-9	Sequence 9, Appl
871	172	4.4	357	4	US-09-270-767-58936	Sequence 58936, A	944	166.5	4.2	723	4	US-09-423-753-27	Sequence 27, Appl
872	172	4.4	721	3	US-08-981-392-5	Sequence 5, Appl	945	166.5	4.2	723	4	US-09-641-612-6	Sequence 6, Appl
873	172	4.4	721	4	US-09-908-322-5	Sequence 5, Appl	946	166	4.2	124	6	5514582-38	Patent No. 5514582
874	171.5	4.3	238	3	US-08-944-483-39	Sequence 39, Appl	947	166	4.2	124	6	5514582-38	Patent No. 5514582
875	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App	948	166	4.2	237	3	US-08-768-859A-1	Sequence 1, Appl
876	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App	949	166	4.2	237	3	US-08-767-820A-1	Sequence 1, Appl
877	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App	950	166	4.2	237	3	US-08-622-046B-7	Sequence 7, Appl
878	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl	951	166	4.2	237	3	US-08-944-483-38	Sequence 38, Appl
879	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App	952	166	4.2	237	3	US-09-100-264-3	Sequence 3, Appl
880	171.5	4.3	259	3	US-08-749-699-85	Sequence 85, Appl	953	166	4.2	237	4	US-09-303-339-2	Sequence 2, Appl
881	171.5	4.3	259	3	US-09-012-692-190	Sequence 190, App	954	166	4.2	237	4	US-08-843-076D-7	Sequence 7, Appl
882	171.5	4.3	259	3	US-08-906-613-190	Sequence 190, App	955	166	4.2	237	4	US-09-303-208-1	Sequence 1, Appl
883	171.5	4.3	259	4	US-09-004-729-85	Sequence 85, Appl	956	166	4.2	243	3	US-08-944-483-70	Sequence 70, Appl
884	171.5	4.3	262	2	US-08-790-137-1	Sequence 1, Appl	957	166	4.2	441	4	US-09-949-016-10792	Sequence 10792, A
885	171.5	4.3	262	2	US-08-790-137-3	Sequence 3, Appl	958	166	4.2	923	4	US-09-439-711C-2	Sequence 2, Appl
886	171.5	4.3	262	2	US-08-681-151-4	Sequence 4, Appl	959	165.5	4.2	240	1	US-08-472-228A-1	Sequence 1, Appl
887	171.5	4.3	262	2	US-08-824-874-4	Sequence 4, Appl	960	165.5	4.2	240	3	US-09-146-831-1	Sequence 1, Appl
888	171.5	4.3	262	3	US-08-807-151-4	Sequence 4, Appl	961	165.5	4.2	240	5	PCT-US96-09303-1	Sequence 1, Appl
889	171.5	4.3	262	3	US-09-210-084-4	Sequence 4, Appl	962	165.5	4.2	333	1	US-08-597-545-2	Sequence 2, Appl
890	171.5	4.3	262	3	US-09-478-957-4	Sequence 4, Appl	963	165.5	4.2	333	1	US-08-457-135-2	Sequence 2, Appl
891	171.5	4.3	262	4	US-09-764-762-4	Sequence 4, Appl	964	165	4.2	101	3	US-09-374-135-4	Sequence 4, Appl
892	171.5	4.3	262	4	US-09-618-359-9	Sequence 9, Appl	965	164	4.2	351	3	US-09-345-041-11	Sequence 11, Appl
893	171.5	4.3	666	3	US-09-341-587-1	Sequence 1, Appl	966	164	4.2	351	4	US-09-358-055B-11	Sequence 11, Appl
894	171.5	4.3	1785	3	US-09-341-587-3	Sequence 3, Appl	967	164	4.2	351	4	US-09-593-238-11	Sequence 11, Appl
895	171	4.3	262	4	US-09-025-059-4	Sequence 4, Appl	968	164	4.2	812	4	US-09-192-012-9	Sequence 9, Appl
896	171	4.3	262	4	US-09-755-100A-14	Sequence 14, Appl	969	163	4.1	441	4	US-09-949-016-11196	Sequence 11196, A
897	171	4.3	287	4	US-09-270-767-33263	Sequence 33263, A	970	163	4.1	607	4	US-09-907-794A-180	Sequence 180, App
898	171	4.3	287	4	US-09-270-767-48480	Sequence 48480, A	971	163	4.1	607	4	US-09-905-125A-180	Sequence 180, App
899	171	4.3	290	4	US-09-949-016-8166	Sequence 8166, Ap	972	163	4.1	607	4	US-09-802-775A-180	Sequence 180, App
900	171	4.3	717	4	US-09-601-040A-6	Sequence 6, Appl	973	163	4.1	607	4	US-09-806-700-190	Sequence 190, App
901	171	4.3	729	4	US-09-601-040A-2	Sequence 2, Appl	974	163	4.1	607	4	US-09-903-603A-190	Sequence 190, App
902	171	4.3	737	4	US-09-866-028-15	Sequence 15, Appl	975	163	4.1	607	4	US-09-904-920A-190	Sequence 190, App
903	171	4.3	737	4	US-09-944-457-15	Sequence 15, Appl	976	163	4.1	607	4	US-09-909-064-190	Sequence 190, App

977	163	4.1	607	4	US-09-905-381A-190	Sequence 190, App	1050	156	4.0	238	5	PCT-US95-06157-8	Sequence 8, Appl
978	163	4.1	607	4	US-09-906-618-190	Sequence 190, App	1051	156	4.0	244	3	US-08-768-859A-10	Sequence 10, Appl
979	162.5	4.1	1290	1	US-08-470-350B-2	Sequence 2, Appl	1052	156	4.0	244	3	US-08-767-820A-10	Sequence 10, Appl
980	161.5	4.1	251	3	US-08-944-483-28	Sequence 28, Appl	1053	156	4.0	244	3	US-08-622-046B-5	Sequence 5, Appl
981	161.5	4.1	832	3	US-08-981-392-6	Sequence 6, Appl	1054	156	4.0	244	3	US-08-622-046B-16	Sequence 16, Appl
982	161.5	4.1	832	4	US-09-908-322-6	Sequence 6, Appl	1055	156	4.0	244	3	US-09-100-264-5	Sequence 5, Appl
983	161.5	4.1	1025	4	US-09-834-309-5	Sequence 5, Appl	1056	156	4.0	244	4	US-08-843-076B-5	Sequence 5, Appl
984	161	4.1	270	4	US-09-949-016-7712	Sequence 7712, Ap	1057	156	4.0	244	5	PCT-US95-06157-10	Sequence 10, Appl
985	161	4.1	293	4	US-09-509-908-2	Sequence 2, Appl	1058	156	4.0	261	3	US-08-768-859A-6	Sequence 6, Appl
986	160.5	4.1	238	4	US-09-664-595A-15	Sequence 15, Appl	1059	156	4.0	261	3	US-08-767-820A-19	Sequence 19, Appl
987	160.5	4.1	263	4	US-09-949-016-6072	Sequence 9072, Ap	1060	156	4.0	261	3	US-08-876-820A-6	Sequence 6, Appl
988	160.5	4.1	319	4	US-09-270-767-42672	Sequence 42672, A	1061	156	4.0	261	3	US-08-622-046B-3	Sequence 3, Appl
989	160.5	4.1	661	4	US-09-949-016-6157	Sequence 6157, Ap	1062	156	4.0	261	3	US-08-622-046B-14	Sequence 14, Appl
990	160.5	4.1	665	4	US-09-949-016-10776	Sequence 10776, A	1063	156	4.0	261	3	US-09-100-264-7	Sequence 7, Appl
991	160	4.1	207	4	US-10-000-489-54	Sequence 46, Appl	1064	156	4.0	261	3	US-08-983-0750-7	Sequence 7, Appl
992	160	4.1	234	4	US-08-944-483-46	Sequence 10712, A	1065	156	4.0	261	3	US-08-843-076B-3	Sequence 3, Appl
993	160	4.1	268	4	US-09-949-016-60712	Sequence 10712, A	1066	156	4.0	261	5	PCT-US95-06157-6	Sequence 6, Appl
994	160	4.1	2871	4	US-09-538-092-1076	Sequence 1076, Ap	1067	156	4.0	278	5	US-09-949-016-7711	Sequence 7711, Ap
995	159.5	4.0	228	2	US-08-768-982-11	Sequence 11, Appl	1068	156	4.0	278	2	US-08-651-974-1	Sequence 1, Appl
996	159.5	4.0	228	2	US-09-296-219-11	Sequence 11, Appl	1069	155.5	3.9	247	2	US-09-213-390-1	Sequence 1, Appl
997	159.5	4.0	276	4	US-09-270-767-32048	Sequence 32048, A	1070	155.5	3.9	267	2	US-08-872-855-11	Sequence 11, Appl
998	159.5	4.0	276	4	US-09-270-767-47265	Sequence 47265, A	1071	155.5	3.9	830	3	US-08-872-855-11	Sequence 5, Appl
999	159	4.0	237	2	US-08-844-024-2	Sequence 2, Appl	1072	155	3.9	2489	4	US-09-911-842A-5	Sequence 5, Appl
1000	159	4.0	237	2	US-08-718-547-2	Sequence 2, Appl	1073	154.5	3.9	228	1	US-08-278-091-7	Sequence 7, Appl
1001	158.5	4.0	283	4	US-09-244-111-2	Sequence 2, Appl	1074	154.5	3.9	228	1	US-08-472-173-7	Sequence 7, Appl
1002	158.5	4.0	385	1	US-08-597-545-1	Sequence 1, Appl	1075	154.5	3.9	228	1	US-08-487-167-7	Sequence 7, Appl
1003	158.5	4.0	385	1	US-08-457-135-1	Sequence 1, Appl	1076	154.5	3.9	228	2	US-08-487-167-7	Sequence 7, Appl
1004	158.5	4.0	385	4	US-09-144-027A-10	Sequence 10, Appl	1077	154.5	3.9	228	2	US-08-482-816-7	Sequence 7, Appl
1005	158.5	4.0	833	1	US-08-264-534-6	Sequence 6, Appl	1078	154.5	3.9	228	2	US-08-296-149-7	Sequence 7, Appl
1006	158.5	4.0	833	1	US-08-083-590A-2	Sequence 2, Appl	1079	154.5	3.9	228	2	US-08-801-499-7	Sequence 7, Appl
1007	158.5	4.0	833	1	US-08-465-500-6	Sequence 6, Appl	1080	154.5	3.9	228	2	US-08-615-371-7	Sequence 7, Appl
1008	158.5	4.0	833	1	US-08-346-126-6	Sequence 6, Appl	1081	154.5	3.9	228	3	US-09-074-650-7	Sequence 7, Appl
1009	158.5	4.0	833	2	US-08-346-128-6	Sequence 6, Appl	1082	154.5	3.9	228	3	US-09-074-659-7	Sequence 7, Appl
1010	158.5	4.0	833	3	US-08-533-384-2	Sequence 2, Appl	1083	154.5	3.9	228	3	US-08-482-816-7	Sequence 7, Appl
1011	158.5	4.0	833	3	US-08-893-828-6	Sequence 6, Appl	1084	154.5	3.9	228	3	US-09-106-466A-7	Sequence 7, Appl
1012	158	4.0	156	3	US-09-261-416-6	Sequence 6, Appl	1085	154.5	3.9	228	3	US-09-106-466A-7	Sequence 7, Appl
1013	157.5	4.0	190	2	US-08-845-998-4	Sequence 4, Appl	1086	154	3.9	101	3	US-09-374-135-6	Sequence 6, Appl
1014	157.5	4.0	190	3	US-09-206-537-4	Sequence 4, Appl	1087	154	3.9	224	1	US-08-944-83-10	Sequence 40, Appl
1015	157.5	4.0	190	3	US-09-430-854-4	Sequence 4, Appl	1088	154	3.9	227	3	US-08-944-83-10	Sequence 2, Appl
1016	157.5	4.0	226	4	US-09-601-040A-28	Sequence 28, Appl	1089	154	3.9	248	2	US-08-921-426-4	Sequence 4, Appl
1017	157.5	4.0	228	3	US-08-944-483-55	Sequence 55, Appl	1090	154	3.9	248	2	US-08-816-915-4	Sequence 4, Appl
1018	157.5	4.0	255	3	US-08-906-769-91	Sequence 91, Appl	1091	154	3.9	248	3	US-08-816-915-4	Sequence 4, Appl
1019	157.5	4.0	255	3	US-08-906-616-91	Sequence 91, Appl	1092	154	3.9	248	5	PCT-US95-07743-4	Sequence 37, Appl
1020	157.5	4.0	255	3	US-08-817-795-91	Sequence 91, Appl	1093	154	3.9	248	5	US-08-824-084-1	Sequence 4, Appl
1021	157.5	4.0	255	3	US-08-639-075A-91	Sequence 91, Appl	1094	154	3.9	268	2	US-09-210-084-1	Sequence 1, Appl
1022	157.5	4.0	255	3	US-09-012-431-91	Sequence 91, Appl	1095	154	3.9	268	4	US-09-764-762-1	Sequence 1, Appl
1023	157.5	4.0	255	3	US-09-012-692-91	Sequence 91, Appl	1096	154	3.9	268	4	US-09-764-762-1	Sequence 33762, A
1024	157.5	4.0	255	3	US-08-906-613-91	Sequence 91, Appl	1097	154	3.9	321	4	US-09-270-767-33762	Sequence 48979, A
1025	157.5	4.0	255	5	PCT-US95-14442A-91	Sequence 91, Appl	1098	154	3.9	321	4	US-09-270-767-48979	Sequence 48979, A
1026	157	4.0	185	3	US-08-906-769-141	Sequence 141, App	1099	154	3.9	1466	6	US-08-944-83-10	Sequence 40, Appl
1027	157	4.0	185	3	US-08-906-616-141	Sequence 141, App	1100	154	3.9	1466	6	US-08-921-426-4	Sequence 4, Appl
1028	157	4.0	185	3	US-08-639-075A-141	Sequence 141, App	1101	154	3.9	1466	6	US-08-816-915-4	Sequence 4, Appl
1029	157	4.0	185	3	US-09-012-431-141	Sequence 141, App	1102	154	3.9	1466	6	US-09-210-084-1	Sequence 1, Appl
1030	157	4.0	185	3	US-09-012-692-141	Sequence 141, App	1103	154	3.9	1537	6	US-09-764-762-1	Sequence 33762, A
1031	157	4.0	185	3	US-08-906-613-141	Sequence 141, App	1104	154	3.9	1537	6	US-09-764-762-1	Sequence 33762, A
1032	157	4.0	610	6	US-08-906-613-141	Sequence 141, App	1105	154	3.9	1537	6	US-09-764-762-1	Sequence 33762, A
1033	157	4.0	610	6	US-08-906-613-141	Sequence 141, App	1106	154	3.9	1537	6	US-09-764-762-1	Sequence 33762, A
1034	157	4.0	647	4	US-09-949-016-10272	Sequence 10272, A	1107	154	3.9	1537	6	US-09-949-016-10272	Sequence 10272, A
1035	156.5	4.0	312	4	US-09-636-382A-15	Sequence 15, Appl	1108	154	3.9	1537	6	US-09-636-382A-15	Sequence 15, Appl
1036	156.5	4.0	363	4	US-09-845-583A-2	Sequence 2, Appl	1109	154	3.9	1847	6	US-09-845-583A-2	Sequence 2, Appl
1037	156	4.0	237	3	US-08-768-859A-16	Sequence 16, Appl	1110	154	3.9	1847	6	US-09-845-583A-2	Sequence 2, Appl
1038	156	4.0	237	3	US-08-768-859A-21	Sequence 21, Appl	1111	154	3.9	1947	6	US-09-845-583A-2	Sequence 2, Appl
1039	156	4.0	237	3	US-08-767-820A-16	Sequence 16, Appl	1112	154	3.9	1947	6	US-09-845-583A-2	Sequence 2, Appl
1040	156	4.0	237	3	US-08-767-820A-21	Sequence 21, Appl	1113	154	3.9	2039	6	US-09-845-583A-2	Sequence 2, Appl
1041	156	4.0	237	3	US-08-622-046B-1	Sequence 1, Appl	1114	154	3.9	2039	6	US-09-845-583A-2	Sequence 2, Appl
1042	156	4.0	237	3	US-08-622-046B-12	Sequence 12, Appl	1115	154	3.9	2039	6	US-09-845-583A-2	Sequence 2, Appl
1043	156	4.0	237	3	US-08-944-483-37	Sequence 37, Appl	1116	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appl
1044	156	4.0	237	3	US-09-100-264-1	Sequence 1, Appl	1117	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appl
1045	156	4.0	237	3	US-09-100-264-12	Sequence 12, Appl	1118	153.5	3.9	185	3	US-08-705-875A-5	Sequence 5, Appl
1046	156	4.0	237	3	US-08-843-076D-1	Sequence 1, Appl	1119	153.5	3.9	190	2	US-08-843-076D-1	Sequence 1, Appl
1047	156	4.0	237	4	US-08-843-076D-8	Sequence 8, Appl	1120	153.5	3.9	190	3	US-08-843-076D-8	Sequence 8, Appl
1048	156	4.0	238	3	US-08-768-859A-8	Sequence 8, Appl	1121	153.5	3.9	352	4	US-09-430-854-6	Sequence 6, Appl
1049	156	4.0	238	3	US-08-767-820A-8	Sequence 8, Appl	1122	153.5	3.9	352	4	US-09-902-540-5796	Sequence 9796, Ap

1123	153.5	3.9	610	1	US-08-365-470-3	Sequence 3, Appl1	1196	148.5	3.8	111	4	US-09-341-461-30	Sequence 30, Appl1
1124	153.5	3.9	610	3	US-09-209-668-19	Sequence 19, Appl1	1197	148	3.8	113	4	US-09-438-046-23	Sequence 23, Appl1
1125	153.5	3.9	610	3	US-09-009-490A-89	Sequence 89, Appl1	1198	148	3.8	218	3	US-09-578-303-3	Sequence 3, Appl1
1126	153.5	3.9	610	4	US-09-949-016-5942	Sequence 5942, Ap	1199	148	3.8	242	3	US-09-032-215-47	Sequence 47, Appl1
1127	153.5	3.9	1725	4	US-09-562-702A-20	Sequence 20, Appl1	1200	148	3.8	657	4	US-09-949-016-11365	Sequence 11365, A
1128	153.5	3.9	1725	4	US-09-561-818A-20	Sequence 20, Appl1	1201	148	3.8	657	4	US-09-949-016-11366	Sequence 11366, A
1129	153.5	3.9	1786	4	US-09-562-702A-18	Sequence 18, Appl1	1202	148	3.8	657	4	US-09-949-016-11367	Sequence 11367, A
1130	153.5	3.9	1786	4	US-09-561-818A-18	Sequence 18, Appl1	1203	148	3.8	657	4	US-09-949-016-11368	Sequence 11368, A
1131	153	3.9	158	3	US-09-374-135-2	Sequence 2, Appl1	1204	148	3.8	1480	3	US-09-191-647-7	Sequence 7, Appl1
1132	153	3.9	248	3	US-08-906-769-111	Sequence 11, App	1205	148	3.8	1480	3	US-09-540-245A-7	Sequence 7, Appl1
1133	153	3.9	248	3	US-08-906-616-111	Sequence 11, App	1206	148	3.8	1480	5	US-09-540-153-7	Sequence 7, Appl1
1134	153	3.9	248	3	US-08-817-795-111	Sequence 11, App	1207	148	3.8	1480	5	PCT-US91-0905-2	Sequence 2, Appl1
1135	153	3.9	248	3	US-08-639-075A-111	Sequence 11, App	1208	147.5	3.7	137	1	US-08-456-840-48	Sequence 48, Appl1
1136	153	3.9	248	3	US-09-012-431-111	Sequence 11, App	1209	147.5	3.7	137	1	US-08-466-407A-48	Sequence 48, Appl1
1137	153	3.9	248	3	US-09-012-692-111	Sequence 11, App	1210	147.5	3.7	197	2	US-08-892-544-48	Sequence 48, Appl1
1138	153	3.9	248	3	US-08-906-613-111	Sequence 11, App	1211	147.5	3.7	246	3	US-08-906-769-127	Sequence 127, App
1139	153	3.9	248	5	PCT-US95-14442A-111	Sequence 11, App	1212	147.5	3.7	246	3	US-08-906-616-127	Sequence 127, App
1140	153	3.9	254	3	US-09-578-303-5	Sequence 5, Appl1	1213	147.5	3.7	246	3	US-08-639-075A-127	Sequence 127, App
1141	153	3.9	286	4	US-09-270-767-45162	Sequence 45162, A	1214	147.5	3.7	246	3	US-09-012-431-127	Sequence 127, App
1142	152.5	3.9	267	4	US-09-949-016-10711	Sequence 10711, A	1215	147.5	3.7	246	3	US-09-012-692-127	Sequence 127, App
1143	152.5	3.9	642	4	US-08-872-855-10	Sequence 10, Appl1	1216	147.5	3.7	246	3	US-09-012-692-127	Sequence 127, App
1144	152	3.9	247	2	US-08-851-974-4	Sequence 4, Appl1	1217	147.5	3.7	574	6	US-08-906-613-127	Sequence 127, App
1145	152	3.9	247	2	US-09-213-190-4	Sequence 4, Appl1	1218	147.5	3.7	574	6	5378464-3	Sequence 127, App
1146	152	3.9	247	4	US-09-949-016-6457	Sequence 6457, Ap	1219	147.5	3.7	574	6	5378464-3	Sequence 127, App
1147	152	3.9	258	4	US-09-949-016-10661	Sequence 10661, A	1220	147.5	3.7	1765	4	US-09-562-702A-16	Sequence 16, Appl1
1148	152	3.9	1033	4	US-09-834-309-1	Sequence 1, Appl1	1221	147.5	3.7	1765	4	US-09-561-818A-16	Sequence 16, Appl1
1149	151.5	3.8	259	4	US-09-949-016-10954	Sequence 10954, A	1222	147.5	3.7	1766	4	US-09-562-702A-14	Sequence 14, Appl1
1150	151.5	3.8	716	2	US-08-766-982-1	Sequence 1, Appl1	1223	147.5	3.7	1786	4	US-09-561-818A-14	Sequence 14, Appl1
1151	151.5	3.8	716	2	US-08-766-982-1	Sequence 1, Appl1	1224	147.5	3.7	1786	4	US-09-561-7098-9	Sequence 9, Appl1
1152	151	3.8	110	4	US-09-296-219-1	Sequence 21, Appl1	1225	147.5	3.7	4331	4	US-10-006-011A-2	Sequence 869, App
1153	151	3.8	110	4	US-09-341-461-17	Sequence 21, Appl1	1226	147	3.7	229	3	US-09-004-731-44	Sequence 2, Appl1
1154	151	3.8	237	5	US-08-096-946-10	Sequence 10, Appl1	1227	147	3.7	229	3	US-09-004-731-44	Sequence 44, Appl1
1155	151	3.8	237	5	PCT-US94-07329-10	Sequence 10, Appl1	1228	147	3.7	229	4	US-09-004-729-44	Sequence 44, Appl1
1156	151	3.8	237	1	PCT-US95-06157-16	Sequence 16, Appl1	1229	147	3.7	242	3	US-09-004-731-41	Sequence 41, Appl1
1157	150.5	3.8	277	2	US-08-024-868-2	Sequence 2, Appl1	1230	147	3.7	242	3	US-08-749-699-41	Sequence 41, Appl1
1158	150.5	3.8	277	2	US-08-242-097-2	Sequence 2, Appl1	1231	147	3.7	242	4	US-09-004-729-41	Sequence 41, Appl1
1159	150.5	3.8	277	3	US-09-206-695-2	Sequence 2, Appl1	1232	147	3.7	46	4	US-09-949-016-11726	Sequence 11726, A
1160	150.5	3.8	277	4	US-09-000-179-1	Sequence 1, Appl1	1233	146.5	3.7	223	1	US-08-472-173-13	Sequence 13, Appl1
1161	150.5	3.8	277	5	US-09-799-118-2	Sequence 2, Appl1	1234	146.5	3.7	223	1	US-08-483-059-13	Sequence 13, Appl1
1162	150.5	3.8	277	5	PCT-US96-11995-1	Sequence 1, Appl1	1235	146.5	3.7	223	1	US-08-472-173-13	Sequence 13, Appl1
1163	150.5	3.8	500	4	US-09-423-753-2	Sequence 2, Appl1	1236	146.5	3.7	223	2	US-08-487-167-13	Sequence 13, Appl1
1164	150.5	3.8	685	3	US-08-423-753-2	Sequence 3, Appl1	1237	146.5	3.7	223	2	US-08-482-816-13	Sequence 13, Appl1
1165	150.5	3.8	685	3	US-08-872-855-2	Sequence 2, Appl1	1238	146.5	3.7	223	2	US-08-896-149-13	Sequence 13, Appl1
1166	150.5	3.8	685	4	US-09-423-753-25	Sequence 25, Appl1	1239	146.5	3.7	223	2	US-08-801-499-13	Sequence 13, Appl1
1167	150.5	3.8	1064	1	US-09-641-612-7	Sequence 7, Appl1	1240	146.5	3.7	223	2	US-08-615-271-13	Sequence 13, Appl1
1168	150.5	3.8	1064	1	US-08-537-210A-3	Sequence 3, Appl1	1241	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appl1
1169	150	3.8	113	4	US-09-113-825-3	Sequence 3, Appl1	1242	146.5	3.7	223	3	US-09-074-659-13	Sequence 13, Appl1
1170	150	3.8	238	6	US-09-438-046-32	Sequence 22, Appl1	1243	146.5	3.7	223	3	US-09-106-466A-13	Sequence 13, Appl1
1171	150	3.8	238	6	US-08-944-483-31	Sequence 31, Appl1	1244	146.5	3.7	223	3	US-09-106-466A-13	Sequence 13, Appl1
1172	150	3.8	263	4	5180819-4	Patent No. 5180819	1245	146.5	3.7	223	3	US-09-106-467-13	Sequence 13, Appl1
1173	150	3.8	263	4	US-09-653-813-2	Sequence 2, Appl1	1246	146	3.7	137	3	US-10-067-422-32	Sequence 32, Appl1
1174	150	3.8	267	2	US-08-978-404B-46	Sequence 46, Appl1	1247	146	3.7	137	3	US-09-518-046-23	Sequence 23, Appl1
1175	150	3.8	276	1	US-08-467-155A-1	Sequence 1, Appl1	1248	146	3.7	263	4	US-09-653-813-4	Sequence 4, Appl1
1176	150	3.8	276	2	US-08-628-198-1	Sequence 1, Appl1	1249	146	3.7	263	4	US-09-653-813-6	Sequence 6, Appl1
1177	150	3.8	276	3	US-09-201-038-1	Sequence 1, Appl1	1250	145.5	3.7	108	4	US-09-341-461-22	Sequence 22, Appl1
1178	150	3.8	276	5	PCT-US96-07343-1	Sequence 1, Appl1	1251	145.5	3.7	222	3	US-08-906-769-103	Sequence 103, App
1179	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1252	145.5	3.7	222	3	US-08-906-616-103	Sequence 103, App
1180	150	3.8	677	4	US-09-949-016-11370	Sequence 11370, A	1253	145.5	3.7	222	3	US-08-817-795A-103	Sequence 103, App
1181	150	3.8	677	4	US-09-949-016-11371	Sequence 11371, A	1254	145.5	3.7	222	3	US-08-639-075A-103	Sequence 103, App
1182	150	3.8	677	4	US-09-949-016-11372	Sequence 11372, A	1255	145.5	3.7	222	3	US-09-012-431-103	Sequence 103, App
1183	149.5	3.8	46	4	US-10-067-422-17	Sequence 17, Appl1	1256	145.5	3.7	222	3	US-09-012-692-103	Sequence 103, App
1184	149.5	3.8	385	1	US-08-340-539A-2	Sequence 2, Appl1	1257	145.5	3.7	222	3	US-08-906-613-103	Sequence 103, App
1185	149.5	3.8	385	2	US-08-461-592B-2	Sequence 2, Appl1	1258	145	3.7	222	5	PCT-US95-14442A-103	Sequence 103, App
1186	149.5	3.8	1935	4	US-09-949-016-10403	Sequence 10403, A	1259	145	3.7	110	4	US-09-341-461-21	Sequence 21, Appl1
1187	149	3.8	263	1	US-07-906-983-2	Sequence 2, Appl1	1260	145	3.7	222	3	US-08-906-769-81	Sequence 81, Appl1
1188	149	3.8	575	4	US-09-949-016-11264	Sequence 11264, A	1261	145	3.7	222	3	US-08-906-616-81	Sequence 81, Appl1
1189	149	3.8	575	4	US-09-949-016-11265	Sequence 11265, A	1262	145	3.7	222	3	US-08-817-795A-81	Sequence 81, Appl1
1190	149	3.8	575	4	US-09-949-016-11266	Sequence 11266, A	1263	145	3.7	222	3	US-08-639-075A-81	Sequence 81, Appl1
1191	149	3.8	806	4	US-09-949-016-11267	Sequence 11267, A	1264	145	3.7	222	3	US-09-012-431-81	Sequence 81, Appl1
1192	149	3.8	806	4	US-09-949-016-11267	Sequence 11267, A	1265	145	3.7	222	3	US-09-012-692-81	Sequence 81, Appl1
1193	149	3.8	1404	2	US-08-400-159-2	Sequence 2, Appl1	1266	145	3.7	222	3	US-08-906-613-81	Sequence 81, Appl1
1194	149	3.8	1404	3	US-08-611-729A-2	Sequence 2, Appl1	1267	145	3.7	222	5	PCT-US95-14442A-81	Sequence 81, Appl1
1195	149	3.8	1404	4	US-09-195-524-2	Sequence 2, Appl1	1268	145	3.7	372	2	US-08-513-278-4	Sequence 4, Appl1

1269	145	3.7	372	6	5514582-4	Patent No. 5514582	1342	136.5	3.5	224	1	US-08-483-859-12	Sequence 12, Appl
1270	145	3.7	258	6	5514582-4	Patent No. 5514582	1343	136.5	3.5	224	1	US-08-472-173-12	Sequence 12, Appl
1271	144.5	3.7	372	3	US-09-004-721-16	Sequence 16, Appl	1344	136.5	3.5	224	2	US-08-487-167-12	Sequence 12, Appl
1272	144.5	3.7	258	3	US-09-004-721-19	Sequence 19, Appl	1345	136.5	3.5	224	2	US-08-482-816-12	Sequence 12, Appl
1273	144.5	3.7	258	3	US-08-749-699-16	Sequence 16, Appl	1346	136.5	3.5	224	2	US-08-396-149-12	Sequence 12, Appl
1274	144.5	3.7	258	3	US-08-749-699-16	Sequence 19, Appl	1347	136.5	3.5	224	2	US-08-801-499-12	Sequence 12, Appl
1275	144.5	3.7	258	4	US-09-004-729-19	Sequence 16, Appl	1348	136.5	3.5	224	2	US-08-615-271-12	Sequence 12, Appl
1276	144.5	3.7	258	4	US-09-004-729-19	Sequence 19, Appl	1349	136.5	3.5	224	3	US-09-074-660-12	Sequence 12, Appl
1277	144	3.6	163	4	US-09-270-767-60652	Sequence 60652, A	1350	136.5	3.5	224	3	US-09-074-659-12	Sequence 12, Appl
1278	143	3.6	237	3	US-09-004-721-22	Sequence 22, Appl	1351	136.5	3.5	224	3	US-09-106-466A-12	Sequence 12, Appl
1279	143	3.6	237	4	US-08-749-699-22	Sequence 22, Appl	1352	136.5	3.5	224	3	US-09-106-467-12	Sequence 12, Appl
1280	143	3.6	237	3	US-09-004-729-22	Sequence 22, Appl	1353	136.5	3.5	224	3	US-09-106-467-12	Sequence 12, Appl
1281	143	3.6	549	3	US-09-245-041-9	Sequence 9, Appl	1354	136.5	3.5	227	1	US-07-929-198-4	Sequence 4, Appl
1282	143	3.6	549	4	US-09-358-055B-9	Sequence 9, Appl	1355	136.5	3.5	227	2	US-08-978-404B-47	Sequence 47, Appl
1283	143	3.6	549	4	US-09-893-238-9	Sequence 9, Appl	1356	136	3.4	326	2	US-08-640-977-1	Sequence 1, Appl
1284	143	3.6	1260	4	US-09-245-041-2	Sequence 2, Appl	1357	136	3.4	326	4	US-09-976-594-458	Sequence 458, App
1285	143	3.6	1260	4	US-09-358-055B-2	Sequence 2, Appl	1358	135.5	3.4	226	3	US-08-906-616-89	Sequence 89, Appl
1286	143	3.6	1260	4	US-08-893-238-2	Sequence 2, Appl	1359	135.5	3.4	226	3	US-08-906-616-89	Sequence 89, Appl
1287	143	3.6	3075	2	US-08-460-309-5	Sequence 5, Appl	1360	135.5	3.4	226	3	US-08-817-795-89	Sequence 89, Appl
1288	143	3.6	3075	2	US-08-125-077-5	Sequence 5, Appl	1361	135.5	3.4	226	3	US-08-639-075A-89	Sequence 89, Appl
1289	142.5	3.6	226	1	US-07-929-198-6	Sequence 6, Appl	1362	135.5	3.4	226	3	US-09-012-631-89	Sequence 89, Appl
1290	142.5	3.6	240	3	US-08-824-692-23	Sequence 23, Appl	1363	135.5	3.4	226	3	US-09-012-692-89	Sequence 89, Appl
1291	142	3.6	577	2	US-08-435-149-3	Sequence 3, Appl	1364	135.5	3.4	226	3	US-08-906-613-89	Sequence 89, Appl
1292	142	3.6	611	3	US-09-475-460A-32	Sequence 32, Appl	1365	135.5	3.4	226	5	PCT-US95-14442A-89	Sequence 89, Appl
1293	142	3.6	611	4	US-09-748-061A-32	Sequence 32, Appl	1366	135.5	3.4	323	4	US-09-270-767-44375	Sequence 44375, A
1294	142	3.6	1068	1	US-08-537-210A-2	Sequence 2, Appl	1367	135.5	3.4	372	2	US-08-513-278-2	Sequence 2, Appl
1295	142	3.6	1068	3	US-09-113-825-2	Sequence 2, Appl	1368	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1296	142	3.6	1480	1	US-09-182-024A-5	Sequence 5, Appl	1369	135.5	3.4	372	6	5514582-2	Patent No. 5514582
1297	141	3.6	226	3	US-08-944-483-41	Sequence 41, Appl	1370	135	3.4	223	2	US-08-738-113B-9	Sequence 9, Appl
1298	140	3.5	148	4	US-09-618-259-2	Sequence 2, Appl	1371	135	3.4	725	3	US-09-191-647-9	Sequence 9, Appl
1299	140	3.5	148	4	US-09-261-416-7	Sequence 7, Appl	1372	135	3.4	725	3	US-09-191-647-9	Sequence 9, Appl
1300	140	3.5	578	3	US-08-981-392-13	Sequence 13, Appl	1373	135	3.4	725	3	US-09-540-245A-9	Sequence 9, Appl
1301	140	3.5	578	4	US-09-908-322-13	Sequence 3, Appl	1374	134.5	3.4	113	4	US-09-341-461-24	Sequence 24, Appl
1302	140	3.5	997	4	US-09-747-371-3	Sequence 3, Appl	1375	134.5	3.4	223	1	US-07-956-848B-41	Sequence 41, Appl
1303	139.5	3.5	207	4	US-09-244-111-4	Sequence 4, Appl	1376	134.5	3.4	223	1	US-08-471-956A-41	Sequence 41, Appl
1304	139.5	3.5	214	4	US-09-380-682-57	Sequence 57, Appl	1377	134.5	3.4	304	3	US-09-088-651-2	Sequence 2, Appl
1305	139.5	3.5	256	3	US-09-032-215-32	Sequence 32, Appl	1378	134.5	3.4	1525	3	US-09-191-647-2	Sequence 2, Appl
1306	139	3.5	267	3	US-08-906-769-145	Sequence 145, App	1379	134.5	3.4	1525	3	US-09-540-245A-2	Sequence 2, Appl
1307	139	3.5	267	3	US-08-906-616-145	Sequence 145, App	1380	134.5	3.4	1525	3	US-09-540-153-2	Sequence 2, Appl
1308	139	3.5	267	3	US-08-639-075A-145	Sequence 145, App	1381	134	3.4	266	2	US-08-640-977-4	Sequence 747, Ap
1309	139	3.5	267	3	US-09-004-731-67	Sequence 67, Appl	1382	134	3.4	1566	4	US-09-949-016-7247	Sequence 7247, Ap
1310	139	3.5	267	3	US-09-012-431-145	Sequence 145, App	1383	134	3.4	1821	4	US-09-949-016-5938	Sequence 5938, Ap
1311	139	3.5	267	3	US-08-748-699-67	Sequence 67, Appl	1384	133.5	3.4	248	2	US-08-824-692-29	Sequence 29, Appl
1312	139	3.5	267	3	US-09-012-692-145	Sequence 145, App	1385	133	3.4	248	2	US-08-640-977-2	Sequence 2, Appl
1313	139	3.5	267	3	US-08-906-613-145	Sequence 145, App	1386	132	3.3	110	4	US-09-341-461-26	Sequence 26, Appl
1314	139	3.5	267	4	US-09-004-729-67	Sequence 67, Appl	1387	132	3.3	112	4	US-09-341-461-34	Sequence 34, Appl
1315	139	3.5	495	4	US-10-006-011A-4	Sequence 4, Appl	1388	132	3.3	119	4	US-09-438-046-24	Sequence 24, Appl
1316	139	3.5	705	4	US-10-006-011A-3	Sequence 3, Appl	1389	132	3.3	159	3	US-09-020-956-172	Sequence 172, App
1317	139	3.5	1139	1	US-08-537-210A-4	Sequence 4, Appl	1390	132	3.3	159	3	US-09-030-607-172	Sequence 172, App
1318	139	3.5	1139	3	US-09-113-825-4	Sequence 4, Appl	1391	132	3.3	159	3	US-09-313-172	Sequence 172, App
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1321	138.5	3.5	226	2	US-08-557-146-15	Sequence 15, Appl	1394	132	3.3	159	4	US-09-159-812-172	Sequence 172, App
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1323	138.5	3.5	226	2	US-08-944-483-45	Sequence 45, Appl	1396	132	3.3	159	4	US-09-685-166A-172	Sequence 172, App
1324	138.5	3.5	226	3	US-08-983-075D-9	Sequence 9, Appl	1397	132	3.3	159	4	US-09-115-453-172	Sequence 172, App
1325	138	3.5	182	4	US-09-328-925-12	Sequence 12, Appl	1398	132	3.3	159	4	US-09-688-489-172	Sequence 172, App
1326	138	3.5	216	4	US-08-824-692-24	Sequence 24, Appl	1399	132	3.3	159	4	US-09-679-426-172	Sequence 172, App
1327	138	3.5	249	3	US-09-578-303-2	Sequence 2, Appl	1400	132	3.3	159	4	US-09-759-143-172	Sequence 172, App
1328	138	3.5	253	3	US-08-906-769-131	Sequence 131, App	1401	132	3.3	159	4	US-09-651-236-172	Sequence 172, App
1329	138	3.5	253	3	US-08-906-616-131	Sequence 131, App	1402	132	3.3	166	4	US-09-636-215-838	Sequence 838, App
1330	138	3.5	253	3	US-08-639-075A-131	Sequence 131, App	1403	132	3.3	166	4	US-09-685-166A-838	Sequence 838, App
1331	138	3.5	253	3	US-09-012-431-131	Sequence 131, App	1404	132	3.3	166	4	US-09-679-426-838	Sequence 838, App
1332	138	3.5	253	3	US-09-012-692-131	Sequence 131, App	1405	132	3.3	166	4	US-09-759-143-838	Sequence 838, App
1333	138	3.5	253	3	US-08-906-613-131	Sequence 131, App	1406	132	3.3	166	4	US-09-651-236-838	Sequence 838, App
1334	138	3.5	291	1	US-08-467-155A-11	Sequence 11, App	1407	131.5	3.3	215	2	US-09-612-314A-33	Sequence 33, Appl
1335	138	3.5	291	2	US-08-628-198-11	Sequence 11, App	1408	131.5	3.3	810	2	US-08-820-170A-34	Sequence 34, Appl
1336	138	3.5	291	2	US-09-201-038-11	Sequence 11, App	1409	131.5	3.3	810	3	US-09-035-699-34	Sequence 34, Appl
1337	138	3.5	291	5	PCT-US96-07343-11	Sequence 11, Appl	1410	131.5	3.3	810	3	US-09-273-565-34	Sequence 34, Appl
1338	138	3.5	345	4	US-10-000-489-106	Sequence 106, App	1411	131.5	3.3	810	3	US-09-565-538-34	Sequence 34, Appl
1339	138	3.5	583	4	US-09-641-612-2	Sequence 2, Appl	1412	131.5	3.3	810	4	US-09-661-468-34	Sequence 34, Appl
1340	136.5	3.5	109	4	US-09-341-461-33	Sequence 33, Appl	1413	131.5	3.3	810	4	US-09-976-165-34	Sequence 34, Appl
1341	136.5	3.5	224	1	US-08-278-091-12	Sequence 12, Appl	1414	131	3.3	219	2	US-08-925-708-2	Sequence 2, Appl

	1486	127	3.2	2123	4	US-09-949-016-7517	Sequence 7517, Ap
	1489	127	3.2	3070	4	US-09-961-403-7	Sequence 7, Appl
	1490	127	3.2	3084	4	US-09-562-702A-12	Sequence 12, Appl
	1491	127	3.2	3088	4	US-09-562-702A-8	Sequence 8, Appl
	1492	127	3.2	3089	4	US-09-562-702A-4	Sequence 4, Appl
	1493	127	3.2	3106	4	US-09-562-702A-10	Sequence 10, Appl
	1494	127	3.2	3110	4	US-09-562-702A-2	Sequence 2, Appl
	1495	127	3.2	3110	4	US-09-562-702A-6	Sequence 6, Appl
	1496	127	3.2	3110	4	US-09-561-709B-7	Sequence 7, Appl
	1497	127	3.2	3110	4	US-09-917-254-86	Sequence 86, Appl
	1498	127	3.2	3110	4	US-09-949-016-5937	Sequence 5937, Ap
	1499	127	3.2	3111	2	US-08-460-309-4	Sequence 4, Appl
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ALIGNMENTS

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RESULT 1
US-10-067-422-9
; Sequence 9, Application US/10067422
; Patent No. 6743613
; GENERAL INFORMATION:
; APPLICANT: NI et al.
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and
; FILE REFERENCE: PTO04P1
; CURRENT APPLICATION NUMBER: US/10/067,422
; PRIOR FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/685,899
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: PCT/US00/09028
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/152,933
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/147,020
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-067-422-9

Query Match          74.7%; Score 2946.5; DB 4; Length 570;
Best Local Similarity 96.8%; Pred. No. 9.5e-237;
Matches 552; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

Dy      168  MLSEFDYMCQDYDEVRVDGDNRDQIIRKVCNGNERPAPIQSIGSLHVLFHSDDGSKNPD 227
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Oy      228  GFHAIVEITACSSPEFHGTCTVLDKASGYKCACLAGTYGCRCENL----- 274
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Db      61  GFHAIVEITACSSPCFHGTCTVLDKASGYKCACLAGTYGCRCENLLEAGSKIRASED 120
Oy      275  -----LEERNCSDPGGPNYGOKITGGPGLINGRHAIKIGTVVSFFCNNSYYLSGNERTCQ 330
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Oy      331  QNGWMSGKOPICIKACEPKISDLVRRRVLPWQVOSRETFHQLYSAAFSKOKLQSPATK 390
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Oy      391  KPALPFEDLPMGVQHLLTOLQYEICISPFYRKLGSSSRRTCLRTGWSGRAPSCIPICGIE 450
        | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy 451 NITAPKTOGLRMPQAAIYRTSGVHDSLHKGMFLVCSGALVNERTVVAAHCTVDLG 510  
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Db 481 BEQHEHDGIPVSVTDNMFCSWEPTAPSDICTAETGIIAIVSPGRASPEPRMHLGLVS 540  
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Db 541 WSYDKTCSHRLSTFTKVLPEKDIERNMK 570

## RESULT 2

US-08-296-014A-4  
; Sequence 4, Application US/08296014A  
; Patent No. 5716834  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius  
; NUMBER OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; ADDRESS: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22042  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/296,014A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murphy, Jr., Gerald M.  
; REGISTRATION NUMBER: 28,977  
; REFERENCE/DOCKET NUMBER: 1781-105P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 205-8000  
; TELEFAX: (703) 205-8050  
; TELEFAX: 248345  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1019 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-296-014A-4

Query Match 16 9%; Score 665; DB 1; Length 1019;  
Best Local Similarity 25.4%; Pred. No. 1,7e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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Qy 83 PGCTIFENCKSCR-NGSWGTL----- 103

Db 230 PYLLIGETITTCGNGQMGQIIPQCKALVFCPPDLDPVNAHEHKVIGVEQKGFPGTE 289  
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Qy 163 -----QLRFVWLSLEPDYV-----QYDYVEVRD-----GDNRDGQIIRKVCN--E 202  
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Qy 203 RPAPIQS--IGSSILHVLPHSDG--SKNFDGFH-----AIEETIACSS 241  
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Qy 242 SPCEHDTGCVL-----DKAGS--YKACIAGYTGORCENLLEERN-----CSDPGPANGYQKI 293  
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Db 590 HGQS--IDGFYA--GSSIRYSCVLAHLSGTEVTTCTTGTWAPKPRCIKVTICQNPV 645  
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Qy 399 -LPMGYQLHTLOQLEICSPFFYRLGLSSRRCTLRGKMGGRAPSCPIPGKIENTAP- 455  
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Qy 456 -----KTQGLRMPQAAIYRTSGVHDSLHKGMFLVCSGALVNERTVVAAHCTVDLG 510  
Db 763 IMNGNSTEIQMPQAGISRMLA-----DHMMFLQCGGSLINEKWIYTAHACTVYSA 815  
Qy 511 KVTMIKTADLKVVLGKFFRDDDEKTTQSLQISAILHPYDPLLDADIAIKLKDKA 570  
Db 816 TAEIIDNQFKMYLKGKRYRDSRDDVQVREALEIHNVDNPGNLFDAIATLQKTPV 875  
Qy 571 RISTRVOPICLAARDLSTFSQESHITVAGNVLADVRSPGKNDTLRSQVSVV 624  
Db 876 TLATRVQPICLPT--DITT--REHLEKGTAAVVTGNG--LNNNTYSETTIOQAVLPV 926  
Qy 625 VDSLCEQHEHDGIPVSVTDNMFCSWEPTAPSDICTAETGIIAIVSPGRASPEPRMH 684  
Db 927 VAATCEEGYKEDLPVTENNFCAGYK--KGRYDACSQSGG--PLVFADDSRTERRV 983  
Qy 685 LMGIVSWYDKTCSH--RLSTAFTKVLPEKDIERNMK 717  
Db 984 LEGIVSWGSPSGCGKANQYGGFTKVVNVLFWMIHQ 1017

## RESULT 3

US-08-596-405-4  
; Sequence 4, Application US/08596405  
; Patent No. 5858706  
; GENERAL INFORMATION:  
; APPLICANT: Ding, Jeak Ling  
; APPLICANT: Ho, Bow  
; TITLE OF INVENTION: The Cloned Factor C cDNA of the  
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius  
; NUMBER OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
; ADDRESS: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Birch, Stewart, Kolasch & Birch  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: USA



```

ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,405
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-596-405-4

Query Match      16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMRCECEYDIEVCVCPKRE-----VGYTIPCCRNENECDSCLIH 82
DB 184 PNGWMSNFPKCR-----ECAMVSPBHGKVALSGDMIEGATL-----RFSCHS----- 229
QY 83 PGCTIFENCSCR-NGSWGTL----- 103
DB 230 PYVLIGETLTCQNGMNGOIPCKNLVPCPLDPVNAHAKVIGVEQYQGPQSGTE 289
QY 104 -----DDFYVKGFYCAEGR--AGWYGG--DCMR-----GGOVLR-- 133
DB 290 VTTTSGSNYFLMGDTDKCNPDGSGWSGSGSCVAVADREVDGSKAVDPLDDYGEVPIH 349
QY 134 APKQQLILES-----YPLNAHCEWTIHA--KEGFYI----- 162
DB 350 CPAGCSLTATGWTGTATYHLESLVCRAIHAQKLPNSGAVHVVNNPYSDFLSDLNGI 409
QY 163 ---QLRFMLSLBEDYV-----CQDYVEYRD-----GDRDQIIRKVCN--E 202
DB 410 KSEBELKLSRFRDYVRSSTAGKSGCPDGMFEVDENCYVVTSKORAMBRAGVCTMAA 469
QY 203 RPARIQS--IGSSLHVLPHSDG--SKNDFGH-----AIYEITACSS 241
DB 470 RLVLVDVAVPNSLTETLRKGLTTTIGLHRLDAEKPIWELMDRSNVVNLNLTFWAS 529
QY 242 SPCHDGTCLV-----DKAGS--YKCACTAGYTGRCENULEERN-----CSDPGAPVNGYOKI 293
DB 530 GEPONENICYMDIQLDQLOSWYKTKSCFOPSSPACMDLSDRKAKCDDPSLENGATL 589
QY 294 TGGPGLINGHAKIGTVSPFCNNNSYVLSGNEKRTCOONGSWSGKOPICIK--ACREPKI 351
DB 590 HGGS--IDGFYA--GSSIRYSCVLAHLSTGETVCTTNGTWSAPKRCIKVITCQRPV 645
QY 352 SDLVRRVLPQVQSRFPLHOLYSAAFSKOKLO---SAPTKKALPFGD----- 398
DB 646 PSYGVSEIKP---PSRTNISIRVSGPFLRLPLRLPLARAKPPKRSOSOPSTVDLASK 702
QY 399 --LPMGVOHLHTLOQYECISPFYRLGSSRRCLRTKMGSGRAASCIPIGKIENITAP- 455
DB 703 VKLPBEGHYRGSRAIYTCESHYIELLSQGRCDNSNGWSGRAPSCIPVCGRSDSPSPF 762
QY 456 -----KTQGLRMPWQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVAHAHCVTDLG 510
DB 763 IMMGNSTREIQGMQWAGISRWLA-----DHNWVFLQCGGSLNENKMITVAHAHCVTYS 815

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QY 511 KVTMITADLKVVLGKFRYDDDRDEKTIQSLQISAIILHPNVPILDLADIALIKLIDKA 570
DB 816 TAILIDPNQFKMYLKGXYDDSDRDDYVQYREALERHVNPNDPGNLNPIDIALIQKTPV 875
QY 571 RISTRVOPICLAAARLSTSFQESH-----TVAGMNVLADVRSPGKNDLTRSGVSV 624
DB 876 TLTRVQPICLPT--DITF--REHLKEGTLAVVTGM-----LNENNTYSETIQOAVLPV 926
QY 625 VDSLCEQHEHDHGPVSYDNMFCAWSPEPTASDICTAETGIAVSPGRASPEPRWH 684
DB 927 VASTCEBEGKEADLUTYTENNFCAGYK--KGRYDACSQSGG--PLVFADSRTERRW 983
QY 685 LMGLVMSYDKTCSH-RLSTAFKVLPEKOWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGFYKVVFLSWIRQ 1017

RESULT 4
US-08-877-620-4
Sequence 4, Application US/08877620
Patent No. 5985590
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
TITLE OF INVENTION: roundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolaach & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,620
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-877-620-4

Query Match      16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMRCECEYDIEVCVCPKRE-----VGYTIPCCRNENECDSCLIH 82
DB 184 PNGWMSNFPKCR-----ECAMVSPBHGKVALSGDMIEGATL-----RFSCHS----- 229
QY 83 PGCTIFENCSCR-NGSWGTL----- 103

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Db      984 LEGIVSWGSPGGKANKQYGFTRKANVFLSMIRO 1017

RESULT 6
US-09-626-795-4
; Sequence 4, Application US/09626795
; Patent No. 6719973
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis
; FILE REFERENCE: 4810-6137
; CURRENT APPLICATION NUMBER: US/09/626,795
; CURRENT FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Carcinoscopus rotundicauda
US-09-626-795-4

Query Match      16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.7e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

Qy      34 PGAEWNIMCRCECEYDQIECVCPGKRE-----VVGYYTIPCCRNENECDSCLIH 82
      184 PNGQMSNFPKRCIR-----ECAMWSPEHGKVNALSGMIGATL-----RFGCDs----- 229
      83 PGCTIFENCKSCR-NGSWGTL----- 103
      230 PYVLIGGETILTCQNGQMGNGQIPQCKNLVFCPDLDPVNAHAKYKIGVEQKYGQFPQGT 289
      104 -----DDFYVKGKFCACER--AGWYGG--DCMR-----CGQVLR-- 133
      290 VVTYCGSNYFLMGFDLTKCNPDGSGWSGSPSCVAVADREVDCSKAVDFLDVGEVRIH 349
      134 APKQIILLES-----YPLNAHCWNTIHA-----KQFVYI----- 162
      350 CPAGCSLTAGTGWCTAIYHELSSVCRAIHAHGKLPNGGAVHVVNNGPYDFLGSDLNGI 409
      163 -----QLRFMLSLBEDYM-----COYDVEVRD-----GDNRDGQIIRKVCNG--E 202
      410 KSEELKSLARSPRDYVRSSTPAKSGCPDGFVEDENCCVYTSQKRAMERAGVCTMAA 469
      203 RPAPIQS--IGSSLHLVPHSDG--SKNFDGRH-----AIYEETIACSS 241
      470 RLAVLDKDVIPNSLTETLRGKGLTTWTIGLHRLDAEKPIWELMDRNSNVVLDNLTFMAS 529
      242 SPCHDGTCLV-----DKAGS--YKQACLAGYTGRCENLLEBRN-----GSDPGGPNYQXI 293
      530 GEPENETNCYMDIQDQISVWTKYKSCFQPSFACMMDLSDRNKAKCDDPSLENGATL 589
      294 TGGGGLINGHAKIGTIVVSFFCNNSYVLISGNEKATCOONGSEWSGKOPICIK--ACREPKI 351
      590 HGOS--IDGFYA--GSSIRYSCVLAHLISGTEYVCTTNGWMSAPKRCIKVITCQNPV 645
      352 SDLVRRVRLPMQVSRPTPLHQLVSAFSSQKIQ--SAPTKPALPFGD----- 398
      646 PSYGSVEIKP--PSRTNISIRVGSFPLRLPLPLARAKAPPKPRSSQSPSTVDLASK 702
      399 --LPMGOHLATQOYCISPFYRLGSSRRTCLRTKMGSRAPSCIPICXIENTAP- 455
      703 VKLPEGHYRVSRAIYTCESRYELLDSQGRCDNSNWSGRPASCLPVCGRSDSPSPF 762
      456 -----KTQGLRWPMQAAIYRTSGVHDGSLHKGAMFLVCSGALVNERTVVAACHVTDLG 510
      763 IMNNSNFEIGMPWQAGISRWLA-----DHMMFLOCSSGLNEMKIYVAACHVTYSA 815
      511 KVTMIKTADLKVNLGKRYRDDDEKTIQSLQISAIILHPNYDPIILLADIAIKLIDKA 570
      816 TAEIIDNQFMVYIGKYRRDSDDDYQVVEALEIHVNPYDGNINFDIALIQLKTPV 875

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Qy      571 RISTRVQPICTLAASRLSTSPQESH-----TVAGNVLADYRSPGKNDITRSGVSV 624
      876 TLITRVQPICTLP--DITF---REHLKEGTLAVTGMG---LNENNTYSEITIQOAVLPV 926
Qy      625 VDSLCECHEDHIGIVSVTDMNFCASWEPTAVSDICTAETGSLAIVSPFGRASPEPRM 684
      927 VASTCEGKEDLPITYENNFCAGYK--KGRYDCSGDSGG--PLVFPADSRTERRW 983
Qy      685 IMGVSWSYDKTCSH--RLSTAFYKVLFPKDWIER 717
      984 LEGIVSWGSPGGKANKQYGFTRKANVFLSMIRO 1017

RESULT 7
US-08-296-014A-2
; Sequence 2, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscopus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Birch, Stewart, Kolaesch & Birch
; STREET: 810 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-014A-2

Query Match      16.9%; Score 665; DB 1; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1.8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

Qy      34 PGAEWNIMCRCECEYDQIECVCPGKRE-----VVGYYTIPCCRNENECDSCLIH 82
      248 PNGQMSNFPKRCIR-----ECAMWSPEHGKVNALSGMIGATL-----RFGCDs----- 293
      83 PGCTIFENCKSCR-NGSWGTL----- 103
      294 PYVLIGGETILTCQNGQMGNGQIPQCKNLVFCPDLDPVNAHAKYKIGVEQKYGQFPQGT 353
      104 -----DDFYVKGKFCACER--AGWYGG--DCMR-----CGQVLR-- 133
      354 VVTYCGSNYFLMGFDLTKCNPDGSGWSGSPSCVAVADREVDCSKAVDFLDVGEVRIH 413

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QY 134 APKGQILLES-----YPLNAHCEWTIHA-----KRGFVI-----162
DB 414 CPAGCSLTAAGTGWGTALYHELSSVCRAAIHAGKLPNSGGAHVHVNNGPYSDFLGSDINGI 473
QY 163 ---OLRFVMLSLFEDYM-----COYDVEVRD-----GDNRDGQIILKRYCGN--E 202
DB 474 KSEELKSLARFRFDYVSSSTAGKSCGPDGWFEDENCYVVTSKQRAWEBAQGYCTMAA 533
QY 203 RPAPIQS--IGSSLHVLFHSDG-SKNFDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLHRLDAEKPFIMELMDRSNVVINDMLTFWAS 593
QY 242 SPCHDGTCVL---DKAGS--YKACACLAGYTGQRCENULEERN---CSDPGPVGXYOKI 293
DB 594 GEPGENETNCVYMDIODQLOSVWTKKSCFPSSFACMMDLSRNNAKCDDPSGLENGATL 653
QY 294 TGGPGLINGRAKIGTGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPXI 351
DB 654 HGQS--IDGFYA--GSSIRYGCYVLIHLSGTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 352 SDLVRRRLPMOVOSRETPHLQVSAFSAFQKQKQ---SAPTKKRALPFGD-----398
DB 710 PSYGSVEIKP---PSRTNISIRVGSFPLRLPLPLAARAKPPKPRSSQPTVLDLASK 766
QY 399 --LPMGYQHHTQLOYEICISPFYRLGSSRRTCLRTKWSGRAPSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRAIYTESRYELLGSGQRCDNMGWSGRPASCIPLVCGRSDSPSPFP 826
QY 456 -----KTQGLRMPMOAIIYRRTSGVHDSLHKAMFLVCSGALVNERVVAACVYDGLG 510
DB 827 IMNGNSTEIGQPMWQAGISRMLA-----DHNNMFLOCGGSLNEKIVTAACVYYSA 879
QY 511 KVTMIKTADLVKLVGKFRDDDRDEKTIQSLQISAIILHPNYDPIILDADIAILKLDKA 570
DB 880 TAEIIDPNQFMVYLGKYYRDSRDDVYQVREALEIHVNNPYDGNLNFIDIALIQLKTPV 939
QY 571 RISTRVQPICLAASRDISTSFQESH-----TVAGNVLAADVRSPEGKNDTLRSGVSV 624
DB 940 TLTRVQPICLPT--DITF---REHLKEGTLAVVTWGMG---LNNNTYSETIOQAVLPV 990
QY 625 VDSLCEGHEHDHGIPIVSTDNMFPCASWEPTAPSDICAEITGTAIVAFSPERAPBPMH 684
DB 991 VAASTCEGYKEADPLVTENMFPCAGYK-KGYDAGSGDSGG--PLVFADDSRTERRKV 1047
QY 685 IMGIVMSYDTCSH-RLSTAFTKVLFPKDWIER 717
DB 1048 LEGIVMSGSPGCGKANQYGETTKVNVFLSMIRQ 1081

RESULT 8
US-08-596-405-2
; Sequence 2, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jaek Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horsehoe Crab, Carcinus scorpheus
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/596,405
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-405-2

```

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Query Match 16.9%; Score 665; DB 2; Length 1083;
Best Local Similarity 25.4%; Pred. No. 1,8e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNTMCECEYDIECVCPGKRE-----VVGTYIPCCRNENECDSCLIH 82
DB 248 PNGQMSNFPKRCR---ECAMVSSPEHGKVALNSGDMIGATL-----RFSQDS-----293
QY 83 PGCTIFENCKSCR-NGSMGCTL-----103
DB 294 PYVILIGETILTCGNGNGMNQIIPQCKNLVFCRDLDPVNNHAHKYKIGVEQKYQFPQCTE 353
QY 104 -----DDFYVKGFCYACER--AGWYGG--DCNR-----CGQVLR--133
DB 354 VTYTCSGNYFLMGFDLTKCNPDGSMGSGQPSGVADREYDCSKAVDPLDVGEPVRIH 413
QY 134 APKGQILLES-----YPLNAHCEWTIHA-----KRGFVI-----162
DB 414 CPAGCSLTAAGTGWGTALYHELSSVCRAAIHAGKLPNSGGAHVHVNNGPYSDFLGSDINGI 473
QY 163 ---OLRFVMLSLFEDYM-----COYDVEVRD-----GDNRDGQIILKRYCGN--E 202
DB 474 KSEELKSLARFRFDYVSSSTAGKSCGPDGWFEDENCYVVTSKQRAWEBAQGYCTMAA 533
QY 203 RPAPIQS--IGSSLHVLFHSDG-SKNFDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVIPNSLTETLRGKGLTTWTWIGLHRLDAEKPFIMELMDRSNVVINDMLTFWAS 593
QY 242 SPCHDGTCVL---DKAGS--YKACACLAGYTGQRCENULEERN---CSDPGPVGXYOKI 293
DB 594 GEPGENETNCVYMDIODQLOSVWTKKSCFPSSFACMMDLSRNNAKCDDPSGLENGATL 653
QY 294 TGGPGLINGRAKIGTGVVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPXI 351
DB 654 HGQS--IDGFYA--GSSIRYGCYVLIHLSGTETVCTTNGTWSAPKRCIKVITCQNPV 709
QY 399 --LPMGYQHHTQLOYEICISPFYRLGSSRRTCLRTKWSGRAPSCIPICGKIENITAP- 455
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QY 456 -----KTQGLRMPMOAIIYRRTSGVHDSLHKAMFLVCSGALVNERVVAACVYDGLG 510
DB 827 IMNGNSTEIGQPMWQAGISRMLA-----DHNNMFLOCGGSLNEKIVTAACVYYSA 879
QY 511 KVTMIKTADLVKLVGKFRDDDRDEKTIQSLQISAIILHPNYDPIILDADIAILKLDKA 570
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Db 940 TLTRVQICLPT--DITT--REHLKEGLAVVTGNG---LNENNTSETIQOAVLPV 990  
Qy 625 VDSLCEBOHEDHGIPVSTDNMFCAWSEPTAPSDICTAETGCIAAVSPGRASPEPRWH 684  
Db 991 VAASTCEEGYKADLPLVTENNFCAGYK-KGRYDACSGBSGG--PLVFADSRTERRW 1047  
Qy 685 LMGVMSYDKTCSH-RLSTAFTKVLPEFKWMIER 717  
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNVEFLSMIRQ 1081

RESULT 9  
US-08-877-620-2  
Sequence 2, Application US/08877620  
Patent No. 5985590  
GENERAL INFORMATION:  
APPLICANT: Ding, Jeak Ling  
APPLICANT: Ho, Bow  
TITLE OF INVENTION: The Cloned Factor C cDNA of the  
TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius  
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Kolasch & Birch  
STREET: 810 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22042  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/877,620  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/596,405  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy, Jr., Gerald M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1781-105P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-877-620-2

Query Match 16.94; Score 665; DB 2; Length 1083;  
Best Local Similarity 25.44; Pred. No. 1.8e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

Qy 34 PGAEWNTMCECEYDIECVPCPKR-----VGYTTPCCRNENEDSCLIH 82  
Db 248 PNCQMSFPKRCIR---ECAMVSPRHKVNALSGMIGATL-----RFSQDS--- 293  
Qy 83 PGCTIFENCKSCR-NGSMGTL----- 103  
Db 294 PYVLIGETLTCQNGNGMGOIPLCKKLVPCRPDLVPVNAHKKKIGVEKQYGGPQCTE 353  
Qy 104 -----DFTYVKGFFCAECR--AGWYGG--DCKR-----CGQVLR-- 133  
Db 354 VVTYSGSNVFLMGFDLTKCNPDGSGWSGSPSCVAVADREVDCSKAVDPLDVGEPVRIH 413

Qy 134 APFGQILLS-----YPLNAHCWTHA---KPGFV----- 162  
Db 414 CPAGCSLITAGTGWTAIYHLSVCAAIHAGCLPNSGGAHVHVNNGPYSDFLGDLNGI 473  
Qy 163 ---QLAFWHLSEFDN-----CQDYVEVRD-----GDNRDGOIKRVCN--E 202  
Db 474 KSEELSLARSFFRDVSSSTAGKSCPDGWFEBVENCYVTSKORAMEAQAQVCTNMAA 533  
Qy 203 RPAPIOS--IGSSIAHLFHSDG-SKNFDFH-----AIYEITACSS 241  
Db 534 RLAVLDKVDVPLNLTETLNGKGLTTTWIGLHRLDAKRFIWMELMDRSNVLANNLTFMAS 593  
Qy 242 SPGFHDGTCVL-----DKAGS-YKACIAGYTGRCENLLEBN---CSDFGSPVNGYQKI 293  
Db 594 GEPGNETNVCYMDIOPLOSVMTKSCFQPSFPAQMDLSDRKAKCDPDGSLENGHATL 653  
Qy 294 TGPBGLINRHAKIGTVSPFNNSVYLSGNERKTCQCNEMSGKQPICK--ACREPKI 351  
Db 654 HGGS--IDGFYA--GSSIRYSCVHLVLSGETVCTTNGTWGAPKPRCIKITQONPV 709  
Qy 352 SDLVRRRLPMQVSRBETPLHOLYSAFSSKQLO---SAPTKPALPFGD----- 398  
Db 710 PYSYSEIKP--PSTNNSIRVSGSEPLRLPLPLAPRAKPPRRSSQSPSTVDLASK 766  
Qy 399 --LPMGYOHLATQLOECISPFYRLGSSRRCTLRTGKSGRAPSCIPICKLENTAP- 455  
Db 767 VKLPEGHYRVGSAIYTCESRYELLGSGQRCDNSGNGSGRPASCIPVCGRSDSPSPF 826  
Qy 456 ----KTQGLRWQALYHRTSGVHDGSLHKAMFLVCSGALVNERTVVAAHCTYDLG 510  
Db 827 INNGNSTEIGQWPMQGISRWLA-----DHNMFQCGGSLNEMKIYTAHCVYSA 879  
Qy 511 KVMITKADLVKLVGKPRVDRDEKTIOSLSAIIHPNYPILDLADIAILKLDKA 570  
Db 880 TAEIIPNCFKTLKATYRDSRDDYVVRLELHVNNVDGNINFIATLITKTPV 939  
Qy 571 RISTRVQICLAPSDLSFSQSHI-----TVAGNNVLADYRSGPKNDLRSQVSV 624  
Db 940 TLTRVQICLPT--DITT--REHLKEGLAVVTGNG---LNENNTSETIQOAVLPV 990  
Qy 625 VDSLCEBOHEDHGIPVSTDNMFCAWSEPTAPSDICTAETGCIAAVSPGRASPEPRWH 684  
Db 991 VAASTCEEGYKADLPLVTENNFCAGYK-KGRYDACSGBSGG--PLVFADSRTERRW 1047  
Qy 685 LMGVMSYDKTCSH-RLSTAFTKVLPEFKWMIER 717  
Db 1048 LEGIVSWGSPSGCGKANQYGGFTKVNVEFLSMIRQ 1081

RESULT 10  
US-09-287-368-2  
Sequence 2, Application US/09287368A  
Patent No. 6645724  
GENERAL INFORMATION:  
APPLICANT: Ding, Jeak Ling  
APPLICANT: HO, Bow  
TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin  
TITLE OF INVENTION: From a Sample Using Recombinant Factor C  
FILE REFERENCE: 1781-0165P  
CURRENT APPLICATION NUMBER: US/09/287,368A  
CURRENT FILING DATE: 1999-04-07  
EARLIER APPLICATION NUMBER: 09/201,786  
EARLIER FILING DATE: 1998-12-01  
EARLIER APPLICATION NUMBER: 09/081,767  
EARLIER FILING DATE: 1998-05-21  
EARLIER APPLICATION NUMBER: 60/058,816  
EARLIER FILING DATE: 1997-09-19  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 2  
LENGTH: 1083  
TYPE: PRT  
ORGANISM: Carinoscorpius rotundicauda

FEATURE:  
OTHER INFORMATION: any n or xaa = Unknown  
US-09-287-368-2

16.9%; Score 665; DB 4; Length 1083;

Query Match  
Best Local Similarity 25.4%; Pred. No. 1.8e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEWNIMCECECYDIECVCPKRE-----VVGYYTIPCCRNENECDCLIH 82
DB 248 PNGQMSNFPKRCIR-----ECAMVSSPEHGKYNALSGDMIEGATL-----RFSCDS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 294 PYVLIGQETLTCQNGQMNQIPOCKNLVFCPDLDPVNAHAKYKIGVEQKYGOFPQGTB 353
QY 104 -----DDFYKGFYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTSGNRYFLMGFDTLKCNPDGSMGSGSPSCYKVAADREVDCSKAVDFLDVGEPRYIH 413
QY 134 APKQIILLES-----YPLNAHCEWTIHA---KRGFVI----- 162
DB 414 CPACGSLTAGTGWGTATAYHELSSVCRAIHAIGKLPNSGGAHVHVNNGPYDFLSDLNGI 473
QY 163 ---QLRFTVMSLEFDYH-----COYDYVEYRD-----GNRDGQIHKRYCGN--E 202
DB 474 KSEBELKSLARSPFDYVSSSTAGKSGCPDGMFEVDENCYVYTSKORAMERAOQVCTMAA 533
QY 203 RPAPIQS--IGSSLHVLHFDG--SKNFDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVYNSLTETLRGKGLTTTWTGHLRLDAEKPFIMELMDRNVNLNDLWTWAS 593
QY 242 SPCHDGTCLV---DKAGS--YKACIAGYTGORCENLBERN---CSPDGPVNGYQKI 293
DB 594 GEPGNETNCVYMDIODOQSVWTKKSCFQPSFACMDLSDRNKAKCDDPGSLNGHATL 653
QY 294 TGGEGILINGHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGQS--IDGFYA--GSSIRYSCEVLHAYLSTETVCTTNGTWSAPKPRCIKVITCONPV 709
QY 352 SDVLRRLVPMQVOSRETPHLQVSAFSSKQKQ---SAPTKKRALPFGD----- 398
DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAKAPPKRRSSOPSTVDLASK 766
QY 399 --LPMGYOHLHTOLOYECISPFYRLGSSRRCTCLRTGKMSGRABSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRALYTCESRYEELGSGRRCDNSNGMWSGRPASCIPIVCGRSDSPSPF 826
QY 456 -----KTQGLRMPQOAIYRRTSGVHDSGLHKAMFLVCSGALYNERTVVAACVTDLG 510
DB 827 IWNQNSTEIQMPQOAGISRWLA-----DHNMMFLOCGGSLINEKMIYVAACVYISA 879
QY 511 KVTMIKTADLKVVYLGKPYRDDDRDEKTIQSLQISAILIHPYDPILLDADIAIKLDDKA 570
DB 880 TAEIIDPNQFKMYLGKTYRDSRDDDDYQVREALEIHVNPYDPGNALFDIALIQLKTPV 939
QY 571 RISTRVOPICLAASRDISTSFQESH-----TVAGNVLADVRSPEGKNDTLRSGVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGNG---LNENNTYSTIIQOAVLPV 990
QY 625 VDSLICEQHEHDHGIPIVSVTDNMFCAWEPTAPSDICTAETGGLAIVSFPGRASPEPRWH 684
DB 991 VAASTICEEGYKEADPLTLVTENMFCAGYK--KGRYDACSGLSDG--PLVFADSRTERRV 1047
QY 685 LMGLVSWGYDKTCSH--RLSTAFTKYLPRKDWIER 717
DB 1048 LEGIVSWGSPGCGKANOYGGFTKYNVFLSWIRQ 1081
```

RESULT 11  
US-09-626-795-2  
Sequence 2, Application US/09626795  
Patent No. 6719973

GENERAL INFORMATION:  
APPLICANT: DING, Jeak Ling  
APPLICANT: HO, Bow  
TITLE OF INVENTION: Use of Recombinant Factor C to Induce Bacteriostasis  
FILE REFERENCE: 4810-61737  
CURRENT APPLICATION NUMBER: US/09/626,795  
CURRENT FILING DATE: 2000-07-26  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 1083  
TYPE: PR1  
ORGANISM: Carcinoscopus rotundicauda  
US-09-626-795-2

16.9%; Score 665; DB 4; Length 1083;

Query Match  
Best Local Similarity 25.4%; Pred. No. 1.8e-46;  
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

```
QY 34 PGAEWNIMCECECYDIECVCPKRE-----VVGYYTIPCCRNENECDCLIH 82
DB 248 PNGQMSNFPKRCIR-----ECAMVSSPEHGKYNALSGDMIEGATL-----RFSCDS----- 293
QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 294 PYVLIGQETLTCQNGQMNQIPOCKNLVFCPDLDPVNAHAKYKIGVEQKYGOFPQGTB 353
QY 104 -----DDFYKGFYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
DB 354 VTYTSGNRYFLMGFDTLKCNPDGSMGSGSPSCYKVAADREVDCSKAVDFLDVGEPRYIH 413
QY 134 APKQIILLES-----YPLNAHCEWTIHA---KRGFVI----- 162
DB 414 CPACGSLTAGTGWGTATAYHELSSVCRAIHAIGKLPNSGGAHVHVNNGPYDFLSDLNGI 473
QY 163 ---QLRFTVMSLEFDYH-----COYDYVEYRD-----GNRDGQIHKRYCGN--E 202
DB 474 KSEBELKSLARSPFDYVSSSTAGKSGCPDGMFEVDENCYVYTSKORAMERAOQVCTMAA 533
QY 203 RPAPIQS--IGSSLHVLHFDG--SKNFDGFH-----AIYEITACSS 241
DB 534 RLAVLDKDVYNSLTETLRGKGLTTTWTGHLRLDAEKPFIMELMDRNVNLNDLWTWAS 593
QY 242 SPCHDGTCLV---DKAGS--YKACIAGYTGORCENLBERN---CSPDGPVNGYQKI 293
DB 594 GEPGNETNCVYMDIODOQSVWTKKSCFQPSFACMDLSDRNKAKCDDPGSLNGHATL 653
QY 294 TGGEGILINGHAKIGTVSPFCNNSYVLSGNEKRTCOQNGEMSGKOPICIK--ACREPKI 351
DB 654 HGQS--IDGFYA--GSSIRYSCEVLHAYLSTETVCTTNGTWSAPKPRCIKVITCONPV 709
QY 352 SDVLRRLVPMQVOSRETPHLQVSAFSSKQKQ---SAPTKKRALPFGD----- 398
DB 710 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLARAKAPPKRRSSOPSTVDLASK 766
QY 399 --LPMGYOHLHTOLOYECISPFYRLGSSRRCTCLRTGKMSGRABSCIPICGKIENITAP- 455
DB 767 VKLPEGHYRVGSRALYTCESRYEELGSGRRCDNSNGMWSGRPASCIPIVCGRSDSPSPF 826
QY 456 -----KTQGLRMPQOAIYRRTSGVHDSGLHKAMFLVCSGALYNERTVVAACVTDLG 510
DB 827 IWNQNSTEIQMPQOAGISRWLA-----DHNMMFLOCGGSLINEKMIYVAACVYISA 879
QY 511 KVTMIKTADLKVVYLGKPYRDDDRDEKTIQSLQISAILIHPYDPILLDADIAIKLDDKA 570
DB 880 TAEIIDPNQFKMYLGKTYRDSRDDDDYQVREALEIHVNPYDPGNALFDIALIQLKTPV 939
QY 571 RISTRVOPICLAASRDISTSFQESH-----TVAGNVLADVRSPEGKNDTLRSGVSV 624
DB 940 TLTRVQPICLPT--DITT---REHLKEGTLAVVTGNG---LNENNTYSTIIQOAVLPV 990
QY 625 VDSLICEQHEHDHGIPIVSVTDNMFCAWEPTAPSDICTAETGGLAIVSFPGRASPEPRWH 684
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Db 991 VAASTCEEGYKADLPLVTENNFCAGYK-KGRYDACSDDSGG--PLVAFDSDRTERRNV 1047

Qy 685 LMGIVSMXYDKTCSH-RLSTAFKVLPPFKWMIER 717

Db 1048 LEGIVSMGSPSGCGKANQYGGFTKNVFLSMIRQ 1081

RESULT 12

US-09-949-016-6138

/ Sequence 6138, Application US/09949016

/ Patent No. 6812339

/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.

/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001307

/ CURRENT APPLICATION NUMBER: US/09/949,016

/ CURRENT FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768

/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498

/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 6138

/ LENGTH: 699

/ TYPE: PRT

/ ORGANISM: Human

US-09-949-016-6138

Query Match 12.2%; Score 482; DB 4; Length 699;

Best Local Similarity 24.9%; Pred. No. 1,76-31; Indels 228; Gaps 39;

Matches 178; Conservative 93; Mismatches 215; Indels 228; Gaps 39;

Qy 69 CNEBNECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCYACBAGWY---GGD 124

Db 143 CEREBEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNT 180

Qy 125 C-MRCGQVLRAPKQILL-----ESYPLNAHCMTTHAKRPGVIOQLRFVMLSLEPDY-- 176

Db 181 CVCESDNLFTORTGIVTSPDPNPYPKSECLYTIIEBGMVNLQFEDI---FDIQH 237

Qy 177 ----CQYDVEVRDGNRRCQIIRKVCGERPAPISIGSSLHVLFHSDGSKNPFDFHAI 232

Db 238 PEVPCPYDIKIKVGP---KVLGPGCEKAPBPISTOSHVLILPHSDNSAENRGMRL- 292

Qy 233 YEETACSSSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEBRNCSDPGGPVNGYOK 292

Db 293 -----STRAA-----GNECPRL-----QP--PVH----- 309

Qy 293 ITGGPGLINGRAKIGTVSFF-----CNSY-VLSGNEK-----TCQNGEWSGKQ 339

Db 310 -----GKIPSOAKY-----FFKDQVLYSCDTGYKVLKONVEMDTFOIELCKDGTWSNKI 359

Qy 340 PIC-ICACBEPKISDLVRRRLVLMQVOSRETPHLQYSAFSGKQKLSAPTKKRALPFGD 398

Db 360 PTCKIYDCRAP-----GEB 372

Qy 399 LPMGYOHLHT-----OLOYECISPFYRLGSSR--RTCLRTGKWS---GRA-PSC 442

Db 373 LEHGLITFTSRNNLTYYKSEIKISCOEPYKMLNNNTGITYTCSAQGVMMNKVLGRSLPTC 432

Qy 443 IPICG-----KIENITAPKTOGLRWPQOAIYRRTSGVHDSLHKGAMFLVCSGA 492

Db 433 LPTCGLPKFSRKLMAIFN-GRPAQGT--PWIAML-----SHLNGQPF--CGGS 478

Qy 493 LVNERVVVAARV---TDLGKTY-----MIKTADLVKLVGKPYRDDDEKTIQSLQIS 544

Db 479 LLESSWIVAAHCHLHSLDPLDRLSDLSPSDKIILGKMR--LSDSENEOHLGVK 536

Qy 545 AILHNVDPDILLDADIALIKLIDKARISTRVQPICLAASRDISTFQE-SHITVAGMNV 603

Db 537 HTLLHPQDVPNTFENDVALVELLESBVINAFAFWPILCPBGPQ-----QGANVIVSGWK 591

Qy 604 LADVSPGKNDTLKSGVSVSDSLCEBQHDHGIPIVSTDNMFCASEPTAPSDICTA 663

Db 592 QFLQRF---ETLWEIELEPIVDHSTCOKAYAP--LKKKVTYDMICAG-EKGGADACAG 644

Qy 664 ETGGIAAVSPGRASPEPRRMLMGVSMXYDKTCSHRLSTAFKVLPPFKWMIER 717

Db 645 DSGGPMVTLNRRG---QWLVGVTVSMGDGKKDRVC-VYSYIHNNDWIQR 693

RESULT 13

US-09-949-016-11182

/ Sequence 1182, Application US/09949016

/ Patent No. 6812339

/ GENERAL INFORMATION:

/ APPLICANT: VENTER, J. Craig et al.

/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

/ TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001307

/ CURRENT APPLICATION NUMBER: US/09/949,016

/ CURRENT FILING DATE: 2000-04-14

/ PRIOR APPLICATION NUMBER: 60/241,755

/ PRIOR FILING DATE: 2000-10-20

/ PRIOR APPLICATION NUMBER: 60/237,768

/ PRIOR FILING DATE: 2000-10-03

/ PRIOR APPLICATION NUMBER: 60/231,498

/ PRIOR FILING DATE: 2000-09-08

/ NUMBER OF SEQ ID NOS: 207012

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 11182

/ LENGTH: 717

/ TYPE: PRT

/ ORGANISM: Human

US-09-949-016-11182

Query Match 12.0%; Score 475; DB 4; Length 717;

Best Local Similarity 24.6%; Pred. No. 6,96-31; Indels 228; Gaps 38;

Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;

Qy 69 CNEBNECDSCLIHPGCTIFENCKSCRNCSWGTLDDFYVKGFCYACBAGWY---GGD 124

Db 161 CEREBEELSCDHY-----CHN-----YIGGYCS-CRFGYILHTDNT 198

Qy 125 C-MRCGQVLRAPKQILL-----ESYPLNAHCMTTHAKRPGVIOQLRFVMLSLEPDY-- 174

Db 199 CVCESDNLFTORTGIVTSPDPNPYPKSECLYTIIEBGMVNLQFEDI---FDIEDH 255

Qy 175 --YMOQYDVEVRDGNRRCQIIRKVCGERPAPISIGSSLHVLFHSDGSKNPFDFHAI 232

Db 256 PEVPCPYDIKIKVGP---KVLGPGCEKAPBPISTOSHVLILPHSDNSAENRGMRL- 310

Qy 233 YEETACSSSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEBRNCSDPGGPVNGYOK 292

Db 311 -----STRAA-----GNECPRL-----QP--PVH----- 327

Qy 293 ITGGPGLINGRAKIGTVSFF-----CNSY-VLSGNEK-----TCQNGEWSGKQ 339

Db 328 -----GKIPSOAKY-----FFKDQVLYSCDTGYKVLKONVEMDTFOIELCKDGTWSNKI 377

Qy 340 PIC-ICACBEPKISDLVRRRLVLMQVOSRETPHLQYSAFSGKQKLSAPTKKRALPFGD 398

Db 378 PTCKIYDCRAP-----GEB 390

Qy 399 LPMGYOHLHT-----OLOYECISPFYRLGSSR--RTCLRTGKWS---GRA-PSC 442

Db 391 LEHGLITFTSRNNLTYYKSEIKISCOEPYKMLNNNTGITYTCSAQGVMMNKVLGRSLPTC 450

Qy 443 IPICG-----KIENITAPKTOGLRWPQOAIYRRTSGVHDSLHKGAMFLVCSGA 492

Db 451 LPTCGLPKFSRKLMAIFN-GRPAQGT--PWIAML-----SHLNGQPF--CGGS 496

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QY 493 LUNERTVVAANRV-----TDLGKVMITKADLKVLGKFRYRDDDEKTIQSLQIS 544
DB 497 LLSGSMIVLWALHCHSLDPEDEPTLRSDLSPSDFKILIGKMR--LISDENOHLGYK 554
QY 545 AILHNVPDILDLADIAILKLDKARISTRVOPICLAASRLDSTFSOE-SHTTVGMNV 603
DB 555 HTLHQYDPTNRENDVALVELLESFVLNAFVMPICLPEBPQ-----QEGAMIVSGMK 609
QY 604 LADVRSGFNKDTLRSGVSVVDSLCEQEDHGIPIVSTDNMFCAWEPAPSDICTA 663
DB 610 QFQRRP-----ETLMEIPIVDHSTCQKAYAP--LKKVTRDMICAG--EKEGKDACAG 662
QY 664 ETGCIANVSFPGASPEPRHMLGMVSMYDTCSHRLSTAFKULPFDWMIR 717
DB 663 DSGGPMVTLNRRG-----QWYLVGVSMGDCGCKDRYG--VVSYIHNNKDWIOR 711

RESULT 14
US-09-949-016-7775
; Sequence 7775, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7775
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7775

Query Match 10.1%; Score 399.5; DB 4; Length 691;
Best Local Similarity 22.6%; Pred. No. 1.3e-24;
Matches 173; Conservative 79; Mismatches 243; Indels 269; Gaps 34;

QY 128 CGOVLAR--APK-----GQILSSYP-----LMAHCETIAKDPFVQLRFLVMSLEPDY 175
DB 16 CGSVATPFLGPKMBPVVFGRLASPGFGEYANDQERRMTLTAPEGYRLRLFTFPDLFLSH 75
QY 176 MCOYDVEVRDGNRDQIIRKVCNME---RPAF---IQSIGSLHVLFHS DGS--KN 225
DB 76 LCEYDFPKLSSG---AKVLATLCGGESTDTERAPGQDTFYSIGSSLDIFRDSINEKP 111
QY 226 FDFGHAII--EETAGSSP-----CFHDTCLVDKAGSYKACACLAGYTOR---CENL 274
DB 132 FTGFEAFYAEDIDECQVARGEARPTCDH--CHNHGFGFYCSGAGYVLRHKKRTCSAL 188
QY 275 -----LEE----- 277
DB 189 CSGOVFTQSRGELSSPEYPPRPYKLSCTYSISLEBSFVILDRVESFDVETHPETLCY 248
QY 278 -----RNCSDP 283
DB 249 DPLKIQTDREHREHFGCKTLPHRIETKSNVTITFTVDES GHTGKIHVTSIAQPCPY 308
QY 284 GGPVNGYQKTTGGEGLINGRHAK--IGTVVSFFCNSY-VLSG-----NEKRTCOQNGEW 335
DB 309 MAPPNGH-----VSPVQAKYILKDSFSIFCETGTELLQGLPLKSFVAVCQKDGSW 359
QY 336 SGKQPTC-IKACREPKISDLVRRVRLPM-QVQSEFTPLHQLYGAAPSKQLQSAPTKPA 393
DB 360 DRMPACISIVDCGPD-----YLPGRVEYITGGVTTYKAV----- 396
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QY 394 LPFGDLPMGYGHLHQLQYECTISPRY--RLGSSRRCTCLRTGKMG-----RAPSCPTIG 447
DB 397 -----IQSCETEFYTMKVDNGKYYCEADGWTSGKSGKSPVCPVG 440
QY 448 KIENITAPKTOGLR-----WPMQAIYRRTSGVHDSLHKAMFLVCSGALVNERTVV 501
DB 441 LSARTTGRHIVYGQAKRQKEDFPWVLLIGST-----AAGALLYDNWVLT 485
QY 502 AAHCYTDLQKVMITKADLKVLGKFRYRDDDEKTIQSLQ-----ISAIIHENV-D 553
DB 486 AAHAAYE-----QKHASALDIRMG-----TLKRLSPHYQAGSEAVFIHEGYTH 530
QY 554 PILLDADIAILKLDKARISTRVOPICLAASRLDSTFSQESHITYAGNVLVADVSPGR 613
DB 531 DAGFNDIALILKNNKVININSNITPICRKEASEGFMRTDICTAGSWG-----LTGRFL 586
QY 614 NDTLRSGVSVVDSLCEQEDHGIPIVSTDNMFCAWEPAPSDICTAETGCIANA 672
DB 587 ANNLMTVDIPYDHQKCTAAYEKPRYPRGSVTANMLCAGLE--SGGKDCRGDSGG--ALV 643
QY 673 FPGRASPEPRHMLGMVSMYDTCSHRLSTAFKULPFDWMIR 716
DB 644 F--LDSETRMFVGGIVSGSMNCGEAGQGYVYTKVINYIPIWE 685
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RESULT 15
US-09-027-337-2
; Sequence 2, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotsoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; FILE REFERENCE: D6064
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides
; OTHER INFORMATION: 23 to 2589 of Sequence 1
; Patent No. 5972616
; US-09-027-337-2

Query Match 8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.8e-18;
Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLARPKQI-----LLESYPLNHCETIAKDPFVQLRFLVMSLEPDY----- 176
DB 340 CGGRLEKKAQGTENSPYPPHYPNIDCTWNIE---VNNQHVAVKSYKFFYLEGCVPA 394
QY 177 --CQYDVEVRDGNRDQIIRKVCNME---RPAF---IQSIGSLHVLFHS DGSKNPDGFAIYE 234
DB 395 GTCPRDHYVING-----EKYCGERSQFVTVSNKNIYTRFHS DQSTVDGFLAAY- 444
QY 235 EITAGSSPFCFHDGTC-----VLDKAGSYKACIAGY----- 266
DB 445 -LSYDSDPCPGQFTCRGCIKELRCGMADCTHSDELNCS CDAGHOFCKNFKCP 503
QY 267 -----TGRCENLLEBRNCSDPGPGVNGYQKTTGGEGLINGRHAKIGTVVSFFCNSY 320
DB 504 LFWVCDSVNDCGNSDEQCSCP-----AQTFRCSNGKC 537
QY 321 LSG-----NEKRTCOQNGEWGSKOPICIKACREPKISDLVRRVRLPMQVQSEFTPLHQLYS 376
DB 538 LSKSQQCNKQDCGSDSDASCPKVVVTC----- 567
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QY 377 AAFSKQKQASPTKKRALPFQDLEPMGYOHLHTQLOQECISPFYRRLGSSRRRTCLRTGKMS 436
Db 568 -----TK-----HT---YRCLNGL-----CLSKGN-- 584
QY 437 GRAPSCIPICGKIENITAPKTO-----GLR-----WPMQAIYRRTS 473
Db 585 -----PECDSKEDCDSDGDEKDCGGLRSFTRQARVVGSTDADEGEWPMQVSLHALGQ 637
QY 474 GYHDGSLHKGAWFLVCSGALVNERVVAAHCVTDLGKVTMIKTADLKVVLGKRYRDDDR 533
Db 638 G-----H-----ICGASLISPMWLVSAAHCYIDRGRFRYSDEPTQWTAFLG-LHDQSQR 684
QY 534 DEKTIQSLQISATILHFNYPILLDADIALIKLDKARISTRVOPICLAASRDLSISFOE 593
Db 685 SABGVQERRLRKRIISHPFNDFTFDYDIALLELEKPAEYSSMVRPICLP--DASHVFP 741
QY 594 SH-ITVAGMWVLADVRSPPFNKDTLRSGVSVYDLSLCEQHEDHGI PVSVTDNMPCASW 652
Db 742 GKAIWTGM--GHTQYGGTGAIILOKGEIRVINQTTCENL-----LPQOITPRMNCVGF 793
QY 653 EPTAPSDICTAETCG-IAAVSPGRASPEPRMHLMGIVSNVYDKTCSHRLSTAFTKVLPE 711
Db 794 -LSGGVDSGCGSDSGPLSSVEADGRI-----FGAGVSVNG-DGCAQRNKPQVYTRLLPE 845
QY 712 KDNIERN 718
Db 846 RDMIKEN 852
```

Search completed: July 12, 2005, 17:09:15  
Job time : 56 secs

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GenCore version 5.1.6  
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OM protein - protein search, using bw model

Run on: July 12, 2005, 17:09:12 ; Search time 163 Seconds

(without alignments)  
1706.496 Million cell updates/sec

Perfect score: 3945  
Sequence: 1 MEIGCWTOGLTFPLQLLLIS.....LSTAFKVLPEKMIERNKK 720

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1726218 seqs, 386331768 residues

Total number of hits satisfying chosen parameters: 1726218

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubppaa/US10E\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/2/pubppaa/US10F\_PUBCOMB.pep:\*  
19: /cgn2\_6/ptodata/2/pubppaa/US11\_PUBCOMB.pep:\*  
20: /cgn2\_6/ptodata/2/pubppaa/US11A\_PUBCOMB.pep:\*  
21: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pep:\*  
22: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
27	3945	100.0	720	10	US-09-997-428-231 Sequence 231, App
562	3945	100.0	720	14	US-10-174-587-170 Sequence 170, App
626	3945	100.0	720	14	US-10-063-742-38 Sequence 38, App
741	3945	100.0	720	17	US-10-972-317-38 Sequence 38, App
742	3939	99.8	720	14	US-10-004-551-4 Sequence 4, App
743	3939	99.8	720	14	US-10-098-871-26 Sequence 26, App
744	3921.5	99.4	737	16	US-10-408-765A-1796 Sequence 1796, App
745	3500.5	88.7	649	15	US-10-374-639-17 Sequence 17, App
746	3500.5	88.7	649	15	US-10-333-574-17 Sequence 17, App
747	3089.5	78.3	567	14	US-10-004-551-2 Sequence 2, App
748	2946.5	74.7	570	13	US-10-067-422-9 Sequence 9, App
749	2413	61.2	455	11	US-09-833-245-1401 Sequence 1401, App

750	1708.5	43.3	323	11	US-09-833-245-1402 Sequence 1402, App
751	672	17.0	1019	14	US-10-183-992-4 Sequence 4, App
752	672	17.0	1019	16	US-10-480-254-4 Sequence 4, App
753	665	16.9	1019	14	US-10-183-993-8 Sequence 8, App
754	665	16.9	1019	16	US-10-638-125-4 Sequence 4, App
755	665	16.9	1019	16	US-10-480-254-8 Sequence 8, App
756	665	16.9	1083	14	US-10-183-992-6 Sequence 6, App
757	665	16.9	1083	14	US-10-638-125-2 Sequence 2, App
758	665	16.9	1083	16	US-10-480-254-6 Sequence 6, App
759	475	12.1	699	15	US-10-388-322-2 Sequence 2, App
760	475	12.0	699	18	US-10-820-155-93 Sequence 93, App
761	471	11.9	728	14	US-10-148-671-5 Sequence 5, App
762	469.5	11.9	679	9	US-09-874-198-6 Sequence 6, App
763	469.5	11.9	679	9	US-09-874-198-6 Sequence 6, App
764	468	11.9	728	15	US-10-388-322-4 Sequence 4, App
765	468	11.9	728	18	US-10-820-155-92 Sequence 92, App
766	461	11.7	728	17	US-10-239-032-1 Sequence 1, App
767	403.5	10.2	688	9	US-09-874-198-7 Sequence 7, App
768	403.5	10.2	688	9	US-09-874-198-7 Sequence 7, App
769	403.5	10.2	705	10	US-09-808-602-94 Sequence 94, App
770	403.5	10.2	705	10	US-09-800-198-81 Sequence 81, App
771	403.5	10.2	705	15	US-10-257-021-66 Sequence 66, App
772	401.5	10.2	686	9	US-09-874-198-2 Sequence 2, App
773	401.5	10.2	686	9	US-09-874-198-2 Sequence 2, App
774	401.5	10.2	686	18	US-10-974-148-12 Sequence 12, App
775	401.5	10.2	686	18	US-10-820-155-90 Sequence 90, App
776	400.5	10.2	686	15	US-10-388-322-3 Sequence 3, App
777	400.5	10.2	686	15	US-10-332-713-2 Sequence 2, App
778	398.5	10.1	671	15	US-10-332-713-3 Sequence 3, App
779	336	8.5	760	9	US-09-925-301-1024 Sequence 1024, App
780	334	8.5	673	9	US-09-874-198-8 Sequence 8, App
781	334	8.5	673	9	US-09-874-198-8 Sequence 8, App
782	334	8.5	688	18	US-10-820-155-81 Sequence 81, App
783	332	8.4	855	15	US-10-072-012-354 Sequence 354, App
784	332	8.4	855	15	US-10-072-012-420 Sequence 420, App
785	331.5	8.4	855	15	US-10-037-411-132 Sequence 132, App
786	331.5	8.4	1019	14	US-09-776-191-64 Sequence 64, App
787	331.5	8.4	1019	14	US-10-157-031-267 Sequence 267, App
788	331.5	8.4	1019	15	US-10-156-218A-31 Sequence 31, App
789	330.5	8.4	1019	16	US-10-729-807-37 Sequence 37, App
790	330.5	8.4	1019	16	US-10-408-765A-2243 Sequence 2243, App
791	329.5	8.4	3389	16	US-10-016-248-47 Sequence 47, App
792	329.5	8.4	3389	16	US-10-408-765A-2286 Sequence 2286, App
793	329.5	8.3	3508	15	US-10-016-248-46 Sequence 46, App
794	329	8.3	3564	15	US-10-016-248-45 Sequence 45, App
795	328.5	8.3	1274	15	US-10-467-042-11 Sequence 11, App
796	328.5	8.3	1274	20	US-11-046-866-11 Sequence 11, App
797	328.5	8.3	1783	14	US-10-276-934-12 Sequence 12, App
798	328.5	8.3	1800	14	US-10-276-934-10 Sequence 10, App
799	328.5	8.3	1866	14	US-10-276-934-9 Sequence 9, App
800	328.5	8.3	2008	14	US-10-276-934-11 Sequence 11, App
801	328.5	8.3	2306	14	US-10-276-934-14 Sequence 14, App
802	328.5	8.3	2352	14	US-10-276-934-13 Sequence 13, App
803	328	8.3	762	16	US-10-729-807-1 Sequence 1, App
804	328	8.3	851	15	US-10-276-934-1798 Sequence 1798, App
805	328	8.3	851	15	US-10-296-115-1143 Sequence 1143, App
806	328	8.3	855	15	US-10-295-027-1185 Sequence 1185, App
807	328	8.3	855	15	US-10-072-012-353 Sequence 353, App
808	328	8.3	855	15	US-10-072-012-412 Sequence 412, App
809	328	8.3	449	9	US-09-925-302-612 Sequence 612, App
810	327.5	8.3	449	10	US-09-925-302-612 Sequence 612, App
811	327.5	8.3	449	15	US-10-453-827-884 Sequence 884, App
812	327	8.3	727	15	US-10-072-012-44 Sequence 44, App
813	327	8.3	727	15	US-10-072-012-44 Sequence 44, App
814	327	8.3	855	14	US-10-099-700A-2 Sequence 2, App
815	327	8.3	855	14	US-10-190-030B-2 Sequence 2, App
816	327	8.3	855	14	US-10-302-840A-2 Sequence 2, App
817	327	8.3	855	14	US-10-267-219-2 Sequence 2, App
818	327	8.3	855	14	US-10-112-221A-2 Sequence 2, App
819	327	8.3	855	14	US-10-104-271-2 Sequence 2, App
820	327	8.3	855	14	US-10-147-211A-2 Sequence 2, App
821	327	8.3	855	15	US-10-156-214A-2 Sequence 2, App
822	327	8.3	855	15	US-10-156-214A-2 Sequence 2, App









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GenCore version 5.1.6

OM protein - protein search, using sw model  
Run on: July 12, 2005, 17:13:58 ; Search time 78 Seconds  
(without alignments)

3570.096 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

Sequence: 1 MEICWTQLGLTFLQLLLS.....LSTAFKVLPRKDIERNRK 720

Scoring table:

Gapop 60.0, Gapext 60.0

Searched: 2105692 seqs, 38676081 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Database: A.GeneSeq.16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1980s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## Description

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66695	standard;	protein;	720	AA.	
DE	Membrane-bound protein	PRO1344.				
PN	MO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 3;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 2						
ID	AAU29108	standard;	protein;	720	AA.	
DE	Human PRO polypeptide sequence	#85.				
PN	MO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 3						
ID	AA87544	standard;	protein;	720	AA.	
DE	Human PRO1344.					
PN	MO200116318-A2.					
PD	08-MAR-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 4						
ID	AA65218	standard;	protein;	720	AA.	
DE	Human PRO1344 (UN0659)	protein sequence SEQ ID NO:221.				
PN	MO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 4;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 5						
ID	ABG9569	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein	PRO1344.				
PN	US2002119130-A1.					
PD	29-AUG-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 5;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 6						
ID	ABU58484	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#85.				
PN	US2003027272-A1.					
PD	06-FEB-2003.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 7						
ID	ABU88032	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein	PRO1344.				
PN	US2003032127-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 8						
ID	ABU84347	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)	#85.				
PN	US2003032112-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 9						
ID	ABR66221	standard;	protein;	720	AA.	
DE	Human secreted polypeptide	PRO1344, SEQ ID NO:170.				
PN	US2003027278-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 10						
ID	ABR65611	standard;	protein;	720	AA.	
DE	Human secreted polypeptide	PRO1344, SEQ ID NO:170.				
PN	US2003036159-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 11						
ID	ABU99551	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein (PRO)	#85.				
PN	US2003040070-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 12						
ID	ABU58033	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#65.				
PN	US2003027163-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 13						
ID	ABU59111	standard;	protein;	720	AA.	
DE	Novel human secreted or transmembrane protein	PRO1344.				
PN	US2002132252-A1.					
PD	19-SEP-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 14						
ID	ABU82623	standard;	protein;	720	AA.	
DE	Human secreted/transmembrane protein	PRO1344.				
PN	US2003032023-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 15						
ID	ABU82790	standard;	protein;	720	AA.	
DE	Human PRO polypeptide	#85.				
PN	US2003032113-A1.					
PD	13-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			
RESULT 16						
ID	ABU89911	standard;	protein;	720	AA.	
DE	Novel human secreted and transmembrane protein	PRO1344.				
PN	US2003036147-A1.					
PD	20-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match		100.0%;	Score 720;	DB 6;	Length 720;	
Best Local Similarity		100.0%;	Pred. No. 0;			

RESULT 17  
ID ABR68160 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US200302764-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 18  
ID ABU60542 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein; #94.  
PN US2002160384-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 19  
ID ABU96213 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 20  
ID ABU92644 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 21  
ID ABO08721 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 22  
ID ABO02773 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 23  
ID ABR74927 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 24  
ID ABR94689 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 25  
ID ABU13924 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002103125-A1.  
PD 01-AUG-2002.  
PA (GETH ) GENENTECH LTD.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 26  
ID ABU85662 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;

RESULT 27  
ID AEU98622 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 28  
ID ABU98037 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 29  
ID ABU91743 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 30  
ID ABU89436 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 31  
ID ABU86277 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 32  
ID ABU67490 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 33  
ID ABU80518 standard; protein; 720 AA.  
DE Human PRO protein #85.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 34  
ID ABU72509 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003003531-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 35  
ID ABU90894 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003018173-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 36  
ID ABO33953 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003009013-A1.  
PD 09-JAN-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 37
ID ABR99436 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 38
ID ABR98826 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 39
ID ABO16349 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 40
ID HUM92249 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 41
ID ABO18890 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 42
ID ABR76311 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 43
ID ABO191970 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 44
ID ABO85047 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 45
ID ABO00186 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 46
ID ABO1518 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 47
ID ABO02163 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 48
ID ABO8737 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 49
ID ABO83432 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 50
ID ABO06233 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 51
ID ABR59269 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 52
ID ABO09331 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ABO19195 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ABO11213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ABR66831 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
ID ABO16044 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 57  
ID ABO13750 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 58  
ID ABU71524 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344.  
PN US2003013855-A1.  
PD 16-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 59  
ID ABU65653 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, SEQ ID 170.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 60  
ID ABO07501 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032117-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 61  
ID ABO03688 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036128-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 62  
ID ABR67136 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027266-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 63  
ID ABO15739 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054483-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 64  
ID ABUS6020 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003022298-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 65  
ID ABU72305 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2002182638-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 66  
ID ABU65348 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032102-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;

RESULT 67  
ID ABU95293 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036117-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 68  
ID ABU71196 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003036143-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 69  
ID ABO07806 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032130-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 70  
ID ABR70047 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032138-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 71  
ID ABR69380 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036132-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 72  
ID ABO01521 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003008353-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 73  
ID ABU81323 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017542-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 74  
ID ABR60120 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032137-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 75  
ID ABU90978 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003018168-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 76  
ID ABR67855 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027269-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;

RESULT 77  
ID ABR65243 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027268-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 78  
ID ABR6465 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027274-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 79  
ID ABR7187 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032135-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 80  
ID ABUS9258 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, #94.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 81  
ID ABUS357 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022295-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 82  
ID ABUS9047 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003022297-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 83  
ID ABUS3127 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 84  
ID ABUS94983 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 85  
ID ABUS9531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 86  
ID ABUS4042 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 87  
ID ABUS3693 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 88  
ID ABO25955 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 89  
ID ABR64938 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 90  
ID ABO27299 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003009012-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 91  
ID ABR68770 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 92  
ID ABO06586 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 93  
ID ABR99131 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 94  
ID ABUS7015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 95  
ID ABUS85967 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 96  
ID ABUS82254 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 97  
ID ABUS7265 standard; protein; 720 AA.

DE Human PRO polypeptide #85.  
 PN US2003036138-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 98  
 ID ABU83737 standard; protein; 720 AA.  
 DE Human secreted/cranemembrane protein (PRO) #85.  
 PN US2003032109-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 99  
 ID ABO08111 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003040066-A1.  
 PD 27-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 100  
 ID ABU92494 standard; protein; 720 AA.  
 DE Human secreted/cranemembrane protein PRO1344.  
 PN US2003045684-A1.  
 PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 101  
 ID ABU81822 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003032104-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 102  
 ID ABU65986 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003036157-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 103  
 ID ABU81164 standard; protein; 720 AA.  
 DE Human secreted polypeptide PRO1344.  
 PN US2003027212-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 104  
 ID ABR59815 standard; protein; 720 AA.  
 DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
 PN US2003032120-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 105  
 ID ABU94003 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003036155-A1.  
 PD 20-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 106  
 ID ABU99856 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003022296-A1.  
 PD 30-JAN-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 107  
 ID ABR66526 standard; protein; 720 AA.  
 DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003027281-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 108  
 ID ABR90944 standard; protein; 720 AA.  
 DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
 PN US2003040058-A1.  
 PD 27-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 109  
 ID ABO53279 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003027986-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 110  
 ID ABU58964 standard; protein; 720 AA.  
 DE Human secreted/cranemembrane protein, #94.  
 PN US2002142961-A1.  
 PD 03-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 111  
 ID ABU94371 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003017540-A1.  
 PD 23-JAN-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 112  
 ID ABU79253 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003032106-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 113  
 ID ABU86582 standard; protein; 720 AA.  
 DE Human secreted/cranemembrane protein (PRO) #85.  
 PN US2003032129-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 114  
 ID ABU86887 standard; protein; 720 AA.  
 DE Novel human secreted and cranemembrane protein PRO1344.  
 PN US2003032131-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 115  
 ID ABU94676 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003032103-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 116  
 ID ABO04603 standard; protein; 720 AA.  
 DE Human PRO polypeptide #85.  
 PN US2003032107-A1.  
 PD 13-FEB-2003.  
 Query Match 100.0%; Score 720; DB 6; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 RESULT 117  
 ID ABR70352 standard; protein; 720 AA.  
 DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003032139-A1.  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Query Match  
RESULT 118  
ID ABR92342 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003022187-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 119  
ID ABR98517 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 120  
ID ABR65916 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 121  
ID ABR64633 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 122  
ID ABR59407 standard; protein; 720 AA.  
DE Novel human secreted or transmembrane protein PRO1109.  
PN US2003027985-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 123  
ID ABR79558 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 124  
ID ABR92949 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 125  
ID ABR95908 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 126  
ID ABR91128 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 127  
ID ABR90221 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036153-A1.  
PD 20-FEB-2003.

Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 128  
ID ABR09636 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 129  
ID ABR10908 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 130  
ID ABR70962 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 131  
ID ABR98281 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183493-A1.  
PD 05-DEC-2002.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 132  
ID ABR87570 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 133  
ID ABR91438 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 134  
ID ABR89286 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003036634-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 135  
ID ABR84652 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 136  
ID ABR69742 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
RESULT 137  
ID ABR80119 standard; protein; 720 AA.  
DE Human PRO protein #85.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 138  
ID AB082493 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002183494-A1.  
PD 05-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 139  
ID AB092173 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003017476-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 140  
ID AB093388 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 141  
ID AB009941 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 142  
ID AB009026 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 143  
ID AB096457 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003027993-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 144  
ID AB010879 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 145  
ID AB010594 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein #85.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 146  
ID AB081631 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 147  
ID AB072127 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003023042-A1.

PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 148  
ID AB095603 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 149  
ID AB096812 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 150  
ID ABR70657 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 151  
ID AB005008 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 152  
ID AB008416 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 153  
ID AB088570 standard; protein; 720 AA.  
DE Human secreted and transmembrane polypeptide PRO1344.  
PN US2002197615-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 154  
ID AB034084 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 155  
ID AB005623 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032118-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 156  
ID ABR74012 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036135-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 157  
ID ABR95604 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.



PN US2003054455-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 158  
ID ABR80901 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049741-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 159  
ID ABR81206 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049743-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 160  
ID ABM0902 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049769-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 161  
ID ABR8504 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068743-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 162  
ID ABM77325 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054479-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 163  
ID ABO28809 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068685-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 164  
ID ABO31554 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068725-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 165  
ID ABM07971 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068752-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 166  
ID ABO40451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068682-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 167  
ID ABO35876 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068701-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 168  
ID ABO44015 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068755-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 169  
ID ADA77922 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003073180-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 170  
ID ABM24810 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104539-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 171  
ID ABO03078 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036131-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 172  
ID ABR90334 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040075-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 173  
ID ABM17248 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054459-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 174  
ID ABR94994 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044930-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 175  
ID ABR95299 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040071-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 176  
ID ABO40451 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068682-A1.

ID ADB17095 standard; protein; 720 AA.  
PD Human transmembrane PRO polypeptide (Seqid 38).  
PN US2003050462-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 177  
ID ABO21537 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054471-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 178  
ID ABR97801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064452-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 179  
ID ABR87589 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068705-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 180  
ID ABR7630 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054473-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 181  
ID ABR27860 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064440-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 182  
ID ABR06141 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068704-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 183  
ID ABR03647 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068722-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 184  
ID ABR35098 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073183-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 185  
ID ABR26335 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003104549-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 186  
ID ABO48117 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003045749-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 187  
ID ABR92859 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064462-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 188  
ID ABO24620 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003065159-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 189  
ID ADA37742 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US200308297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 190  
ID ABR11631 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064447-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 191  
ID ABR02732 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073184-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 192  
ID ABR16028 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064463-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 193  
ID ABO27589 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064451-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 194  
ID ABR29080 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068721-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 195  
ID ABO07056 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068699-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 196  
ID ABO21150 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068707-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 197  
ID ABO09496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073175-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 198  
ID ABO41366 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068695-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 199  
ID ABO36181 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068703-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 200  
ID ABO43710 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068732-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 201  
ID ABO16959 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082717-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 202  
ID ABO76106 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104548-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 203  
ID ABO25725 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104542-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 204  
ID ABO26030 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104543-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 205  
ID ADA21428 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 206  
ID ABO03383 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036127-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 207  
ID ABO02468 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003040061-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 208  
ID ABO44257 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO 1344.  
PN US2003018172-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 209  
ID ABR90639 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036130-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 210  
ID ABR73707 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054468-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 211  
ID ABO16959 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054470-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 212  
ID ABR94384 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049917-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 213  
ID ABR75891 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003044929-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 214  
ID ABR71267 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059880-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 215  
ID ABR93164 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064465-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 216  
ID ABR93469 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054478-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 217  
ID ADA10215 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein, PRO1344.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 218  
ID ABR87894 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068718-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 219  
ID ABO27894 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064454-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 220  
ID ABO30029 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064461-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 221  
ID ABO33338 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068724-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 222  
ID ABO04926 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068727-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 223  
ID ABO23705 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068772-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 224  
ID ABO36486 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068714-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 225  
ID ABO35571 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068758-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 226  
ID ABO39536 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068776-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 227  
ID ABO10411 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003069407-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 228  
ID ABO11936 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104555-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 229  
ID ABO52082 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049768-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 230  
ID ABO52387 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049771-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 231  
ID ADA19900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003069394-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 232  
ID ABO23705 standard; protein; 720 AA.

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DE Human secreted/transmembrane protein (PRO) #85.
PN US200303134-A1.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-FEB-2003.
RESULT 233
ID ADB17283 standard; protein; 720 AA.
DE Human transmembrane PRO polypeptide (SeqID 38).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
RESULT 234
ID ADAL7759 standard; protein; 720 AA.
DE Human PRO1344 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
RESULT 235
ID ABR97191 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
RESULT 236
ID ABR86979 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 237
ID ABM11021 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 238
ID ABM28165 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 239
ID ABO32164 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 240
ID ABM15291 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 241
ID ABM06446 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 242
ID ABM04257 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 243
ID ABM22370 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 244
ID ABM07666 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 245
ID ABO40756 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 246
ID ABM35403 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 17-APR-2003.
RESULT 247
ID ABM33166 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 08-MAY-2003.
RESULT 248
ID ABO52692 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 249
ID ABO50252 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 250
ID ABU99246 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 27-FEB-2003.
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RESULT 251
ID ABO04298 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 27-FEB-2003.
ID ABO05928 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 27-FEB-2003.
ID ABO18468 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054480-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
ID ADA27867 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
RESULT 255
ID ABR97496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059885-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 27-MAR-2003.
ID ABR80596 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049740-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 257
ID ABW01207 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049770-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 258
ID ABR88809 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 17-APR-2003.
RESULT 259
ID ABM13461 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064457-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 03-APR-2003.
RESULT 260
ID ABM20845 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068711-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 261
ID ABO41976 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049745-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 262
ID ABO42586 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003048751-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 13-MAR-2003.
RESULT 263
ID ABM10106 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003067478-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 264
ID ABO38621 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068773-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 10-APR-2003.
RESULT 265
ID ABM32861 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073185-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 17-APR-2003.
RESULT 266
ID ABM22675 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 08-MAY-2003.
RESULT 267
ID ABM74886 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 22-MAY-2003.
RESULT 268
ID ADA79714 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 17-APR-2003.
RESULT 269
ID ABR96276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;
PD 20-MAR-2003.
RESULT 270
ID ABM02427 standard; protein; 720 AA.
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DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US200305986-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 271  
ID ABR86369 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049758-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 272  
ID ABR86674 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049772-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 273  
ID ABR1638 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064448-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 274  
ID ABR29690 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064456-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 275  
ID ABO29114 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 276  
ID ABR23895 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068735-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 277  
ID ABR23285 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068753-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 278  
ID ABR22065 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068742-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 279  
ID ABO37706 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.

PN US2003068756-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 280  
ID ABR28470 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082715-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 281  
ID ABR28775 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003082716-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 282  
ID ABR66419 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068737-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 283  
ID ABR75801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104547-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 284  
ID ABR34081 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003096359-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 285  
ID ABR34386 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003100061-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 286  
ID ABO20317 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003032125-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 287  
ID ABO21232 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054454-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;  
RESULT 288  
ID ABO22147 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054477-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 6; Length 720;  
Pred. No. 0;

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RESULT 289
ID AD20072 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
PN US200305522-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ABO34185 standard; protein; 720 AA.
DE Human secreted/transmembrane polypeptide PRO 1344.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ABR96581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADA94447 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ABR85759 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ABR9741 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ABM00597 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ABM00292 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ABO29724 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ABM23590 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ABR23985 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ABO38316 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ABO45616 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ABM20540 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADA81441 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ABO16654 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ABO18280 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ABO22707 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ABO23012 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 308  
ID ABR92554 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064446-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 309  
ID ABR81511 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049744-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 310  
ID ABM77935 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049783-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 311  
ID ABR89724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073171-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 312  
ID ABM26640 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003032121-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 313  
ID ABM13766 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064458-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 314  
ID ABO28504 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064460-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 315  
ID ABO30334 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003064464-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 316  
ID ABM07361 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068702-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 317  
ID ABM03952 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

PN US2003068734-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 318  
ID ABO37096 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068719-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 319  
ID ABO41671 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068729-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 320  
ID ABO35266 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068738-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 321  
ID ABM25115 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104540-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 322  
ID ABO47507 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049742-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 323  
ID ABO47812 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049747-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 324  
ID ABO48422 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049750-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 325  
ID ABO51472 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049786-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 326  
ID ABO51777 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049767-A1.  
PD 13-MAR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 327  
ID ABO50557 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049779-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 328  
ID ABR79661 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040059-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 329  
ID ABM16943 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040078-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 330  
ID ABO17975 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003044918-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 331  
ID ABO20927 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003032132-A1.  
PD 13-FEB-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 332  
ID ABR96886 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054462-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 333  
ID ADA38672 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein PRO1344.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 334  
ID ABM12241 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064445-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 335  
ID ABM16333 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064449-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 336  
ID ABM24200 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064441-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 337  
ID ABM14681 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068656-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 338  
ID ABM04562 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068712-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 339  
ID ABM06751 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068730-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 340  
ID ABM09191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073174-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 341  
ID ABO39231 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003068775-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 342  
ID ABM75496 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104545-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 343  
ID ABM25420 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104541-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 344  
ID ABM19930 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104554-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 345  
ID ABO46836 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049762-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

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Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ABO47141 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADA83239 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ABR71572 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ABR72182 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ABR98521 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036129-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ABO06891 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ABR84844 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ABR73402 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ABR76496 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ABR73097 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID AEM18163 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 357
ID ABO20622 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ABO25365 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ABO25670 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ABR94079 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADA92793 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ABR79986 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID AEM11326 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ABO32933 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ABO30639 standard; protein; 720 AA.
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DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003064466-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 366  
ID ABO30944 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003064468-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 367  
ID ABW27250 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068760-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 368  
ID ABW29995 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068769-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 369  
ID ABW05531 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003045700-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 370  
ID ABW15596 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068698-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 371  
ID ABW08581 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068759-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 372  
ID ABO42281 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049748-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 373  
ID ABO38011 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003068765-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 374  
ID ABO45921 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049754-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 375  
ID ABM66724 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068688-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 376  
ID ADB20282 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003082767-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 377  
ID ABM19625 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104552-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 378  
ID ABO49337 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003048774-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 379  
ID ABO49642 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003049775-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 380  
ID ADA78534 standard; protein; 720 AA.  
DE Human secreted/cranmembrane protein (PRO) #85.  
PN US2003073181-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 381  
ID ABR88199 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068720-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 382  
ID ADA00369 standard; protein; 720 AA.  
DE Human secreted/cranmembrane polypeptide PRO 1344.  
PN US2003027992-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 6; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 383  
ID ABW26945 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068739-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ABO03342 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ABO39841 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ABO49947 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ABO50862 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ABO05318 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ABR74622 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ABR77101 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ABM17858 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ABR95909 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ABO21842 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ABO20012 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ABO24315 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ABR86064 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID ABM10716 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID ABM76715 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 399
ID ABR89419 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 400
ID ABM12546 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 401
ID ABM05836 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 402
ID ABO34961 standard; protein; 720 AA.
DE Human PRO polypeptide #85.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 403  
ID ABM03037 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068764-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 404  
ID ABM19015 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104550-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 405  
ID ABM19320 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104551-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 406  
ID ABO46531 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049761-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 407  
ID ABO49032 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049757-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 408  
ID ABR69075 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003027273-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 409  
ID ABR89114 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036119-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 410  
ID ABR72487 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036120-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 411  
ID ABR74317 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003036161-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 412  
ID ABO16585 standard; protein; 720 AA.

DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003044921-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 413  
ID ABR80291 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049739-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 414  
ID ABM01512 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059882-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 415  
ID ABM02122 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059884-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 416  
ID ABR87284 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068687-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 417  
ID ABM12851 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073186-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 418  
ID ABM30605 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064443-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 419  
ID ABM24505 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064444-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 420  
ID ABO29419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068697-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 421  
ID ABO31249 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068710-A1.

PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 422  
ID ABR14376 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US200306868-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 423  
ID ABR09801 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073178-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 424  
ID ABR038926 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068774-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 425  
ID ABR34691 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104538-A1.  
PD 05-JUN-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 426  
ID ABR051167 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049781-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 427  
ID ABR003993 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003036158-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 428  
ID ABR010463 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003036151-A1.  
PD 20-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 429  
ID ABR053170 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 430  
ID ABR17706 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003040067-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 431  
ID ABR78916 standard; protein; 720 AA.  
PD 10-APR-2003.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054456-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 432  
ID ABR024010 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054482-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 433  
ID ABR93774 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003054457-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 434  
ID ABR01817 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003059883-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 435  
ID ABR78240 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003049764-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 436  
ID ABR90029 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003073177-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 437  
ID ADA22354 standard; protein; 720 AA.  
DE Human secreted/transmembrane polypeptide PRO1344.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 438  
ID ABR27555 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064442-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 439  
ID ABR13156 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003064450-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 440  
ID ABR031859 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068731-A1.  
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 441
ID ABM14071 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 442
ID ABM08276 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 443
ID ABO40146 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 444
ID ABM74581 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 445
ID ABM33776 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 446
ID ABM20235 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 447
ID ABO48727 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 448
ID ABO22540 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 449
ID ABR72792 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 450
ID ABO15434 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 451
ID ABR85149 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 452
ID ABO15129 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 453
ID ABO17264 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 454
ID ABM17553 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 455
ID ADA06520 standard; protein; 720 AA.
DE Human secreted/transmembrane PRO polypeptide #65.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 456
ID ADA39213 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 457
ID ABR85454 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 458
ID ABM77020 standard; protein; 720 AA.
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 459
ID ABO28199 standard; protein; 720 AA.
DE Human secreted/transmembrane protein (PRO) #85.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 7; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 460
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ID AEM22980 standard; protein; 720 AA. SEQ ID NO:170.  
DE Human secreted polypeptide PRO1344, DB 7; Length 720;  
PN US2003068757-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 461  
ID AEM30300 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068723-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 462  
ID AEM21760 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068741-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 463  
ID AEM21455 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068744-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 464  
ID AEM14986 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068766-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 465  
ID ABO31061 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068694-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 466  
ID ABO36791 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068715-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 467  
ID ABO37401 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003068726-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 468  
ID AEM75191 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003104544-A1.  
PD 05-JUN-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 469  
ID AEM33471 standard; protein; 720 AA.

DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068357-A1.  
PD 22-MAY-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 470  
ID ABO46226 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003049760-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 471  
ID ADA82605 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003049755-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 472  
ID ADB85611 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049735-A1.  
PD 13-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 473  
ID ADB96239 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 474  
ID AEM31825 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068680-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 475  
ID AEM31215 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068762-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 476  
ID ADB85913 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003054472-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 477  
ID AEM32130 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068708-A1.  
PD 10-APR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 478  
ID AEM32435 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068713-A1.  
PD 10-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 479  
ID ADB68290 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003065161-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 480  
ID ADB68097 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060600-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 481  
ID AEM31520 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068761-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 482  
ID ABM30910 standard; protein; 720 AA.  
DE Human secreted polypeptide PRO1344, SEQ ID NO:170.  
PN US2003068771-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 483  
ID ADB90914 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003083473-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 484  
ID ADC57711 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 485  
ID ADC55075 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 486  
ID ADC11942 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 487  
ID ADC06994 standard; protein; 720 AA.  
DE Human PRO1344 protein.  
PN US2003060602-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 488

ID ADC56364 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 489  
ID ADC17173 standard; protein; 720 AA.  
DE Mammalian PRO polypeptide (Seqid 38).  
PN US2003065143-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 490  
ID ADC07419 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 491  
ID ADC11409 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 492  
ID ADC14671 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073208-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 493  
ID ADC52366 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003138882-A1.  
PD 24-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 494  
ID ADC14531 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 495  
ID ADD08063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068623-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 496  
ID ADC8188 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 497  
ID ADD07530 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 498

RESULT 498  
ID ADG82421 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 499  
ID ADD05643 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003087376-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 500  
ID ADD06601 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073090-A1.  
PD 17-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 501  
ID ADD06650 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2002193300-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 502  
ID ADC83097 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003059783-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 503  
ID ADD55204 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077593-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 504  
ID ADD36042 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003105298-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 505  
ID ADD56162 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003077594-A1.  
PD 24-APR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 506  
ID ADD54600 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2002133253-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 507  
ID ADE26754 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003087304-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 508  
ID ADE26221 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003087305-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 509  
ID ADF67158 standard; protein; 720 AA.  
DE Human PRO1344 amino acid sequence SEQ ID NO:231.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 510  
ID ADG01043 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003078387-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 511  
ID ADG08596 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180793-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 512  
ID ADG02638 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207397-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 513  
ID ADG01345 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207399-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 514  
ID ADF95520 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207398-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 515  
ID ADF95217 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180795-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 516  
ID ADG12335 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207392-A1.  
PD 06-NOV-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 517  
ID ADH24070 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180918-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 518  
ID ADH34096 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180858-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 519  
ID ADH29929 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180859-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 520  
ID ADH23900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180919-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 521  
ID ADH08995 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003207395-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 522  
ID ADG85304 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180904-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 523  
ID ADH24580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180907-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 524  
ID ADH37436 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181646-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 525  
ID ADH02025 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180837-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 526  
ID ADH37606 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.

PN US2003181648-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 527  
ID ADG85644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180905-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 528  
ID ADH24240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180914-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 529  
ID ADH38534 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181643-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 530  
ID ADG83655 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180794-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 531  
ID ADH29463 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180860-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 532  
ID ADH27579 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180906-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 533  
ID ADH37776 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181647-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 534  
ID ADH37953 standard; protein; 720 AA.  
DE Human secreted and transmembrane protein PRO1344 CDNA.  
PN US2003181649-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 535  
ID ADH57373 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180920-A1.

PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 536  
ID ADH53515 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181636-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 537  
ID ADH53685 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181641-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 538  
ID ADH52021 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181638-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 539  
ID ADH49876 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181639-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 540  
ID ADI25386 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181696-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 541  
ID ADH90179 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181698-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 542  
ID ADI25556 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181669-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 543  
ID ADH97730 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181672-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 544  
ID ADI35412 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.

Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 545  
ID ADI03578 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181656-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 546  
ID ADI11935 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181686-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 547  
ID ADH90009 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181697-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 548  
ID ADH99904 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 549  
ID ADH98410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181707-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 550  
ID ADI11085 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181682-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 551  
ID ADI11595 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181684-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 552  
ID ADH98240 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181709-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 553  
ID ADH98580 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181708-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 554  
ID ADI35412 standard; protein; 720 AA.  
DE Human PRO polypeptide #65.  
PN US2003050457-A1.  
PD 13-MAR-2003.

RESULT 554  
ID ADH98070 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181673-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 555  
ID ADI05058 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180848-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 556  
ID ADI03408 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181654-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 557  
ID ADI04803 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181657-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 558  
ID ADH78257 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181658-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 559  
ID ADI19601 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181676-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 560  
ID ADH90349 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181659-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 561  
ID ADI03068 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181653-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 562  
ID ADH77917 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181666-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 563

ID ADH97900 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181674-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 564  
ID ADI01285 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190669-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 565  
ID ADI01980 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181652-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 566  
ID ADI03238 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181655-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 567  
ID ADI11425 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181681-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 568  
ID ADI02327 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181650-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 569  
ID ADI11765 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181685-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 570  
ID ADI05402 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003190716-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 571  
ID ADH79474 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191290-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 572  
ID ADI19431 standard; protein; 720 AA.

DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181675-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 573  
ID ADI05332 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181677-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 574  
ID ADH79644 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191288-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 575  
ID ADI01470 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181678-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 576  
ID ADI01640 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181679-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 577  
ID ADI01810 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181680-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 578  
ID ADH79814 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191289-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 579  
ID ADI04632 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003171550-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 580  
ID ADI02768 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181651-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 581  
ID ADH78087 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.

PN US2003181667-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 582  
ID ADI25726 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181670-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 583  
ID ADI25896 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181671-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 584  
ID ADK55408 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073821-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 585  
ID ADH98750 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191284-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 586  
ID ADH79991 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003191287-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 587  
ID ADI32776 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003207396-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 588  
ID ADM30310 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003073813-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 589  
ID ADL93722 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003040013-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 7; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 590  
ID ADC52176 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003130483-A1.

PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 591  
ID ADE74307 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003211572-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 592  
ID ADE74919 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein (PRO) #85.  
PN US2003211574-A1.  
PD 13-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 593  
ID ADF35357 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003194760-A1.  
PD 16-OCT-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 594  
ID ADG11607 standard; protein; 720 AA.  
DE Human PRO1344 polypeptide.  
PN US2003228655-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 595  
ID ADP96132 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215909-A1.  
PD 20-NOV-2003.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 596  
ID ADG04403 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215912-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 597  
ID ADG00563 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003215911-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 598  
ID ADH06608 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180852-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 599  
ID ADH06438 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180853-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 600

ID ADG68859 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180855-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 601  
ID ADH27749 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180912-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 602  
ID ADH25690 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180913-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 603  
ID ADH33722 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181645-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 604  
ID ADG82819 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003215910-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 605  
ID ADH02365 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180839-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 606  
ID ADH07972 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180845-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 607  
ID ADG69369 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180846-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 608  
ID ADH39190 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180917-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 609  
ID ADH26100 standard; protein; 720 AA.



DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003068770-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 610  
ID ADG83930 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180842-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 611  
ID ADH19477 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 612  
ID ADG85474 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003166848-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 613  
ID ADH06268 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180854-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 614  
ID ADH30098 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180856-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 615  
ID ADH24410 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180910-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 616  
ID ADH33069 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2003068768-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 617  
ID ADG69539 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180844-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 618  
ID ADH07802 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.

PN US2003180851-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 619  
ID ADG85614 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180861-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 620  
ID ADH39360 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180916-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 621  
ID ADH33552 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181637-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 622  
ID ADH33892 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003181644-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 623  
ID ADH01102 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180838-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 624  
ID ADG69709 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180843-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 625  
ID ADH20970 standard; protein; 720 AA.  
DE Human secreted/transmembrane protein PRO1344.  
PN US2003224358-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 626  
ID ADH02195 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003180841-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 720; DB 8; Length 720;  
PRED. No. 0;  
RESULT 627  
ID ADG69199 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003180847-A1.  
PD 25-SEP-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 628
ID ADG65984 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 629
ID ADH24920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 630
ID ADH39537 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 631
ID ADH20010 standard; protein; 720 AA.
DE Human secreted/transmembrane protein PRO1344.
FN US200319856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 632
ID ADH02535 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
FN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 633
ID ADG69029 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 634
ID ADH07632 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 635
ID ADG6154 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 636
ID ADH24750 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 637
ID ADH25798 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 638
ID ADH38364 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 639
ID ADH57203 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 640
ID ADH52191 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 641
ID ADH49557 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 642
ID ADH90519 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 643
ID ADI11255 standard; protein; 720 AA.
DE Human PRO polypeptide #19.
FN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 644
ID ADH98920 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 645
ID ADI02150 standard; protein; 720 AA.
DE Novel human secreted and transmembrane protein PRO1344.
FN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 720; DB 8; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
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Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 646  
ID ADH90689 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181701-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 647  
ID ADJ54808 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004023321-A1.  
PD 05-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 648  
ID ADJ98564 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187197-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 649  
ID ADJ98734 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187228-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 650  
ID ADH78893 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181703-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 651  
ID ADJ99127 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003186408-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 652  
ID ADJ99297 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187196-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 653  
ID ADJ98915 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187242-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 654  
ID ADH79063 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003181702-A1.  
PD 25-SEP-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 655  
ID ADK00923 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2003186407-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 656  
ID ADK14444 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2003187229-A1.  
PD 02-OCT-2003.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 657  
ID ADJ64579 standard; protein; 720 AA.  
DE Human PRO polypeptide #85.  
PN US2004038337-A1.  
PD 26-FEB-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 658  
ID ADM31475 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048334-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 659  
ID ADM36522 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004053358-A1.  
PD 18-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 660  
ID ADM40327 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004048335-A1.  
PD 11-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 661  
ID ADM80893 standard; protein; 720 AA.  
DE Human PRO polypeptide #19.  
PN US2004058411-A1.  
PD 25-MAR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 662  
ID ADN37935 standard; protein; 720 AA.  
DE Novel human secreted and transmembrane protein PRO1344.  
PN US2004091959-A1.  
PD 13-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 100.0%; Score 720; DB 8; Length 720;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 663  
ID AAB70531 standard; protein; 567 AA.  
DE Human PRO1 protein sequence SEQ ID NO:2.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 77.2%; Score 556; DB 4; Length 567;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 664

Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 664  
ID AAB70531 standard; protein; 567 AA.  
DE Human PRO1 protein sequence SEQ ID NO:2.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 77.2%; Score 556; DB 4; Length 567;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 664

ID AA88280 standard; protein; 720 AA.  
DE Human TANGO 215 protein.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 71.9%; Score 518; DB 3; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 665  
ID AAB70532 standard; protein; 720 AA.  
DE Human PRO2 protein sequence SEQ ID NO:4.  
PN WO200110902-A2.  
PD 15-FEB-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.9%; Score 518; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 666  
ID AAU00401 standard; protein; 720 AA.  
DE Human secreted protein, POLY13.  
PN WO200119856-A2.  
PD 22-MAR-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 71.9%; Score 518; DB 4; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 667  
ID ADH89028 standard; protein; 720 AA.  
DE Human POLYX polypeptide #11.  
PN US200319858-A1.  
PD 23-OCT-2003.  
PA (SHIM/) SHIMKETS R. A.  
PA (PERN/) PERMANDES E.  
PA (HERR/) HERRMANN J L.  
PA (LIUX/) LIU X.  
PA (YANG/) YANG M.  
PA (BOLD/) BOLDOS F L.  
PA (SMIT/) SMITHSON G.  
PA (RAST/) RASTELLI L.  
Query Match 71.9%; Score 518; DB 8; Length 720;  
Best Local Similarity 99.7%; Pred. No. 0;  
RESULT 668  
ID AAM41706 standard; protein; 499 AA.  
DE Human polypeptide SEQ ID NO 6637.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 61.9%; Score 446; DB 4; Length 499;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 669  
ID AAB85891 standard; protein; 737 AA.  
DE Human serine protease-like protein (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 670  
ID AAB93670 standard; protein; 737 AA.  
DE Human protein sequence SEQ ID NO:13202.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 671  
ID ADU69990 standard; protein; 737 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1796.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 61.9%; Score 446; DB 7; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 672  
ID ADN04640 standard; protein; 737 AA.

DE Antiporiatic protein sequence #505.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 673  
ID AD885034 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SeqID36.  
PN WO200403386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 674  
ID AD885022 standard; protein; 737 AA.  
DE Human atopic dermatitis-related protein sequence SeqID24.  
PN WO200403386-A1.  
PD 15-APR-2004.  
PA (GENO-) GENOX RES INC.  
PA (UYJU-) UNIV JUNTENDO.  
Query Match 61.9%; Score 446; DB 8; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 675  
ID AAB85893 standard; protein; 762 AA.  
DE Human serine protease-like protein (hc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 61.9%; Score 446; DB 4; Length 762;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 676  
ID ADL06662 standard; protein; 417 AA.  
DE Human 3T3 cell conversion promoter FP938.  
PN CN1403477-A.  
PD 19-MAR-2003.  
PA (SHAN-) SHANGHAI XINSHIJI GENE TECHN DEV CO LTD.  
Query Match 53.6%; Score 386; DB 7; Length 417;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 677  
ID AAE19180 standard; protein; 649 AA.  
DE Human protease, PRS-17 protein.  
PN WO200208396-A2.  
PD 31-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 52.1%; Score 375; DB 5; Length 649;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 678  
ID AAM39920 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3065.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 49.9%; Score 359; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 679  
ID AAM39957 standard; protein; 359 AA.  
DE Human polypeptide SEQ ID NO 3102.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 49.9%; Score 359; DB 4; Length 359;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 680  
ID AAB49533 standard; protein; 570 AA.  
DE Clone HPEBY75.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 49.3%; Score 355; DB 3; Length 570;  
Best Local Similarity 100.0%; Pred. No. 0;  
RESULT 681

ID AAE20817 standard; protein; 455 AA.  
DE Human gene 5 encoded secreted protein HSLG075, SEQ ID NO:79.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 682  
ID AEG64652 standard; protein; 455 AA.  
DE Human albumin fusion protein #1327.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 683  
ID ADL77919 standard; protein; 455 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1401.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 38.5%; Score 277; DB 8; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.5e-261;  
RESULT 684  
ID ADR41485 standard; protein; 551 AA.  
DE Human CD-like molecule HSDP41, SEQ ID NO:284.  
PN WO200226830-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.5%; Score 277; DB 5; Length 551;  
Best Local Similarity 100.0%; Pred. No. 5.4e-261;  
RESULT 685  
ID AAE20797 standard; protein; 323 AA.  
DE Human gene 5 encoded secreted protein HSLG075, SEQ ID NO:59.  
PN WO200218435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.3%; Score 276; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 686  
ID AEG64653 standard; protein; 323 AA.  
DE Human albumin fusion protein #1328.  
PN WO200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 38.3%; Score 276; DB 5; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 687  
ID ADL77920 standard; protein; 323 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1402.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 38.3%; Score 276; DB 8; Length 323;  
Best Local Similarity 100.0%; Pred. No. 3.2e-260;  
RESULT 688  
ID AAM24485 standard; protein; 234 AA.  
DE Human EST encoded protein SEQ ID NO: 2010.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 25.4%; Score 183; DB 4; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.5e-169;  
RESULT 689  
ID AAM41743 standard; protein; 146 AA.  
DE Human polypeptide SEQ ID NO 6674.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 15.8%; Score 114; DB 4; Length 146;  
Best Local Similarity 100.0%; Pred. No. 2.2e-102;

RESULT 690  
ID AAB09927 standard; protein; 719 AA.  
DE Murine TANGO 215 protein.  
PN WO200018904-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
Query Match 8.5%; Score 61; DB 3; Length 719;  
Best Local Similarity 100.0%; Pred. No. 5.2e-50;  
RESULT 691  
ID AAB85892 standard; protein; 720 AA.  
DE Mouse serine protease-like protein (mc-PLACE1009992).  
PN WO200109349-A1.  
PD 08-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 8.5%; Score 61; DB 4; Length 720;  
Best Local Similarity 100.0%; Pred. No. 5.2e-50;  
RESULT 692  
ID AAY11743 standard; protein; 103 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 343.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 5.3%; Score 38; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 2.5e-28;  
RESULT 693  
ID AAY11763 standard; protein; 34 AA.  
DE Human 5' EST secreted protein SEQ ID NO: 363.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST-) GENSET.  
Query Match 2.1%; Score 15; DB 2; Length 34;  
Best Local Similarity 100.0%; Pred. No. 2.6e-06;  
RESULT 694  
ID AAB49539 standard; peptide; 12 AA.  
DE Clone HEPHY75 peptide fragment.  
PN WO200061774-A2.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.7%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
RESULT 695  
ID AAY72114 standard; peptide; 12 AA.  
DE Human serine protease epidermal growth factor (EGF)-like domain.  
PN WO200068247-A2.  
PD 16-NOV-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.7%; Score 12; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00086;  
RESULT 696  
ID AAR93594 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS14 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 697  
ID AAR76945 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS13 (residues 276-306).  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 698  
ID AAR93590 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS20 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU-) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 699

ID AAR93593 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS11 residues 276-306.  
PN WO9509308-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 700  
ID AAR93588 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS18 residues 276-306.  
PN WO9509308-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 1.2%; Score 9; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
RESULT 701  
ID AAY82996 standard; protein; 101 AA.  
DE CUB domain from murine BMP-1.  
PN WO200009691-A2.  
PD 24-FEB-2000.  
PA (UROG-) UROGENESYS INC.  
PA (AFAR/) AFAR D E.  
PA (HUBE/) HUBERT R. S.  
PA (LEON/) LEONG K.  
PA (RAIT/) RAITANO A. B.  
PA (SAFE/) SAFFRAN D C.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.2%; Score 9; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
RESULT 702  
ID AAY27043 standard; protein; 110 AA.  
DE Amino acid sequence of human Bmp-1 CUB1 domain.  
PN WO9937757-A1.  
PD 29-JUL-1999.  
PA (TULA) TULANE EDUCATIONAL FUND.  
PA (INRM) INST NAT SANTE & RECH MEDICALE.  
Query Match 1.2%; Score 9; DB 2; Length 110;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
RESULT 703  
ID ABM84572 standard; protein; 622 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO:4821.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.2%; Score 9; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 704  
ID ABM80969 standard; protein; 622 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81651, SEQ:2500.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 1.2%; Score 9; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 27;  
RESULT 705  
ID AAP0618 standard; protein; 730 AA.  
DE Human Bone Morphogenic Protein-1 of lambda U2OS-1.  
PN WO8800205-A.  
PD 14-JAN-1988.  
PA (GENY) GENENTECH INC.  
Query Match 1.2%; Score 9; DB 1; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 706  
ID AAW13669 standard; protein; 730 AA.  
DE C-proteinase encoded by clone pcP-1.  
PN WO9706242-A1.  
PD 20-FEB-1997.  
PA (UYXE-) UNIV JEFFERSON THOMAS.  
Query Match 1.2%; Score 9; DB 2; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 707  
ID ADP65217 standard; protein; 730 AA.  
DE Human bone morphogenetic protein 1, isoform 1, precursor, PCP.

PN WO2003072827-A1.  
PD 04-SEP-2003.  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
Query Match 1.2%; Score 9; DB 7; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 708  
ID ABM80967 standard; protein; 730 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO2042, SEQ:2496.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GERTH) GENENTECH INC.  
Query Match 1.2%; Score 9; DB 8; Length 730;  
Best Local Similarity 100.0%; Pred. No. 31;  
RESULT 709  
ID AAW75919 standard; protein; 788 AA.  
DE C-proteinase sequence used to cleave procollagene.  
PN US5807981-A.  
PD 15-SEP-1998.  
PA (FIBR-) FIBROGEN INC.  
Query Match 1.2%; Score 9; DB 2; Length 788;  
Best Local Similarity 100.0%; Pred. No. 33;  
RESULT 710  
ID ADH41541 standard; protein; 821 AA.  
DE Novel human protein NOV8e.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 711  
ID ADH41549 standard; protein; 821 AA.  
DE Novel human protein NOV8i.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 712  
ID ADH41533 standard; protein; 821 AA.  
DE Novel human protein NOV8a.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 713  
ID ADH41543 standard; protein; 821 AA.  
DE Novel human protein NOV8f.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 714  
ID ADH41545 standard; protein; 821 AA.  
DE Novel human protein NOV8g.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 715  
ID ADH41547 standard; protein; 821 AA.  
DE Novel human protein NOV8h.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 821;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 716  
ID ADM87216 standard; protein; 823 AA.  
DE Human protein SEQ ID NO:309.  
PN WO2004009834-A2.

PD 29-JAN-2004.  
PA (NOVE-) NUVELO INC.  
Query Match 1.2%; Score 9; DB 8; Length 823;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 717  
ID AMB80968 standard; protein; 823 AA.  
DE Tumour-associated antigenic target (TAT) polypeptide PRO81650, SEQ:2498.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 1.2%; Score 9; DB 8; Length 823;  
Best Local Similarity 100.0%; Pred. No. 34;  
RESULT 718  
ID ABG79188 standard; protein; 970 AA.  
DE Human colloid-like 2-like protein #2.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 5; Length 970;  
Best Local Similarity 100.0%; Pred. No. 40;  
RESULT 719  
ID ADH41539 standard; protein; 970 AA.  
DE Novel human protein NOV8d.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 970;  
Best Local Similarity 100.0%; Pred. No. 40;  
RESULT 720  
ID AAW13670 standard; protein; 986 AA.  
DE C-proteinase encoded by clone pcp-2.  
PN WO9706242-A1.  
PD 20-FEB-1997.  
PA (UYJE-) UNIV JEFFERSON THOMAS.  
Query Match 1.2%; Score 9; DB 2; Length 986;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 721  
ID ABB90755 standard; protein; 986 AA.  
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 242.  
PN WO200210217-A2.  
PD 07-FEB-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 1.2%; Score 9; DB 5; Length 986;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 722  
ID ABUS4462 standard; protein; 986 AA.  
DE Human tumour endothelial marker TEM 25.  
PN WO200283874-A2.  
PD 24-OCT-2002.  
PA (UYJO-) UNIV JOHNS HOPKINS.  
Query Match 1.2%; Score 9; DB 6; Length 986;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 723  
ID ADH11578 standard; protein; 986 AA.  
DE Human bone morphogenic protein (BMP) polypeptide #6.  
PN US2003224501-A1.  
PD 04-DEC-2003.  
PA (YOUN/) YOUNG P E.  
PA (RUBE/) RUBEN S M.  
Query Match 1.2%; Score 9; DB 8; Length 986;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 724  
ID AD018558 standard; protein; 986 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1377.  
PN WO200404838-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.2%; Score 9; DB 8; Length 986;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 725  
ID ABG79187 standard; protein; 992 AA.  
DE Human colloid-like 2-like protein #1.  
PN WO200264791-A2.  
PD 22-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 5; Length 992;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 726  
ID ADH41535 standard; protein; 992 AA.  
DE Novel human protein NOV8d.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 992;  
Best Local Similarity 100.0%; Pred. No. 41;  
RESULT 727  
ID AAY32240 standard; protein; 1015 AA.  
DE Human colloid-like protein mtl1-2.  
PN WO9951730-A2.  
PD 14-OCT-1999.  
PA (WISC-) WISCONSIN ALUMNI RES FOUND.  
Query Match 1.2%; Score 9; DB 3; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 42;  
RESULT 728  
ID ADH41537 standard; protein; 1015 AA.  
DE Novel human protein NOV8c.  
PN WO2003102159-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.2%; Score 9; DB 8; Length 1015;  
Best Local Similarity 100.0%; Pred. No. 42;  
RESULT 729  
ID ABB71111 standard; protein; 1464 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 40125.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 1.2%; Score 9; DB 4; Length 1464;  
Best Local Similarity 100.0%; Pred. No. 58;  
RESULT 730  
ID ABB77068 standard; peptide; 11 AA.  
DE AC2885 antibody light chain hypervariable region CDR1'.  
PN WO200216436-A2.  
PD 28-FEB-2002.  
PA (NOVS-) NOVARTIS AG.  
PA (NOVS-) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 1.1%; Score 8; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
RESULT 731  
ID ADH17899 standard; peptide; 11 AA.  
DE Human ISH12/19D12 CDR (complementarity determining region)-L1 peptide.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE-) SCHERING CORP.  
Query Match 1.1%; Score 8; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
RESULT 732  
ID ADM41606 standard; peptide; 11 AA.  
DE Interleukin-1 receptor type 1 antibody light chain variable region CDR1.  
PN WO2004022718-A2.  
PD 18-MAR-2004.  
PA (AMGE-) AMGEN INC.  
Query Match 1.1%; Score 8; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.4;  
RESULT 733  
ID AAB36802 standard; protein; 50 AA.  
DE Human epigen EGF-like domain.  
PN WO2003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOM-) BIOCROMOLAR RES INST LTD.  
PA (HALI-) HALI INST MEDICAL RES VALTER & ELIZA.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 1.1%; Score 8; DB 6; Length 50;  
Best Local Similarity 100.0%; Pred. No. 25;  
RESULT 734





PN WO2004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIGEN INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 107;  
Pred. No. 51;  
RESULT 753  
ID ADO07307 standard; protein; 107 AA.  
DE Human proteolytic A10-CKI light chain, used in catalytic antibody.  
PN WO2004033658-A2.  
PD 22-APR-2004.  
PA (INTE-) INTEGRIGEN INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 107;  
Pred. No. 51;  
RESULT 754  
ID ABB03399 standard; protein; 124 AA.  
DE Human musculoskeletal system related polypeptide SEQ ID NO 1346.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 4; Length 124;  
Pred. No. 58;  
RESULT 755  
ID ABB12693 standard; protein; 124 AA.  
DE Novel human musculoskeletal system antigen #313.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 6; Length 124;  
Pred. No. 58;  
RESULT 756  
ID ADJ28719 standard; protein; 124 AA.  
DE Human musculoskeletal system-associated protein - SEQ ID 1346.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 124;  
Pred. No. 58;  
RESULT 757  
ID ABB77064 standard; protein; 126 AA.  
DE AC2885 antibody light chain variable region.  
PN WO200216436-A2.  
PD 28-FEB-2002.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GRS MBH.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 5; Length 126;  
Pred. No. 59;  
RESULT 758  
ID ADM41553 standard; protein; 126 AA.  
DE Anti-interleukin-1 receptor type 1 antibody kappa chain variable region.  
PN WO2004022718-A2.  
PD 18-MAR-2004.  
PA (AMGE-) AMGEN INC.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 126;  
Pred. No. 59;  
RESULT 759  
ID APP57370 standard; protein; 127 AA.  
DE Anti-FcRL-1 antibody related clone KMTR1 protein SEQ ID NO:35.  
PN WO200294880-A1.  
PD 28-NOV-2002.  
PA (KIRI ) KIRIN BEER KK.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 6; Length 127;  
Pred. No. 60;  
RESULT 760  
ID AAY56718 standard; protein; 128 AA.  
DE Amino acid sequence of chimpanzee V kappa CNA clone 46-4.  
PN WO9955369-A1.  
PD 04-NOV-1999.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 3; Length 128;  
Pred. No. 60;  
RESULT 761

ID ADH17963 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain C (LCC) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 762  
ID ADH17967 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain E (LCE) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 763  
ID ADH17969 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain F (LCF) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 764  
ID ADH17932 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain A (LCA) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 765  
ID ADH17965 standard; protein; 128 AA.  
DE Human modified 15H12/19D12 light chain D (LCD) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 766  
ID ADH17934 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain B (LCB) protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 767  
ID ADH17893 standard; protein; 128 AA.  
DE Human 15H12/19D12 light chain variable region protein.  
PN WO2003100008-A2.  
PD 04-DEC-2003.  
PA (SCHE ) SCHERING CORP.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 8; Length 128;  
Pred. No. 60;  
RESULT 768  
ID AAY76009 standard; protein; 152 AA.  
DE Murine TGF-alpha homologue murt1, SEQ ID 187.  
PN WO9955865-A1.  
PD 04-NOV-1999.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 3; Length 152;  
Pred. No. 70;  
RESULT 769  
ID AAB55948 standard; protein; 152 AA.  
DE Skin cell protein, SEQ ID NO: 187.  
PN WO200069884-A2.  
PD 23-NOV-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
Query Match  
Best Local Similarity 1.1%; Score 8; DB 4; Length 152;  
Pred. No. 70;  
RESULT 770  
ID ABB72148 standard; protein; 152 AA.

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DE Murine proteain isolated from skin cells SEQ ID NO: 187.  
PN WO200190357-A1.  
PD 29-NOV-2001.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
ID AAY93714 standard; protein, 155 AA.  
DE The kappa chain of immunoglobulin clone 2.1.3.  
PN WO200037504-A2.  
PD 29-JUN-2000.  
PA (PRIZ-) PRIZER INC.  
Query Match 1.1%; Score 8; DB 3; Length 155;  
Best Local Similarity 100.0%; Pred. No. 71;  
RESULT 772  
ID AAF53906 standard; protein, 155 AA.  
DE Human 2.1.3 anti-CTLA-4 antibody kappa chain.  
PN EPI262193-A1.  
PD 04-DEC-2002.  
PA (PRIZ-) PRIZER PROD INC.  
Query Match 1.1%; Score 8; DB 6; Length 155;  
Best Local Similarity 100.0%; Pred. No. 71;  
RESULT 773  
ID ADF52330 standard; protein, 157 AA.  
DE Human anti-MCP-1 variable region light chain #9.  
PN WO2004016769-A2.  
PD 26-FEB-2004.  
PA (ABGE-) ABGENIX INC.  
Query Match 1.1%; Score 8; DB 8; Length 157;  
Best Local Similarity 100.0%; Pred. No. 72;  
RESULT 774  
ID ADM41575 standard; protein, 233 AA.  
DE Anti-interleukin-1 receptor type 1 antibody light chain.  
PN WO2004022718-A2.  
PD 18-MAR-2004.  
PA (AMGE-) AMGEN INC.  
Query Match 1.1%; Score 8; DB 8; Length 233;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 775  
ID ABU70774 standard; protein, 235 AA.  
DE Human adipocyte Selected Interacting domain, STD, #405.  
PN WO200286122-A2.  
PD 31-OCT-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 1.1%; Score 8; DB 6; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
RESULT 776  
ID ADN24003 standard; protein, 302 AA.  
DE Bacterial polypeptide #656.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.1%; Score 8; DB 8; Length 302;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
RESULT 777  
ID AAY79332 standard; protein, 467 AA.  
DE Human EGF repeat-containing protein EGF-Hy1.  
PN WO200017357-A1.  
PD 30-MAR-2000.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 3; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
RESULT 778  
ID ABU22131 standard; protein, 596 AA.  
DE Protein encoded by Prokaryotic essential gene #7658.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
  
Query Match 1.1%; Score 8; DB 6; Length 596;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 779  
ID ADG93413 standard; protein, 807 AA.  
DE Maize lipoxygenase (LOX) polypeptide #22.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 1.1%; Score 8; DB 7; Length 807;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
RESULT 780  
ID ADG93411 standard; protein, 807 AA.  
DE Maize lipoxygenase (LOX) polypeptide #21.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Query Match 1.1%; Score 8; DB 7; Length 807;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
RESULT 781  
ID ABP68935 standard; protein, 859 AA.  
DE Human polypeptide SEQ ID NO 982.  
PN WO200270539-A2.  
PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 5; Length 859;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 782  
ID AAM43394 standard; protein, 1019 AA.  
DE Singapore horseshoe crab factor C proenzyme (CrFC 21).  
PN SC42456-A1.  
PD 15-AUG-1997.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 783  
ID AAY05750 standard; protein, 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO9915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 784  
ID AAW94302 standard; protein, 1019 AA.  
DE Horseshoe crab Factor C protein #2.  
PN US5858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 785  
ID AAY42490 standard; protein, 1019 AA.  
DE Recombinant N-terminally truncated Horseshoe crab Factor C protein.  
PN US5985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 3; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 786  
ID AAB60935 standard; protein, 1019 AA.  
DE Horseshoe crab recombinant Factor C #2.  
PN WO200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 4; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 787  
ID ABP72332 standard; protein, 1019 AA.  
DE Horseshoe crab Factor C.  
PN WO2003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK-) BIOWHITTAKER INC.  
Query Match 1.1%; Score 8; DB 6; Length 1019;
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Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 788  
ID AAB72334 standard; protein; 1019 AA.  
DE Horsehoe crab Factor C.  
PN W02003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK-) BIOWHITTAKER INC.  
Query Match 1.1%; Score 8; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
RESULT 789  
ID AAM43393 standard; protein; 1083 AA.  
DE Singapore horsehoe crab factor C proenzyme (CrFC 26).  
PN S642456-A1.  
PD 15-AUG-1997.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 790  
ID AAY05749 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN W09915676-A1.  
PD 01-APR-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 791  
ID AAM94301 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C protein #1.  
PN U55858706-A.  
PD 12-JAN-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 2; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 792  
ID AAY42489 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C protein.  
PN U55985590-A.  
PD 16-NOV-1999.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 3; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 793  
ID AAB60934 standard; protein; 1083 AA.  
DE Horsehoe crab recombinant Factor C #1.  
PN W0200127289-A2.  
PD 19-APR-2001.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.1%; Score 8; DB 4; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 794  
ID AAB72333 standard; protein; 1083 AA.  
DE Horsehoe crab Factor C.  
PN W02003002976-A2.  
PD 09-JAN-2003.  
PA (WHIK-) BIOWHITTAKER INC.  
Query Match 1.1%; Score 8; DB 6; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 4.2e+02;  
RESULT 795  
ID AAB62022 standard; protein; 1238 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12858.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 1.1%; Score 8; DB 4; Length 1238;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 796  
ID AAB94754 standard; protein; 1316 AA.  
DE Human protein sequence SEQ ID NO.15811.  
PN EPI074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.1%; Score 8; DB 4; Length 1316;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 797  
ID ADF28695 standard; protein; 1484 AA.  
DE Neurological therapy-related protein - SED ID 605.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1484;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 798  
ID ADF28692 standard; protein; 1487 AA.  
DE Human peroxidase-like protein - SED ID 602.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1487;  
Best Local Similarity 100.0%; Pred. No. 5.6e+02;  
RESULT 799  
ID ADS10671 standard; protein; 1507 AA.  
DE Human therapeutic protein - SEQ ID 908.  
PN W02004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 1.1%; Score 8; DB 8; Length 1507;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 800  
ID ADF28708 standard; protein; 1538 AA.  
DE Peroxidase-like protein - SED ID 618.  
PN W02003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.1%; Score 8; DB 7; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 801  
ID ADS10672 standard; protein; 1538 AA.  
DE Human therapeutic protein - SEQ ID 909.  
PN W02004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 1.1%; Score 8; DB 8; Length 1538;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 802  
ID ADN39112 standard; protein; 3557 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:430.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.1%; Score 8; DB 7; Length 3557;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 803  
ID ADN39979 standard; protein; 3557 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C349.  
PN W02003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.1%; Score 8; DB 7; Length 3557;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 804  
ID AAB37944 standard; protein; 3570 AA.  
DE Human GSD-33 protein.  
PN W02003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.1%; Score 8; DB 7; Length 3570;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 805  
ID AAE20146 standard; protein; 3571 AA.  
DE Human C3b/C4b complement receptor-like protein.  
PN W0200210388-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 1.1%; Score 8; DB 5; Length 3571;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 806

ID ADL22512 standard; protein; 3571 AA.  
DE Human CNGH0004 antibody protein.  
PN WO2004003147-A2.  
PD 08-JAN-2004.  
PA (GENZ ) CENTOCOR INC.  
Query Match 1.1%; Score 8; DB 8; Length 3571;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 807  
ID AD075791 standard; peptide; 10 AA.  
DE Human 213P1F11 HLA motif bearing epitope #9890.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALILITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.0%; Score 7; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 56;  
RESULT 808  
ID AD077632 standard; peptide; 15 AA.  
DE Human 213P1F11 HLA motif bearing epitope #11721.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALILITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 1.0%; Score 7; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 81;  
RESULT 809  
ID AAR71665 standard; peptide; 30 AA.  
DE Modified urinary plasminogen activator residues 159-188.  
PN JP07039374-A.  
PD 10-FEB-1995.  
PA (SUMI) SUMITOMO SEIYAKU KK.  
Query Match 1.0%; Score 7; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
RESULT 810  
ID ABP78761 standard; protein; 43 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 4052.  
PN WO200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
RESULT 811  
ID AAM23855 standard; protein; 49 AA.  
DE Human EST encoded protein SEQ ID NO: 1380.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 812  
ID ADC33279 standard; protein; 49 AA.  
DE Human novel contig-encoded polypeptide sequence, SEQ ID NO:3361.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 7; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 813  
ID AAM06451 standard; protein; 50 AA.  
DE Human foetal protein, SEQ ID NO: 182.  
PN WO200155339-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 1.0%; Score 7; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
RESULT 814  
ID AAG91460 standard; protein; 54 AA.  
DE C glutamicum protein fragment SEQ ID NO: 5214.  
PN EP108790-A2.  
PD 20-JUN-2001.  
PA (KOW ) KOWA HAKKO KOGYO KK.  
Query Match 1.0%; Score 7; DB 4; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
RESULT 815  
ID AAY02522 standard; protein; 56 AA.  
DE Clone selected after panning a NNK library of the invention.  
PN WO9920749-A1.  
PD 29-APR-1999.  
PA (MEDI-) MEDICAL RES COUNCIL.  
Query Match 1.0%; Score 7; DB 2; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
RESULT 816  
ID ABW71426 standard; protein; 59 AA.  
DE Staphylococcus aureus protein #666.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
RESULT 817  
ID AAU48293 standard; protein; 62 AA.  
DE Propionibacterium acnes immunogenic protein #9189.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 818  
ID ABW44812 standard; protein; 62 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9488.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 62;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
RESULT 819  
ID ABB42063 standard; peptide; 63 AA.  
DE Peptide #9569 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 820  
ID AAM75756 standard; protein; 63 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36062.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 821  
ID AAM62944 standard; protein; 63 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 35049.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 822  
ID ABG57494 standard; peptide; 63 AA.  
DE Human liver peptide, SEQ ID NO 36142.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 63;

Best Local Similarity 100.0%; Pred. No. 3e+02;  
RESULT 823  
ID AAB35189 standard; protein; 74 AA.  
DE Human deaminase-like ORF4162 protein, SEQ ID NO:8324.  
PN W0200190366-A2.  
PD 29-NOV-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 5; Length 74;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
RESULT 824  
ID AAV66472 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #27368.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 825  
ID AAV67610 standard; protein; 76 AA.  
DE Propionibacterium acnes immunogenic protein #28506.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 826  
ID AAM62991 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #27667.  
PN W02001903515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 827  
ID AAM64129 standard; protein; 76 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #28805.  
PN W02001903515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 76;  
Best Local Similarity 100.0%; Pred. No. 3.5e+02;  
RESULT 828  
ID AAE20816 standard; protein; 79 AA.  
DE Human gene 5 encoded secreted protein HSLGU75, SEQ ID NO:78.  
PN W020018435-A1.  
PD 07-MAR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 829  
ID AAG64651 standard; protein; 79 AA.  
DE Human albumin fusion protein #1326.  
PN W0200177137-A1.  
PD 18-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 830  
ID ADU77918 standard; protein; 79 AA.  
DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 1400.  
PN US2004010134-A1.  
PD 15-JAN-2004.  
PA (ROSE/) ROSEN C A.  
PA (HASE/) HASELTINE W A.  
Query Match 1.0%; Score 7; DB 8; Length 79;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 831  
ID AAM64695 standard; protein; 81 AA.  
DE Propionibacterium acnes immunogenic polypeptide #29371.  
PN W02001903515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 81;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
RESULT 832  
ID ADF05104 standard; protein; 83 AA.  
DE Bacterial polypeptide #1217.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 83;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
RESULT 833  
ID AAG03800 standard; protein; 103 AA.  
DE Human secreted protein, SEQ ID NO: 7881.  
PN EP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match 1.0%; Score 7; DB 3; Length 103;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 834  
ID AAV64590 standard; peptide; 105 AA.  
DE Nonclassical cadherin extracellular domain SEQ ID NO:18.  
PN W09957149-A2.  
PD 11-NOV-1999.  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
Query Match 1.0%; Score 7; DB 3; Length 105;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
RESULT 835  
ID AAB06753 standard; protein; 107 AA.  
DE Human ORFX protein sequence SEQ ID NO:13488.  
PN W0200192523-A2.  
PD 06-DEC-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 5; Length 107;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
RESULT 836  
ID AAV27656 standard; protein; 108 AA.  
DE Human protein APP548753.  
PN W020016748-A2.  
PD 13-SEP-2001.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 837  
ID AAG32136 standard; protein; 108 AA.  
DE Mutant B lichenformis secreted polypeptide SeqID 106.  
PN W02001903453-A2.  
PD 13-NOV-2003.  
PA (NOVO-) NOVOZYMES AS.  
Query Match 1.0%; Score 7; DB 8; Length 108;  
Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
RESULT 838  
ID AAM99113 standard; protein; 111 AA.  
DE Bovine zeta 2 prethrombin 2.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 111;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 839  
ID ABO74597 standard; protein; 111 AA.  
DE Pseudomonas aeruginosa polypeptide #6772.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 111;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
RESULT 840  
ID AAM99115 standard; protein; 116 AA.  
DE Human zeta 2 prethrombin 2.  
PN W09855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

RESULT 841  
ID AAG26792 standard; protein; 117 AA.  
DE Zea mays protein fragment SEQ ID NO: 31379.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
RESULT 842  
ID AAG51373 standard; protein; 121 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65194.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 121;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 843  
ID AAG26791 standard; protein; 121 AA.  
DE Zea mays protein fragment SEQ ID NO: 31378.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 121;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 844  
ID ABO73690 standard; protein; 121 AA.  
DE Pseudomonas aeruginosa polypeptide #5865.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 121;  
Best Local Similarity 100.0%; Pred. No. 5.4e+02;  
RESULT 845  
ID AAG11631 standard; protein; 128 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 10420.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 846  
ID AAG51372 standard; protein; 128 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65193.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
RESULT 847  
ID AAG26790 standard; protein; 142 AA.  
DE Zea mays protein fragment SEQ ID NO: 31377.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 142;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 848  
ID ABO63944 standard; protein; 142 AA.  
DE Klebsiella pneumoniae polypeptide seqid 10461.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 142;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 849  
ID AAW41967 standard; protein; 144 AA.  
DE Flea beetle protease SEQ ID NO: 81.  
PN WO9740058-A1.  
PD 30-OCT-1997.  
PA (HESK-) HESKA CORP.  
Query Match 1.0%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 850  
ID AAG50629 standard; protein; 144 AA.  
DE Flea beetle protease PfESP32-144 protein sequence #153.  
PN US6150125-A.  
PD 21-NOV-2000.  
PA (HESK-) HESKA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 144;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
RESULT 851  
ID AAW64494 standard; protein; 148 AA.  
DE Propionibacterium acnes immunogenic protein #25390.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (COR-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 148;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 852  
ID AEW61013 standard; protein; 148 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25689.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (COR-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 148;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
RESULT 853  
ID AAG51371 standard; protein; 151 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65192.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 151;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
RESULT 854  
ID AD145291 standard; protein; 164 AA.  
DE Rice isoprenoid biosynthesis-associated protein #111.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG/) LANGE B M.  
PA (GHAS/) GHASEMIAN M.  
PA (BRIG/) BRIGGS S P.  
PA (COOP/) COOPER B J.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (MOUG/) MOUGAMER T.  
PA (PROV/) PROVART N.  
PA (RICK/) RICKER D.  
PA (ZHUT/) ZHU T.  
Query Match 1.0%; Score 7; DB 8; Length 164;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
RESULT 855  
ID AAY34950 standard; protein; 172 AA.  
DE Amino acid sequence of a Chlamydia pneumoniae protein.  
PN WO9927105-A2.  
PD 03-JUN-1999.  
PA (GERS-) GENSERT.  
Query Match 1.0%; Score 7; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 856  
ID ABU39246 standard; protein; 172 AA.  
DE Protein encoded by Prokaryotic essential gene #24773.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) BLITPA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 172;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
RESULT 857  
ID AAG51370 standard; protein; 184 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65190.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 184;  
Best Local Similarity 100.0%; Pred. No. 7.9e+02;  
RESULT 858  
ID ADC97109 standard; protein; 187 AA.  
DE E. faecium protein sequence SEQ ID 6736.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 187;

Best Local Similarity 100.0%; Pred. No. 8e+02;  
RESULT 859  
ID AAU2597 standard; protein; 194 AA.  
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #44.  
PN W0200162797-A2.  
PD 30-AUG-2001.  
PA (PHDA ) PHARMACIA & UPJOHN CO.  
Query Match 1.0%; Score 7; DB 4; Length 194;  
Best Local Similarity 100.0%; Pred. No. 8.3e+02;  
RESULT 860  
ID AAU29491 standard; protein; 200 AA.  
DE Human G protein-coupled receptor (GPCR) polypeptide #112.  
PN W0200168858-A2.  
PD 20-SEP-2001.  
PA (PHAA ) PHARMACIA & UPJOHN CO.  
Query Match 1.0%; Score 7; DB 4; Length 200;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 861  
ID AAG60779 standard; protein; 200 AA.  
DE Novel G protein coupled receptor (nGPCR-x) #112.  
PN U52002058306-A1.  
PD 16-MAY-2002.  
PA (VOGE/) VOGELI G.  
Query Match 1.0%; Score 7; DB 5; Length 200;  
Best Local Similarity 100.0%; Pred. No. 8.5e+02;  
RESULT 862  
ID AAB65610 standard; protein; 202 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23622.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 863  
ID ADR09068 standard; protein; 202 AA.  
DE Human protein useful for treating neurological disease Seq 2574.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.0%; Score 7; DB 8; Length 202;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 864  
ID AAU45202 standard; protein; 209 AA.  
DE Propionibacterium acnes immunogenic protein #6098.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 209;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 865  
ID AAM41721 standard; protein; 209 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #6397.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match 1.0%; Score 7; DB 6; Length 209;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 866  
ID AAY35451 standard; protein; 210 AA.  
DE Chlamydia pneumoniae transmembrane protein sequence.  
PN W09927105-A2.  
PD 03-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 1.0%; Score 7; DB 2; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 867  
ID ABU27599 standard; protein; 210 AA.  
DE Protein encoded by Prokaryotic essential gene #13126.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 868  
ID ADS41665 standard; protein; 210 AA.  
DE Bacterial polypeptide #20095.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 210;  
Best Local Similarity 100.0%; Pred. No. 8.9e+02;  
RESULT 869  
ID ABU4962 standard; protein; 211 AA.  
DE Protein encoded by Prokaryotic essential gene #35489.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 211;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 870  
ID AAU34556 standard; protein; 212 AA.  
DE E. coli cellular proliferation protein #137.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 871  
ID ABU31486 standard; protein; 212 AA.  
DE Protein encoded by Prokaryotic essential gene #17013.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 872  
ID ABU48063 standard; protein; 212 AA.  
DE Protein encoded by Prokaryotic essential gene #33590.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 873  
ID ABU15066 standard; protein; 212 AA.  
DE Protein encoded by Prokaryotic essential gene #593.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 874  
ID ABU5471 standard; protein; 212 AA.  
DE Protein encoded by Prokaryotic essential gene #30998.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 212;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 875  
ID ABB54972 standard; protein; 213 AA.  
DE Lactococcus lactis protein kdga.  
PN FR2807446-A1.  
PD 12-OCT-2001.  
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
Query Match 1.0%; Score 7; DB 5; Length 213;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 876  
ID ABU40559 standard; protein; 213 AA.  
DE Protein encoded by Prokaryotic essential gene #26086.  
PN W0200277183-A2.  
PD 03-OCT-2002.

PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 213;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 877  
ID ADF04315 standard; protein; 214 AA.  
DE Bacterial polypeptide #428.  
PD US6605709-B1.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 214;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
RESULT 878  
ID ABB65059 standard; protein; 221 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21969.  
PD WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 221;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 879  
ID ADR49443 standard; protein; 221 AA.  
DE Drosophila small endoplasmic reticulum resident protein 3 (emerp3).  
PD EP1447412-A1.  
PD 18-AUG-2004.  
PA (UTVT-) UNIV UTRECHT HOLDING BV.  
Query Match 1.0%; Score 7; DB 8; Length 221;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
RESULT 880  
ID ABO61145 standard; protein; 226 AA.  
DE Klebsiella pneumoniae polypeptide seqid 7662.  
PD US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 226;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 881  
ID AAG51369 standard; protein; 227 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65189.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 227;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 882  
ID AAB92525 standard; protein; 227 AA.  
DE Human protein sequence SEQ ID NO:10677.  
PD EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 1.0%; Score 7; DB 4; Length 227;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 883  
ID ABU40124 standard; protein; 227 AA.  
DE Protein encoded by Prokaryotic essential gene #25651.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 227;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 884  
ID AAG15809 standard; protein; 228 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16207.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 228;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 885  
ID ABU41513 standard; protein; 228 AA.  
DE Protein encoded by Prokaryotic essential gene #27040.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 228;  
Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
RESULT 886  
ID AAG33373 standard; protein; 230 AA.  
DE Zea mays protein fragment SEQ ID NO: 40426.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 230;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 887  
ID ABU27062 standard; protein; 231 AA.  
DE Protein encoded by Prokaryotic essential gene #12589.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 231;  
Best Local Similarity 100.0%; Pred. No. 9.7e+02;  
RESULT 888  
ID AAU33655 standard; protein; 232 AA.  
DE Pseudomonas aeruginosa cellular proliferation protein #99.  
PD WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 889  
ID ABU15506 standard; protein; 232 AA.  
DE Protein encoded by Prokaryotic essential gene #1033.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 232;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 890  
ID AAW41957 standard; protein; 233 AA.  
DE Flea serine protease SEQ ID NO:27.  
PD WO9740058-A1.  
PD 30-OCT-1997.  
PA (HESK-) HESKA CORP.  
Query Match 1.0%; Score 7; DB 2; Length 233;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 891  
ID AAG51368 standard; protein; 234 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65188.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 234;  
Best Local Similarity 100.0%; Pred. No. 9.8e+02;  
RESULT 892  
ID AAG15808 standard; protein; 235 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16206.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 235;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 893  
ID AAG33372 standard; protein; 237 AA.  
DE Zea mays protein fragment SEQ ID NO: 40425.  
PD EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 894  
ID ABU49459 standard; protein; 239 AA.  
DE Protein encoded by Prokaryotic essential gene #34986.  
PD WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 895  
ID AAG33371 standard; protein; 241 AA.  
DE Zea mays protein fragment SEQ ID NO: 40424.  
PD EP1033405-A2.  
PD 06-SEP-2000.



Query Match 1.0%; Score 7; DB 3; Length 241;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 896  
ID ABO77745 standard; protein: 245 AA.  
DE Pseudomonas aeruginosa polypeptide #9920.  
PN U6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 245;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 897  
ID ADC73285 standard; protein: 254 AA.  
DE Human 187H\_H protein - SEQ ID 11.  
PN W02003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN) AJINOMOTO CO INC.  
PA (UMEV) UMEVYAMA H.  
Query Match 1.0%; Score 7; DB 7; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 898  
ID ADK17097 standard; protein: 254 AA.  
DE Nanocarchaeum equitans cancer-associated (CA) protein #524.  
PN W02003093434-A2.  
PD 13-NOV-2003.  
PA (DIVE-) DIVERSA CORP.  
Query Match 1.0%; Score 7; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 899  
ID ADL05143 standard; protein: 255 AA.  
DE M. catarrhalis protein #909.  
PN U6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 8; Length 255;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 900  
ID AAU38252 standard; protein: 257 AA.  
DE Salmonella typhi cellular proliferation protein #143.  
PN W0200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 901  
ID ADA35762 standard; protein: 257 AA.  
DE Acinetobacter baumannii protein #2923.  
PN U6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 6; Length 257;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 902  
ID AAG15807 standard; protein: 258 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16205.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 258;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 903  
ID AAW11545 standard; protein: 259 AA.  
DE Human thrombin Aen9 mutant.  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMO AG.  
Query Match 1.0%; Score 7; DB 2; Length 259;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 904  
ID ABB60565 standard; protein: 259 AA.  
DE Human thrombin variant W215A/E217A B-chain.  
PN W02002100337-A2.  
PD 19-DEC-2002.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 6; Length 259;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 905  
ID ABB60563 standard; protein: 259 AA.  
DE Human thrombin variant W215A B-chain.  
PN W02002100337-A2.  
PD 19-DEC-2002.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 6; Length 259;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 906  
ID AAW72891 standard; protein: 265 AA.  
DE Mycobacterium tuberculosis antigen CFP29.  
PN W0984419-A1.  
PD 08-OCT-1998.  
PA (STAT-) STATENS SERUM INST.  
Query Match 1.0%; Score 7; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 907  
ID AAY21908 standard; protein: 265 AA.  
DE Amino acid sequence of antigen CFP29.  
PN W09924577-A1.  
PD 20-MAY-1999.  
PA (STAT-) STATENS SERUM INST.  
Query Match 1.0%; Score 7; DB 2; Length 265;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 908  
ID AAW41956 standard; protein: 266 AA.  
DE Flea serine protease SEQ ID NO:24.  
PN W09740058-A1.  
PD 30-OCT-1997.  
PA (HESK-) HESKA CORP.  
Query Match 1.0%; Score 7; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 909  
ID AAO17669 standard; protein: 266 AA.  
DE B tropicalis allergen B10 3 protein SEQ ID NO: 4.  
PN W0200230968-A1.  
PD 18-APR-2002.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.0%; Score 7; DB 5; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 910  
ID AAO17668 standard; protein: 266 AA.  
DE B tropicalis allergen B10 3 protein SEQ ID NO: 2.  
PN W0200230968-A1.  
PD 18-APR-2002.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.0%; Score 7; DB 5; Length 266;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 911  
ID AAB62510 standard; protein: 268 AA.  
DE Flea serine protease F1SP2\_268.  
PN U6204010-B1.  
PD 20-MAR-2001.  
PA (HESK-) HESKA CORP.  
Query Match 1.0%; Score 7; DB 4; Length 268;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 912  
ID AAD69394 standard; protein: 271 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1200.  
PN W02003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.0%; Score 7; DB 7; Length 271;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 913  
ID ADO21743 standard; protein: 271 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4563.  
PN W02004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.0%; Score 7; DB 8; Length 271;



ID AAB08633 standard; protein; 295 AA.  
DE Amino acid sequence of a wild type human thrombin.  
PN US610721-A.  
PD 29-AUG-2000.  
PA (GILE-) GILEAD SCI INC.  
Query Match 1.0%; Score 7; DB 3; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 933  
ID AAB60562 standard; protein; 295 AA.  
DE Human thrombin variant W215A.  
PN WO2002100337-A2.  
PD 19-DEC-2002.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 934  
ID AAB60564 standard; protein; 295 AA.  
DE Human thrombin variant W215A/E217A.  
PN WO2002100337-A2.  
PD 19-DEC-2002.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 6; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 935  
ID ADS11062 standard; protein; 295 AA.  
DE Human therapeutic protein - SEQ ID 1299.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 1.0%; Score 7; DB 8; Length 295;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 936  
ID AAO17678 standard; protein; 296 AA.  
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 40.  
PN WO200230968-A1.  
PD 18-APR-2002.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.0%; Score 7; DB 5; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 937  
ID AAO17676 standard; protein; 296 AA.  
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 38.  
PN WO200230968-A1.  
PD 18-APR-2002.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.0%; Score 7; DB 5; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 938  
ID AAO17677 standard; protein; 296 AA.  
DE B tropicalis allergen Bloc 3 polymorphic variant protein SEQ ID NO: 39.  
PN WO200230968-A1.  
PD 18-APR-2002.  
PA (UYSI-) UNIV SINGAPORE NAT.  
Query Match 1.0%; Score 7; DB 5; Length 296;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 939  
ID AAM99107 standard; protein; 308 AA.  
DE Bovine prethrombin 2.  
PN WO9855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 308;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 940  
ID AAM99109 standard; protein; 308 AA.  
DE Human prethrombin 2.  
PN WO9855130-A1.  
PD 10-DEC-1998.  
PA (UYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 308;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 941  
ID AAB87820 standard; protein; 308 AA.

DE Mouse T2R26 amino acid sequence SEQ ID NO:155.  
PN WO200118050-A2.  
PD 15-MAR-2001.  
PA (REGC-) UNIV CALIFORNIA.  
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.0%; Score 7; DB 4; Length 308;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 942  
ID ADR29216 standard; protein; 308 AA.  
DE Taste receptor modulation-related mouse T2R26 protein sequence SeqID155.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC.  
Query Match 1.0%; Score 7; DB 8; Length 308;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 943  
ID ADC94558 standard; protein; 310 AA.  
DE E. faecium protein sequence SEQ ID 4185.  
PN US6583275-B1.  
PD 24-JUN-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 310;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 944  
ID ABR52886 standard; protein; 312 AA.  
DE Protein sequence #SEQ ID 637.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELU-) CELZOME AG.  
Query Match 1.0%; Score 7; DB 6; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 945  
ID ADK62400 standard; protein; 312 AA.  
DE Disease treating protein complex-derived protein #326.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELU-) CELZOME AG.  
Query Match 1.0%; Score 7; DB 7; Length 312;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 946  
ID ADC73300 standard; protein; 313 AA.  
DE Stereostereorelated protein.  
PN WO2003060765-A1.  
PD 24-JUL-2003.  
PA (AJIN-) AJINOMOTO CO INC.  
PA (UMBY-) UMEYAMA H.  
Query Match 1.0%; Score 7; DB 7; Length 313;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 947  
ID AAB72885 standard; protein; 314 AA.  
DE Murine ztrypl.  
PN WO200112788-A2.  
PD 22-FEB-2001.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 948  
ID ABU62253 standard; protein; 314 AA.  
DE Mouse tryptase-like polypeptide Ztryp-1.  
PN US6514741-B1.  
PD 04-FEB-2003.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 6; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 949  
ID ABR62454 standard; protein; 314 AA.  
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (EUIL-) UILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 950

ID ABR62456 standard; protein; 314 AA.  
DE Bovine Factor Xa activated recombinant prethrombin-2.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 951  
ID ABR62453 standard; protein; 314 AA.  
DE Bovine thrombin.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 952  
ID ABR62450 standard; protein; 314 AA.  
DE Bovine recombinant prethrombin-2, expressed in Escherichia coli.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 953  
ID ADCl7377 standard; protein; 314 AA.  
DE Mouse serine protease zltyp1.  
PN US2003119035-A1.  
PD 26-JUN-2003.  
PA (ZYMO-) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 314;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 954  
ID ABP41695 standard; protein; 324 AA.  
DE Human ovarian antigen HNTB23, SEQ ID NO:2827.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 324;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 955  
ID ADS27176 standard; protein; 330 AA.  
DE Bacterial polypeptide #16209.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 956  
ID ADS26796 standard; protein; 330 AA.  
DE Bacterial polypeptide #15829.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 330;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 957  
ID AAB87793 standard; protein; 332 AA.  
DE Rat T2R13 amino acid sequence SEQ ID NO:101.  
PN WO200118050-A2.  
PD 15-MAR-2001.  
PA (REGC ) UNIV CALIFORNIA.  
PA (USHS ) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 1.0%; Score 7; DB 4; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 958

ID ADR29162 standard; protein; 332 AA.  
DE Taste receptor modulation-related rat T2R13 protein sequence SeqID101.  
PN WO2004069191-A2.  
PD 19-AUG-2004.  
PA (SENO-) SENOMYX INC.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 959  
ID ADS26428 standard; protein; 332 AA.  
DE Bacterial polypeptide #15461.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 332;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 960  
ID ADJ49544 standard; protein; 336 AA.  
DE Oil-associated gene related protein #1044.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 336;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 961  
ID ADJ49561 standard; protein; 338 AA.  
DE Oil-associated gene related protein #1061.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 962  
ID ADC31358 standard; protein; 357 AA.  
DE Human novel polypeptide sequence, SEQ ID NO:1440.  
PN WO2003029271-A2.  
PD 10-APR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 7; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 963  
ID ADR09339 standard; protein; 357 AA.  
DE Human protein useful for treating neurological disease Seq 2845.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 1.0%; Score 7; DB 8; Length 357;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 964  
ID ABR62452 standard; protein; 362 AA.  
DE Bovine recombinant prethrombin-2, expressed in CHO cells.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 362;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 965  
ID AAY38815 standard; protein; 375 AA.  
DE Neisseria meningitidis strain A antigen encoded by ORF146.  
PN WO9924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.

Query Match 1.0%; Score 7; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 966  
ID AAY3814 standard; protein; 375 AA.  
DE Neisseria meningitidis antigen encoded by ORF146.  
PN W0924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 967  
ID AAY3817 standard; protein; 375 AA.  
DE Neisseria gonorrhoeae antigenic protein encoded by ORF146.  
PN W0924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 2; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 968  
ID AAY75445 standard; protein; 375 AA.  
DE Neisseria gonorrhoeae ORF 706 protein sequence SEQ ID NO:2364.  
PN W0924578-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 3; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 969  
ID AAY75446 standard; protein; 375 AA.  
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2366.  
PN W0924578-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 3; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 970  
ID AAY75447 standard; protein; 375 AA.  
DE Neisseria meningitidis ORF 706 protein sequence SEQ ID NO:2368.  
PN W0924578-A2.  
PD 11-NOV-1999.  
PA (CHIR-) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 3; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 971  
ID AAY72957 standard; protein; 375 AA.  
DE Neisseria meningitidis virulence protein #47.  
PN W0200185772-A2.  
PD 15-NOV-2001.  
PA (MICR-) MICROSCIENCE LTD.  
Query Match 1.0%; Score 7; DB 5; Length 375;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 972  
ID AAR4197 standard; protein; 376 AA.  
DE CD4/Thrombin fusion protein.  
PN W09318162-A1.  
PD 16-SEP-1993.  
PA (CREA-) CREAGEN INC.  
Query Match 1.0%; Score 7; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 973  
ID AAY42789 standard; protein; 376 AA.  
DE Human CD4/Thrombin fusion protein.  
PN US5961973-A.  
PD 05-OCT-1999.  
PA (CREA/) CREA R.  
Query Match 1.0%; Score 7; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 974  
ID AAU10703 standard; protein; 376 AA.  
DE Human CD4-Thrombin fusion protein.  
PN US6287561-B1.

PD 11-SEP-2001.  
PA (CREA/) CREA R.  
Query Match 1.0%; Score 7; DB 5; Length 376;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 975  
ID AAG21667 standard; protein; 398 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24304.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 398;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 976  
ID ABO80228 standard; protein; 399 AA.  
DE Pseudomonas aeruginosa polypeptide #12403.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 399;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 977  
ID AAY3816 standard; protein; 409 AA.  
DE Neisseria gonorrhoeae antigen encoded by partial ORF146.  
PN W0924578-A2.  
PD 20-MAY-1999.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 2; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 978  
ID ABB0460 standard; protein; 409 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 7450.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 979  
ID ABB79601 standard; protein; 409 AA.  
DE N. gonorrhoeae amino acid sequence SEQ ID 5732.  
PN W0200279243-A2.  
PD 10-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 980  
ID ABB37254 standard; protein; 409 AA.  
DE Protein encoded by Prokaryotic essential gene #22781.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (BLIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 981  
ID ADD1516 standard; protein; 420 AA.  
DE Fruitfly odorant receptor protein (Seqid 68).  
PN W02003020913-A2.  
PD 13-MAR-2003.  
PA (SENT-) SENTIGEN CORP.  
Query Match 1.0%; Score 7; DB 7; Length 420;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 982  
ID ABO65926 standard; protein; 422 AA.  
DE Klebsiella pneumoniae polypeptide seqid 12443.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 422;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 983  
ID AAB03444 standard; protein; 426 AA.  
DE Candida albicans essential growth protein #2.  
PN W0200034481-A2.  
PD 15-JUN-2000.  
PA (JANC) JANSSEN PHARM NV.

Query Match 1.0%; Score 7; DB 3; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 984  
ID ABO61095 standard; protein; 437 AA.  
DE Klebsiella pneumoniae polypeptide seqid 7612.  
PN US6610836-B1.  
PD 26-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 437;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 985  
ID ABB34680 standard; protein; 443 AA.  
DE Protein encoded by Prokaryotic essential gene #20207.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 443;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 986  
ID ABB17062 standard; protein; 444 AA.  
DE Protein encoded by Prokaryotic essential gene #2589.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 444;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 987  
ID ADA34407 standard; protein; 448 AA.  
DE Acinetobacter baumannii protein #1568.  
PN US6562958-B1.  
PD 13-MAY-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 6; Length 448;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 988  
ID AAG21666 standard; protein; 452 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24303.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 452;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 989  
ID AAB26435 standard; protein; 456 AA.  
DE Drosophila melanogaster odorant receptor DOR28.  
PN WO200050566-A2.  
PD 31-AUG-2000.  
PA (UNCO-) UNIV COLUMBIA NEW YORK.  
Query Match 1.0%; Score 7; DB 3; Length 456;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 990  
ID ABB64797 standard; protein; 456 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21183.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PERKE-) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 456;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 991  
ID ADJ32828 standard; protein; 459 AA.  
DE Human prethrombin protein.  
PN US200332414-A1.  
PD 18-DEC-2003.  
PA (MOOR/) MOORE M D.  
Query Match 1.0%; Score 7; DB 8; Length 459;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 992  
ID ABB33733 standard; protein; 461 AA.  
DE Protein encoded by Prokaryotic essential gene #19260.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 461;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

RESULT 993  
ID ABB36590 standard; protein; 461 AA.  
DE Protein encoded by Prokaryotic essential gene #22517.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 461;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 994  
ID AAB60460 standard; protein; 463 AA.  
DE Human cell cycle and proliferation protein CCYPR-8, SEQ ID NO:8.  
PN WO200107471-A2.  
PD 01-FEB-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 4; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 995  
ID ADP23764 standard; protein; 463 AA.  
DE PRO polypeptide SEQ ID NO:942.  
PN WO2004041170-A2.  
PD 21-MAY-2004.  
PA (GETH-) GENENTECH INC.  
Query Match 1.0%; Score 7; DB 8; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 996  
ID ABB73357 standard; protein; 465 AA.  
DE Staphylococcus aureus protein #2597.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 997  
ID ADJ50012 standard; protein; 465 AA.  
DE Oil-associated gene related protein #1512.  
PN US2004025202-A1.  
PD 05-FEB-2004.  
PA (LAUR/) LAURIE C C.  
PA (RAVA/) RAVANELLO M.  
PA (SAVA/) SAVAGE T.  
PA (LEDE/) LEDEAUX J R.  
PA (ROGE/) ROGERS J A.  
Query Match 1.0%; Score 7; DB 8; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 998  
ID ADN21085 standard; protein; 467 AA.  
DE Bacterial polypeptide #3738.  
PN US200323675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 999  
ID AAG21665 standard; protein; 469 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 24302.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 469;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1000  
ID ABB72219 standard; protein; 469 AA.  
DE Staphylococcus aureus protein #1459.  
PN WO200294868-A2.  
PD 28-NOV-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 1.0%; Score 7; DB 6; Length 469;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1001  
ID ADK41715 standard; protein; 470 AA.

DE Soybean amino acid transporter protein.  
PN WO2003066879-A2.  
PD 14-AUG-2003.  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 7; Length 470;  
Pred. No. 1.9e+03;  
RESULT 1002  
ID AAY20047 standard; protein; 481 AA.  
DE B. burgdorferi antigenic protein, t352.aa.  
PN WO9859071-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MED1-) MEDIMMUNE INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 2; Length 481;  
Pred. No. 1.1e+03;  
RESULT 1003  
ID AAM68866 standard; protein; 492 AA.  
DE Photocorhabdus luminescens protein sequence #1963.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 6; Length 492;  
Pred. No. 1.1e+03;  
RESULT 1004  
ID ABO84661 standard; protein; 494 AA.  
DE Mouse cancer-associated protein MP20-004.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 8; Length 494;  
Pred. No. 1.1e+03;  
RESULT 1005  
ID AAW72030 standard; protein; 497 AA.  
DE HSV-2 strain SBS Contig ID 103 ORF#8 protein.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;  
Pred. No. 2e+03;  
RESULT 1006  
ID AAW72132 standard; protein; 497 AA.  
DE HSV-2 strain SBS Contig ID 16 ORF#8 protein.  
PN WO9820016-A1.  
PD 14-MAY-1998.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;  
Pred. No. 2e+03;  
RESULT 1007  
ID AAY20046 standard; protein; 497 AA.  
DE B. burgdorferi antigenic protein, t352.aa.  
PN WO9859071-A1.  
PD 30-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (MED1-) MEDIMMUNE INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 2; Length 497;  
Pred. No. 2e+03;  
RESULT 1008  
ID ABB27287 standard; protein; 497 AA.  
DE Streptococcus polypeptide SEQ ID NO 3750.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 5; Length 497;  
Pred. No. 2e+03;  
RESULT 1009  
ID ABO23531 standard; protein; 497 AA.  
DE Borrelia burgdorferi outer protein #1.  
PN US200303963-A1.  
PD 27-FEB-2003.  
PA (BRAH/) BRAHMACHARI S K.  
PA (RAMA/) RAMACHANDRAN S.  
  
PA (NAND/) NANDI T.  
PA (BHIM/) BHIMARAO C.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 7; Length 497;  
Pred. No. 2e+03;  
RESULT 1010  
ID AAU16169 standard; protein; 498 AA.  
DE Human novel secreted protein, Seq ID 1122.  
PN WO200155322-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 4; Length 498;  
Pred. No. 2e+03;  
RESULT 1011  
ID ABU55238 standard; protein; 498 AA.  
DE Human novel polypeptide #325.  
PN US2002132753-A1.  
PD 19-SEP-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 6; Length 498;  
Pred. No. 2e+03;  
RESULT 1012  
ID ADS41994 standard; protein; 500 AA.  
DE Bacterial polypeptide #20424.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 8; Length 500;  
Pred. No. 2e+03;  
RESULT 1013  
ID ABU01365 standard; protein; 502 AA.  
DE S. pneumoniae type 4 strain protein from coding region #940.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 6; Length 502;  
Pred. No. 2e+03;  
RESULT 1014  
ID ABB81378 standard; protein; 502 AA.  
DE Streptococcus pneumoniae polypeptide SEQ ID NO 295.  
PN WO200283855-A2.  
PD 24-OCT-2002.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 6; Length 502;  
Pred. No. 2e+03;  
RESULT 1015  
ID AAY00189 standard; protein; 503 AA.  
DE Enterococcus faecalis antigenic polypeptide fragment EF094.  
PN WO9850554-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 2; Length 503;  
Pred. No. 2e+03;  
RESULT 1016  
ID ABB43408 standard; protein; 503 AA.  
DE E faecalis EF094 antigenic fragment.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 1.0%; Score 7; DB 5; Length 503;  
Pred. No. 2e+03;  
RESULT 1017  
ID ABU88436 standard; protein; 503 AA.  
DE E. faecalis novel protein #180.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 1.0%; Score 7; DB 6; Length 503;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1018  
ID AB013687 standard; protein; 503 AA.  
DE Enterococcus faecalis EF040 polypeptide #180.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCT INC.  
Query Match 1.0%; Score 7; DB 6; Length 503;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1019  
ID AAB68138 standard; protein; 504 AA.  
DE Amino acid sequence of a partial murine SP64 polypeptide.  
PN FR2798138-A1.  
PD 09-MAR-2001.  
PA (CNRS ) CNRS CENT NAT RECH SCI.  
Query Match 1.0%; Score 7; DB 4; Length 504;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1020  
ID AAG29530 standard; protein; 508 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35152.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 508;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1021  
ID ABUS4588 standard; protein; 509 AA.  
DE Human NOVX polypeptide #47.  
PN WO200281498-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 1.0%; Score 7; DB 6; Length 509;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1022  
ID ADS22207 standard; protein; 513 AA.  
DE Bacterial polypeptide #11240.  
PN US200333675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 513;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1023  
ID AAE29568 standard; protein; 517 AA.  
DE Staphylococcus aureus von Willebrand factor binding protein (vwb).  
PN WO200228882-A1.  
PD 11-APR-2002.  
PA (BIOS-) BIOSTRA PRO AB.  
Query Match 1.0%; Score 7; DB 5; Length 517;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1024  
ID ABUS5877 standard; protein; 518 AA.  
DE Mouse notch ligand jagged 2 protein.  
PN WO200277204-A2.  
PD 03-OCT-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 1.0%; Score 7; DB 6; Length 518;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1025  
ID AAG34033 standard; protein; 518 AA.  
DE Murine notch ligand jagged 2 protein.  
PN WO200290992-A2.  
PD 14-NOV-2002.  
PA (AXOR-) AXORDIA LTD.  
Query Match 1.0%; Score 7; DB 6; Length 518;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1026  
ID ABO75124 standard; protein; 525 AA.  
DE Pseudomonas aeruginosa polypeptide #7299.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 7; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1027  
ID ADO26850 standard; protein; 525 AA.  
DE Human receptors and membrane-associated protein, REMAP-40.  
PN WO2004044159-A2.  
PD 27-MAY-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1028  
ID ABB58809 standard; protein; 542 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3219.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 542;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1029  
ID ADN21059 standard; protein; 543 AA.  
DE Bacterial polypeptide #3712.  
PN US200333675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 543;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1030  
ID AAU37798 standard; protein; 553 AA.  
DE Streptococcus pneumoniae cellular proliferation protein #227.  
PN WO200170955-A2.  
PD 27-SEP-2001.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1031  
ID AAM01018 standard; protein; 553 AA.  
DE CPE 17 protein sequence.  
PN WO200149721-A2.  
PD 12-JUL-2001.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
Query Match 1.0%; Score 7; DB 4; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1032  
ID ABU00989 standard; protein; 553 AA.  
DE S. pneumoniae type 4 strain protein from coding region #558.  
PN WO200277021-A2.  
PD 03-OCT-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1033  
ID ABU45930 standard; protein; 553 AA.  
DE Protein encoded by Prokaryotic essential gene #31457.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1034  
ID ADK48791 standard; protein; 553 AA.  
DE Streptococcus pneumoniae protein, Seq ID NO 5306.  
PN US6699703-B1.  
PD 02-MAR-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 8; Length 553;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;



RESULT 1035  
ID AAG29529 standard; protein; 555 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35151.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 555;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1036  
ID AAU08803 standard; protein; 556 AA.  
DE Human phosphatidyl glycerol phosphate (PGP) synthase.  
PN W0200164895-A2.  
PD 07-SEP-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.0%; Score 7; DB 4; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1037  
ID ADCL14217 standard; protein; 556 AA.  
DE Human enzyme ENZM-23.  
PN W02003042357-A2.  
PD 22-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1038  
ID ADJ57901 standard; protein; 556 AA.  
DE Human 27411 FGP synthase protein.  
PN US2004009553-A1.  
PD 15-JAN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 1.0%; Score 7; DB 8; Length 556;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1039  
ID ABP61060 standard; protein; 557 AA.  
DE Lactobacillus rhamnosus HN001 polypeptide SEQ ID NO 120.  
PN W0200244383-A1.  
PD 06-JUN-2002.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (VIAL-) VIALACTIA BIOSCIENCE NZ LTD.  
Query Match 1.0%; Score 7; DB 5; Length 557;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1040  
ID ADR95837 standard; protein; 558 AA.  
DE Novel S. pneumoniae protein sequence, SEQ ID 4472.  
PN US6800744-B1.  
PD 05-OCT-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 1.0%; Score 7; DB 8; Length 558;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1041  
ID ABP75529 standard; protein; 563 AA.  
DE Human secretory polypeptide SPTM SEQ ID NO 713.  
PN W0200283876-A2.  
PD 24-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 6; Length 563;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1042  
ID ABU18645 standard; protein; 573 AA.  
DE Protein encoded by prokaryotic essential gene #4172.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 1.0%; Score 7; DB 6; Length 573;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1043  
ID AAR35763 standard; protein; 579 AA.  
DE Prothrombin (PT).  
PN W03009804-A1.  
PD 27-MAY-1993.  
PA (SCRI) SCRIPPS RES INST.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1044

ID AAM11544 standard; protein; 579 AA.  
DE Human prothrombin Asn419 mutant.  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMUNO AG.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1045  
ID AAM11546 standard; protein; 579 AA.  
DE Human prothrombin mutant (generic sequence).  
PN W09641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMUNO AG.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1046  
ID AAM99108 standard; protein; 579 AA.  
DE Human prothrombin.  
PN W0985130-A1.  
PD 10-DEC-1998.  
PA (VYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1047  
ID AD133974 standard; protein; 579 AA.  
DE Human meizothrombin analogue mature protein.  
PN W02004007714-A1.  
PD 22-JAN-2004.  
PA (ASAH) ASAH KASEI KK.  
Query Match 1.0%; Score 7; DB 8; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1048  
ID AAM99106 standard; protein; 582 AA.  
DE Bovine prothrombin.  
PN W0985130-A1.  
PD 10-DEC-1998.  
PA (VYEM-) UNIV EMORY.  
Query Match 1.0%; Score 7; DB 2; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1049  
ID AAG29528 standard; protein; 582 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 35150.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1050  
ID ABR62449 standard; protein; 583 AA.  
DE Bovine recombinant prothrombin, expressed in Escherichia coli.  
PN W02003052059-A2.  
PD 26-JUN-2003.  
PA (ELIT) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 583;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1051  
ID ADB28808 standard; protein; 588 AA.  
DE Bacterial polypeptide #17841.  
PN US200233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 588;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1052  
ID ABB66001 standard; protein; 603 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24795.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 603;

Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
RESULT 1053  
ID AAR8741 standard; protein; 615 AA.  
DE Human prothrombin.  
PN WO9313208-A1.  
PD 08-JUL-1993.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1054  
ID AAR90377 standard; protein; 615 AA.  
DE Human prothrombin.  
PN US5476777-A.  
PD 19-DEC-1995.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1055  
ID AAR96216 standard; protein; 615 AA.  
DE Human prothrombin.  
PN US5502034-A.  
PD 26-MAR-1996.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 1.0%; Score 7; DB 2; Length 615;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1056  
ID AAR68137 standard; protein; 616 AA.  
DE Amino acid sequence of the human SPG4 polypeptide.  
PN FR2798138-A1.  
PD 09-MAR-2001.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Query Match 1.0%; Score 7; DB 4; Length 616;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1057  
ID AAW1543 standard; protein; 622 AA.  
DE Human preprothrombin (wild-type).  
PN WO9641868-A2.  
PD 27-DEC-1996.  
PA (IMMO) IMMO AG.  
Query Match 1.0%; Score 7; DB 2; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1058  
ID AA49366 standard; protein; 622 AA.  
DE Platelet membrane glycoprotein IIIa beta subunit protein sequence.  
PN WO9590454-A2.  
PD 07-OCT-1999.  
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
Query Match 1.0%; Score 7; DB 2; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1059  
ID ABG74671 standard; protein; 622 AA.  
DE Human F2 protein.  
PN WO2003016494-A2.  
PD 27-FEB-2003.  
PA (VITI-) VITIVITY INC.  
Query Match 1.0%; Score 7; DB 6; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1060  
ID ADB8851 standard; protein; 622 AA.  
DE Human Factor 2, F2, protein, SEQ ID 2.  
PN WO2003029493-A1.  
PD 10-APR-2003.  
PA (VITI-) VITIVITY INC.  
Query Match 1.0%; Score 7; DB 7; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1061  
ID AD18196 standard; protein; 622 AA.  
DE Human coagulation factor II protein SEQ ID NO.116.  
PN WO2003014381-A1.  
PD 20-FEB-2003.  
PA (AHRA-) AHRAM BIOSYSTEMS INC.  
Query Match 1.0%; Score 7; DB 7; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;

RESULT 1062  
ID AD133975 standard; protein; 622 AA.  
DE Human meizothrombin analogue full-length protein.  
PN WO2004007714-A1.  
PD 22-JAN-2004.  
PA (ASAH) ASAH KASEI KK.  
Query Match 1.0%; Score 7; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1063  
ID ADQ30580 standard; protein; 622 AA.  
DE Pancreas cancer marker - prothrombin precursor.  
PN WO2004055519-A2.  
PD 01-JUL-2004.  
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.  
PA (SINO-) SINGENOMAX CO LTD CHINESE NAT HUMAN GEN.  
Query Match 1.0%; Score 7; DB 8; Length 622;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1064  
ID ABR62455 standard; protein; 625 AA.  
DE Bovine preprothrombin.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 625;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1065  
ID ABR62451 standard; protein; 635 AA.  
DE Bovine recombinant prothrombin, expressed in CHO cells.  
PN WO2003052059-A2.  
PD 26-JUN-2003.  
PA (ELIL) LILLY & CO ELI.  
Query Match 1.0%; Score 7; DB 7; Length 635;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
RESULT 1066  
ID AD127332 standard; peptide; 638 AA.  
DE Amino acid sequence of prethrombin(64S)3scfvalphaHA.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEV) AFEVAN N B.  
Query Match 1.0%; Score 7; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1067  
ID AD127333 standard; peptide; 638 AA.  
DE Amino acid sequence of schA(G4S)3prethrombin.  
PN WO2004019878-A2.  
PD 11-MAR-2004.  
PA (COMP-) COMPOUND THERAPEUTICS INC.  
PA (AFEV) AFEVAN N B.  
Query Match 1.0%; Score 7; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1068  
ID ABB93056 standard; protein; 658 AA.  
DE Hericidially active polypeptide SEQ ID NO 2267.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 1.0%; Score 7; DB 5; Length 658;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
RESULT 1069  
ID ABB58511 standard; protein; 683 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2325.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PERE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 683;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1070  
ID AAG30915 standard; protein; 684 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37042.  
PN EPI033405-A2.  
PD 06-SEP-2000.  
Query Match 1.0%; Score 7; DB 3; Length 684;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
RESULT 1071  
ID ABB03731 standard; protein: 696 AA.  
DE Novel human diagnostic protein #3722.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1072  
ID ABB22196 standard; protein: 713 AA.  
DE Protein encoded by Prokaryotic essential gene #7723.  
PN W0200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1073  
ID ABB68587 standard; protein: 716 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32553.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1074  
ID AAB70937 standard; protein: 763 AA.  
DE S. pombe potassium transporter TRKp protein.  
PN DE19941766-A1.  
PD 15-MAR-2001.  
PA (LICH-) LICHTENBERG-FRATE H.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
RESULT 1075  
ID ABB70253 standard; protein: 776 AA.  
DE C. neoformans amino acid sequence SEQ ID NO:3297.  
PN W02003052076-A2.  
PD 26-JUN-2003.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 776;  
RESULT 1076  
ID ABB14998 standard; protein: 783 AA.  
DE Pseudomonas aeruginosa quorum sensing controlled protein, SEQ ID 553.  
PN W02004083385-A2.  
PD 30-SEP-2004.  
PA (IOWA) UNIV IOWA RES FOUND.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 8; Length 783;  
RESULT 1077  
ID ABB45247 standard; protein: 784 AA.  
DE Rice isoprenoid biosynthesis-associated protein #89.  
PN US2004010815-A1.  
PD 15-JAN-2004.  
PA (LANG-) LANGE B M.  
PA (GHAS-) GHASSEMIAN M.  
PA (BRIG-) BRIGGS S P.  
PA (COOP-) COOPER B.  
PA (GLAZ-) GLAZEBROOK J.  
PA (GOLF-) GOLF S A.  
PA (KATA-) KATAGIRI F.  
PA (KREP-) KREPS J.  
PA (MOUG-) MOUGHAMER T.  
PA (PROV-) PROVART N.  
PA (RICK-) RICKS D.  
PA (ZHUT-) ZHU T.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 8; Length 784;  
RESULT 1078  
ID ABB58512 standard; protein: 787 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 2328.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 787;  
RESULT 1079  
ID AAG90377 standard; protein: 799 AA.  
DE C glutamicum protein fragment SEQ ID NO: 4131.  
PN BPI08790-A2.  
PD 20-JUN-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
RESULT 1080  
ID ABB65785 standard; protein: 799 AA.  
DE C. glutamicum RXA-associated protein #71.  
PN DE10154177-A1.  
PD 08-MAY-2003.  
PA (BADI-) BASF AG.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
RESULT 1081  
ID ABB069076 standard; protein: 805 AA.  
DE Pseudomonas aeruginosa polypeptide #1251.  
PN US6551795-B1.  
PD 22-APR-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
RESULT 1082  
ID AAB47019 standard; protein: 808 AA.  
DE A. thaliana DGL1.  
PN CA2307960-A1.  
PD 06-NOV-2000.  
PA (UNMS) UNIV MICHIGAN STATE.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 4; Length 808;  
RESULT 1083  
ID ABB92279 standard; protein: 808 AA.  
DE Herbicidially active polypeptide SEQ ID NO 1490.  
PN W0200210210-A2.  
PD 07-FEB-2002.  
PA (FARB-) BAYER AG.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 5; Length 808;  
RESULT 1084  
ID ABB95604 standard; protein: 808 AA.  
DE A. thaliana protein 21878 #SEQ ID 42.  
PN W0200308440-A2.  
PD 30-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 7; Length 808;  
RESULT 1085  
ID ABB63822 standard; protein: 808 AA.  
DE Plant lipid metabolism protein PK239 SEQ ID NO:24.  
PN W02004013304-A2.  
PD 12-FEB-2004.  
PA (BADI-) BASF PLANT SCI GMBH.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 3e+03;  
RESULT 1086  
ID ABB07872 standard; protein: 859 AA.  
DE Aluminum resistance gene ALR1.  
PN W09634959-A1.  
PD 07-NOV-1996.  
PA (AUCC-) AUCCLAND UNISERVICES LTD.  
Query Match  
Best Local Similarity 100.0%; Score 7; DB 2; Length 859;  
RESULT 1087  
ID ABB08613 standard; protein: 892 AA.  
DE Novel protein (useful for identifying genetic disorders) #768.  
PN W02003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.

Query Match 1.0%; Score 7; DB 7; Length 892;  
Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
RESULT 1088  
ID ADE31112 standard; protein; 912 AA.  
DE Human diagnostic and therapeutic polypeptide (DITHP), SEQ ID NO 244.  
PN WO2003062376-A2.  
PD 31-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 912;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
RESULT 1089  
ID ABH65063 standard; protein; 921 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 21981.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 921;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
RESULT 1090  
ID ABH62769 standard; protein; 984 AA.  
DE Protein fragment #6 of S. roseosporus biosynthetic gene cluster.  
PN WO200259322-A2.  
PD 01-AUG-2002.  
PA (MIAO/) MIAO V P W.  
PA (BRJA/) BRIAN P.  
PA (BALV/) BALVZ R H.  
PA (SILV/) SILVA C J.  
Query Match 1.0%; Score 7; DB 5; Length 984;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
RESULT 1091  
ID AD72180 standard; protein; 984 AA.  
DE Streptomyces roseosporus daptomycin biosynthesis gene cluster protein #6.  
PN WO2003014297-A2.  
PD 20-FEB-2003.  
PA (CUBI-) CUBIST PHARM INC.  
Query Match 1.0%; Score 7; DB 7; Length 984;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
RESULT 1092  
ID ADM5737 standard; protein; 995 AA.  
DE Recombinant protein production method related polypeptide SEQ ID NO: 8.  
PN WO2004027067-A2.  
PD 01-APR-2004.  
PA (CYMO-) CYMIP AS.  
Query Match 1.0%; Score 7; DB 8; Length 995;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
RESULT 1093  
ID ABH93966 standard; protein; 1047 AA.  
DE Heptadically active polypeptide SEQ ID NO 3177.  
PN WO200210210-A2.  
PD 07-FEB-2002.  
PA (FARB) BAYER AG.  
Query Match 1.0%; Score 7; DB 5; Length 1047;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
RESULT 1094  
ID ABH63005 standard; protein; 1061 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:3254.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 1061;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1095  
ID AAY00188 standard; protein; 1074 AA.  
DE Enterococcus faecalis protein EF094.  
PN WO9850554-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 2; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1096  
ID AAY00206 standard; protein; 1074 AA.  
DE Enterococcus faecalis protein EF102.  
PN WO9850554-A2.

PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 2; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1097  
ID ABP43425 standard; protein; 1074 AA.  
DE E faecalis EF102 protein.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1098  
ID ABP43407 standard; protein; 1074 AA.  
DE E faecalis EF094 protein.  
PN US2002045737-A1.  
PD 18-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 5; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1099  
ID ABH88435 standard; protein; 1074 AA.  
DE E faecalis novel protein #179.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1100  
ID ABH88453 standard; protein; 1074 AA.  
DE E faecalis novel protein #197.  
PN US2003017495-A1.  
PD 23-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1101  
ID ABH13686 standard; protein; 1074 AA.  
DE Enterococcus faecalis EF040 polypeptide #179.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1102  
ID ABH13704 standard; protein; 1074 AA.  
DE Enterococcus faecalis EF040 polypeptide #197.  
PN US6448043-B1.  
PD 10-SEP-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 1.0%; Score 7; DB 6; Length 1074;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
RESULT 1103  
ID ADH87879 standard; protein; 1096 AA.  
DE Enterococcus faecalis polypeptide #2359.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Query Match 1.0%; Score 7; DB 7; Length 1096;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1104  
ID AAE37912 standard; protein; 1104 AA.  
DE Human CGDD-1 protein.  
PN WO2003050253-A2.  
PD 19-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 1.0%; Score 7; DB 7; Length 1104;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
RESULT 1105  
ID AAY96613 standard; protein; 1140 AA.  
DE Streptococcus pneumoniae UvrA-like protein.  
PN GB2345288-A.

PD 05-JUL-2000.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 1.0%; Score 7; DB 3; Length 1140;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
RESULT 1106  
ID ADR88899 standard; protein; 1158 AA.  
DE Anopheles thioester-containing protein (TEP) 16 sequence.  
PN EP1452184-A1.  
PD 01-SEP-2004.  
PA (EMBL-) EMBL.  
Query Match 1.0%; Score 7; DB 8; Length 1158;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
RESULT 1107  
ID ASB66758 standard; protein; 1240 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 27066.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 1240;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
RESULT 1108  
ID ADR88898 standard; protein; 1340 AA.  
DE Anopheles thioester-containing protein (TEP) 1 sequence.  
PN EP1452184-A1.  
PD 01-SEP-2004.  
PA (EMBL-) EMBL.  
Query Match 1.0%; Score 7; DB 8; Length 1340;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1109  
ID AAV717195 standard; protein; 1346 AA.  
DE S. venezuelae macrolide biosynthetic enzyme PkAIIV, SEQ ID NO:37.  
PN W020000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1110  
ID AAV77203 standard; protein; 1346 AA.  
DE S. venezuelae plk (macrolide biosynthesis) gene cluster protein #4.  
PN W020000620-A2.  
PD 06-JAN-2000.  
PA (MINU) UNIV MINNESOTA.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1111  
ID AAB18640 standard; protein; 1346 AA.  
DE Amino acid sequence of narbonolide synthase subunit 4 (PICAIV).  
PN US6117659-A.  
PD 12-SEP-2000.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1112  
ID AAV67204 standard; protein; 1346 AA.  
DE Narbonolide synthase subunit 4 (PICAIV) protein sequence.  
PN W09961599-A2.  
PD 02-DEC-1999.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 3; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1113  
ID ASB71664 standard; protein; 1346 AA.  
DE S. venezuelae narbonolide synthase subunit 4, PICAIV.  
PN W0200297062-A2.  
PD 05-DEC-2002.  
PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1114  
ID ADB09403 standard; protein; 1346 AA.  
DE S. venezuelae narbonolide synthase subunit 4 (PICAIV).  
PN US6509455-B1.  
PD 21-JAN-2003.

PA (KOSA-) KOSAN BIOSCIENCES INC.  
Query Match 1.0%; Score 7; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1115  
ID ADH53447 standard; protein; 1346 AA.  
DE Streptomyces venezuelae narbonolide synthase subunit 4 protein, PICAIV.  
PN US2003162262-A1.  
PD 28-AUG-2003.  
PA (ASHL) ASHLEY G.  
PA (BETL) BETLACH M. C.  
PA (BETL) BETLACH M.  
PA (MCDA) MCDANIEL R.  
PA (TANG) TANG L.  
Query Match 1.0%; Score 7; DB 7; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1116  
ID ADL91922 standard; protein; 1346 AA.  
DE Streptomyces macrolide biosynthetic protein - PkIIV.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER) SHERMAN D. H.  
PA (LIUH) LIU H.  
PA (XUEY) XUE Y.  
PA (ZHAO) ZHAO L.  
Query Match 1.0%; Score 7; DB 8; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
RESULT 1117  
ID ABR53267 standard; protein; 1522 AA.  
DE Protein sequence #SEQ ID 1399.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZONE AG.  
Query Match 1.0%; Score 7; DB 6; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1118  
ID ADG63630 standard; protein; 1522 AA.  
DE Disease treating protein complex-derived protein #838.  
PN EP1338608-A2.  
PD 27-AUG-2003.  
PA (CELL-) CELLZONE AG.  
Query Match 1.0%; Score 7; DB 7; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1119  
ID ADM35845 standard; protein; 1522 AA.  
DE Yeast Okazaki fragment endonuclease Dna2.  
PN KR2002072712-A.  
PD 18-SEP-2002.  
PA (SEOV) SEO Y S.  
Query Match 1.0%; Score 7; DB 7; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1120  
ID ADS43628 standard; protein; 1522 AA.  
DE Bacterial polypeptide #22058.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOV) CAO Y.  
PA (HINK) HINKLE G J.  
PA (SLAT) SLATER S C.  
PA (CHEN) CHEN X.  
PA (GOLD) GOLDMAN B S.  
Query Match 1.0%; Score 7; DB 8; Length 1522;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
RESULT 1121  
ID ABB28343 standard; protein; 1631 AA.  
DE Streptococcus polypeptide SEQ ID NO 5862.  
PN W0200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Query Match 1.0%; Score 7; DB 5; Length 1631;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
RESULT 1122  
ID ADG71666 standard; protein; 1666 AA.

DE Chlamydomonas reinhardtii PTB1 protein, SEQ ID NO:1.  
PN JP2003265186-A.  
PD 24-SEP-2003.  
PA (KAGAKU GIJUTSU SHINKO JIGYODAN.  
PA (UNIV.) UNIV TOKYO.  
Query Match 1.0%; Score 7; DB 7; Length 1666;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
RESULT 1123  
ID ABB65038 standard; protein; 1862 AA.  
DE Human diagnostic and therapeutic protein SEQ ID NO:5287.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 1.0%; Score 7; DB 8; Length 1862;  
Best Local Similarity 100.0%; Pred. No. 6.5e+03;  
RESULT 1124  
ID ABB62819 standard; protein; 1963 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 15249.  
PN WO20011042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 1963;  
Best Local Similarity 100.0%; Pred. No. 6.8e+03;  
RESULT 1125  
ID ADG59382 standard; protein; 2910 AA.  
DE Human cancer-associated (CA) protein sequence SEQ ID NO:18.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 1.0%; Score 7; DB 8; Length 2910;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1126  
ID ABB56630 standard; protein; 2911 AA.  
DE Lung cancer-associated polypeptide #223.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.0%; Score 7; DB 6; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1127  
ID ABO07259 standard; protein; 2911 AA.  
DE Human p53 modifying protein, SEQ ID 219.  
PN WO200299122-A1.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 1.0%; Score 7; DB 6; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1128  
ID ADJ68615 standard; protein; 2911 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID21.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 1.0%; Score 7; DB 7; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1129  
ID ADN38844 standard; protein; 2911 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:162.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 1.0%; Score 7; DB 7; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1130  
ID ADQ18204 standard; protein; 2911 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1021.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 1.0%; Score 7; DB 8; Length 2911;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1131  
ID ABB56402 standard; protein; 2912 AA.  
DE Novel human diagnostic protein #6393.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 1.0%; Score 7; DB 4; Length 2912;  
Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
RESULT 1132  
ID AAE20788 standard; protein; 3095 AA.  
DE Rat C3b/C4b complement receptor like protein.  
PN WO200210199-A2.  
PD 07-FEB-2002.  
PA (AMGE-) AMGEN INC.  
Query Match 1.0%; Score 7; DB 5; Length 3095;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
RESULT 1133  
ID AAB23749 standard; protein; 3972 AA.  
DE S. avermitilis avermectin aglycon synthase protein SEQ ID NO:3.  
PN WO200050605-A1.  
PD 31-AUG-2000.  
PA (KITA) KITASATO INST.  
Query Match 1.0%; Score 7; DB 3; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1134  
ID AAG65264 standard; protein; 3972 AA.  
DE Streptomyces avermitilis protein SEQ ID NO: 4.  
PN WO200162939-A1.  
PD 30-AUG-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (KITA) KITASATO INST.  
Query Match 1.0%; Score 7; DB 4; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1135  
ID AAG65268 standard; protein; 3972 AA.  
DE Streptomyces avermitilis protein derivative SEQ ID NO: 8.  
PN WO200162939-A1.  
PD 30-AUG-2001.  
PA (KYOW) KYOWA HAKKO KOGYO KK.  
PA (KITA) KITASATO INST.  
Query Match 1.0%; Score 7; DB 4; Length 3972;  
Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
RESULT 1136  
ID ABB59051 standard; protein; 4547 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3945.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 4547;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
RESULT 1137  
ID ABB65885 standard; protein; 4899 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 24447.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 1.0%; Score 7; DB 4; Length 4899;  
Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
RESULT 1138  
ID ADJ91934 standard; protein; 11877 AA.  
DE Streptomyces venezuelae pik gene cluster protein.  
PN US2003194784-A1.  
PD 16-OCT-2003.  
PA (SHER) SHERMAN D H.  
PA (LIUH/) LIU H.  
PA (XUEY/) XUE Y.  
PA (ZHAO/) ZHAO L.  
Query Match 1.0%; Score 7; DB 8; Length 11877;  
Best Local Similarity 100.0%; Pred. No. 3.5e+04;  
RESULT 1139  
ID AAV77180 standard; protein; 12199 AA.  
DE S. venezuelae pik gene cluster-encoded protein, SEQ ID NO:6.  
PN WO200006620-A2.  
PD 06-JAN-2000.

PA (MINU) UNIV MINNESOTA.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1140  
ID AAR74921 standard; peptide: 8 AA.  
DE Ureaa plasminogen activator residues 173-180.  
PN W0950908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1141  
ID ADD99639 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2631.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1142  
ID ADD97076 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 70.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1143  
ID ADD99119 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2111.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1144  
ID ADD99105 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2097.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1145  
ID ADD99567 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2559.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1146  
ID ADD98532 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 1524.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1147  
ID ADD99106 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2098.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1148  
ID ADD97325 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 319.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1149  
ID ADD99783 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2775.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1150  
ID ADD99689 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2681.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1151  
ID ADD98760 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 1752.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1152  
ID ADD99217 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2209.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1153  
ID ADD97053 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 47.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1154  
ID ADD98456 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 1448.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1155  
ID ADD99266 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 2258.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1156  
ID ADD97623 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 617.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1157  
ID ADD97659 standard; peptide: 9 AA.  
DE Human 193P1E1B protein peptide fragment 653.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1158  
ID ADD99515 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2507.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1159  
ID ADD99936 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2928.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1160  
ID ADD97875 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 869.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1161  
ID ADD99235 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2227.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1162  
ID ADD99455 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2447.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1163  
ID ADD98169 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 1161.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1164  
ID ADD99017 standard; peptide; 9 AA.  
DE Human 193P1E1B protein peptide fragment 2009.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1165  
ID ADO73283 standard; peptide; 9 AA.  
DE Human 213P1F11 HLA motif bearing epitope #7382.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1166  
ID ADO73127 standard; peptide; 9 AA.

DE Human 213P1F11 HLA motif bearing epitope #7226.  
PN US2004019915-A1.  
PD 29-JAN-2004.  
PA (CHAL/) CHALLITA-EID P M.  
PA (RAIT/) RAITANO A B.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (MORR/) MORRISON R K.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1167  
ID ADP51254 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #1448.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1168  
ID ADP52033 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2227.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1169  
ID ADP52487 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #2681.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1170  
ID ADP49876 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #70.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
RESULT 1171  
ID ADP50967 standard; peptide; 9 AA.  
DE Human 193P1E1B epitope #1161.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.



PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1172  
ID ADP52437 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2631.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1173  
ID ADP51917 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2111.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1174  
ID ADP52734 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2928.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1175  
ID ADP52064 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2258.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1176  
ID ADP52313 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2507.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1177  
ID ADP50125 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #319.  
PN US2004102407-A1.

PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1178  
ID ADP51815 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2009.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1179  
ID ADP51903 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2097.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1180  
ID ADP51330 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #1524.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1181  
ID ADP52581 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2775.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1182  
ID ADP52015 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #2209.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A. B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Length 9;  
RESULT 1183  
ID ADP50125 standard; peptide: 9 AA.  
DE Human 193P1E1B epitope #319.  
PN US2004102407-A1.

Best Local Similarity	100.0%;	Pred.No. 1.8e+06;
RESULT 1183		
ID ADP50423 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #617.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
PA (FARI/) FARIS M.		
PA (HUBE/) HUBERT R S.		
PA (GEWM/) GE W.		
PA (JAKO/) JAKOBOVITS A.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;
RESULT 1184		
ID ADP50675 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #869.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
PA (FARI/) FARIS M.		
PA (HUBE/) HUBERT R S.		
PA (GEWM/) GE W.		
PA (JAKO/) JAKOBOVITS A.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;
RESULT 1185		
ID ADP52365 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #2559.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
PA (FARI/) FARIS M.		
PA (HUBE/) HUBERT R S.		
PA (GEWM/) GE W.		
PA (JAKO/) JAKOBOVITS A.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;
RESULT 1186		
ID ADP51558 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #1752.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
PA (FARI/) FARIS M.		
PA (HUBE/) HUBERT R S.		
PA (GEWM/) GE W.		
PA (JAKO/) JAKOBOVITS A.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;
RESULT 1187		
ID ADP52253 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #2447.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
PA (FARI/) FARIS M.		
PA (HUBE/) HUBERT R S.		
PA (GEWM/) GE W.		
PA (JAKO/) JAKOBOVITS A.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;
RESULT 1188		
ID ADP49853 standard; peptide; 9 AA.		
DE Human 193P1E1B epitope #47.		
PN US2004102407-A1.		
PD 27-MAY-2004.		
PA (RAIT/) RAITANO A B.		
PA (CHAL/) CHALLITA-EID P M.		
Query Match		
Best Local Similarity	100.0%;	Score 6; DB 8; Length 9;

[illegible]

ID ADE00128 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3119.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1197  
ID ADE00321 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3312.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1198  
ID ADD98389 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1381.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1199  
ID ADE00477 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3468.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1200  
ID ADD98946 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1038.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1201  
ID ADE00260 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3251.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1202  
ID ADD97458 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 452.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1203  
ID ADD97779 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 773.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1204  
ID ADD97789 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 783.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1205  
ID ADE00572 standard; peptide; 10 AA.

DE Human 193P1E1B protein peptide fragment 3563.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1206  
ID ADD98579 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1571.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1207  
ID ADD98038 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1030.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1208  
ID ADE00277 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3268.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1209  
ID ADE00419 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3410.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1210  
ID ADE00145 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3136.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1211  
ID ADD97471 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 465.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1212  
ID ADD98312 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 1304.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1213  
ID ADE00322 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 3313.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1214  
ID ADD97241 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 235.

PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1215  
ID ADD97805 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 799.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1216  
ID ADD97809 standard; peptide; 10 AA.  
DE Human 193P1E1B protein peptide fragment 803.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1217  
ID ADN14200 standard; peptide; 10 AA.  
DE HIV B cell epitope #58.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (LIFO/) LI F Q.  
PA (CHUY/) CHU Y.  
PA (QUJ/) QU J.  
Query Match 0.8%; Score 6; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1218  
ID ADP53057 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3251.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1219  
ID ADP53216 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3410.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1220  
ID ADP52943 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3137.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1221  
ID ADP53074 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3268.

PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1222  
ID ADP53118 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3312.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1223  
ID ADP50605 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #799.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1224  
ID ADP52942 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3136.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1225  
ID ADP50579 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #773.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1226  
ID ADP52925 standard; peptide; 10 AA.  
DE Human 193P1E1B epitope #3119.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITA-EID P M.  
PA (FARI/) FARI M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOVIĆ A.

Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1227  
ID ADP50014 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #208.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1228  
ID ADP51691 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #1885.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1229  
ID ADP50035 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #229.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1230  
ID ADP53374 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #3468.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1231  
ID ADP50589 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #783.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1232  
ID ADP50609 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #803.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.

PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1233  
ID ADP53369 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #3563.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1234  
ID ADP50836 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #1030.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1235  
ID ADP51110 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #1304.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1236  
ID ADP50271 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #465.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1237  
ID ADP51377 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #1571.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1238  
ID ADP50609 standard; peptide; 10 AA.  
DE Human 193PIE1B epitope #803.  
PD US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.

ID ADP53119 standard; peptide; 10 AA.  
DE Human 193PE1B epitope #3313.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1239  
ID ADP50041 standard; peptide; 10 AA.  
DE Human 193PE1B epitope #235.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1240  
ID ADP50258 standard; peptide; 10 AA.  
DE Human 193PE1B epitope #452.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1241  
ID ADP51187 standard; peptide; 10 AA.  
DE Human 193PE1B epitope #1381.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1242  
ID ADP50844 standard; peptide; 10 AA.  
DE Human 193PE1B epitope #1058.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.3e+02;  
RESULT 1243  
ID AAR74926 standard; peptide; 11 AA.  
DE Urea plasmidogen activator residues 173-182.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1244

ID AAR74924 standard; peptide; 11 AA.  
DE Urea plasmidogen activator residues 173-183.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1245  
ID AAB68774 standard; peptide; 11 AA.  
DE Saccharopolyspora polyspora module I PKS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1246  
ID AAB68770 standard; peptide; 11 AA.  
DE Rat FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1247  
ID AAB68775 standard; peptide; 11 AA.  
DE Streptomyces venezuelae module I PKS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1248  
ID AAB68771 standard; peptide; 11 AA.  
DE Human FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1249  
ID AAB68772 standard; peptide; 11 AA.  
DE Caenorhabditis elegans FAS peptide #1.  
PN WO200104274-A2.  
PD 18-JAN-2001.  
PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1250  
ID AAF10873 standard; peptide; 11 AA.  
DE Bovine uroplakin II protein fragment (1-11 amino acids).  
PN US6290959-B1.  
PD 18-SEP-2001.  
PA (UNIV) UNIV NEW YORK STATE.  
Query Match 0.8%; Score 6; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
RESULT 1251  
ID AAR74922 standard; peptide; 12 AA.  
DE Urea plasmidogen activator residues 173-183.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1252  
ID AAW88589 standard; protein; 12 AA.  
DE Secreted protein encoded by gene 56 clone HE20F09.  
PN WO9854963-A2.  
PD 10-DEC-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1253  
ID ABB50356 standard; protein; 12 AA.

DE Human secreted protein encoded by gene 56 SEQ ID NO:304.  
PN W0200162891-A2.  
PD 30-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1254  
ID ABR38980 standard; peptide; 12 AA.  
DE Human copolysomerase II alpha inhibitory protein fragment #SEQ ID 6.  
PN W02003002737-A1.  
PD 09-JUN-2003.  
PA (RIKE-) RIKEN KK.  
Query Match 0.8%; Score 6; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1255  
ID ABO44613 standard; protein; 12 AA.  
DE Novel human secreted protein #56.  
PN US2003065160-A1.  
PD 03-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1256  
ID ABO26093 standard; protein; 12 AA.  
DE Human protein from novel secreted protein gene 56.  
PN US6525174-B1.  
PD 25-FEB-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 7; Length 12;  
Best Local Similarity 100.0%; Pred. No. 6.2e+02;  
RESULT 1257  
ID AAB01945 standard; peptide; 13 AA.  
DE Human Endothelase 2 repetitive peptide sequence.  
PN W0200136604-A2.  
PD 23-MAY-2001.  
PA (CORV-) CORVAS INT INC.  
Query Match 0.8%; Score 6; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
RESULT 1258  
ID MAG98215 standard; peptide; 14 AA.  
DE Human SNP associated peptide SEQ ID NO. 857.  
PN W0200148245-A2.  
PD 05-JUL-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1259  
ID ABB56699 standard; peptide; 14 AA.  
DE Human SNP related amino acid sequence SEQ ID NO:1464.  
PN W0200138586-A2.  
PD 31-MAY-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 0.8%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1260  
ID ABG67423 standard; peptide; 14 AA.  
DE Human ADP1 tryptic digest peptide #132.  
PN W0200246767-A2.  
PD 13-JUN-2002.  
PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
Query Match 0.8%; Score 6; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1261  
ID ADZ3531 standard; peptide; 14 AA.  
DE Alzheimer's disease-associated protein isoform tryptic peptide #140.  
PN US2003064411-A1.  
PD 03-APR-2003.  
PA (HERA/) HERATH H M A C.  
PA (PARE/) PAREKH R B.  
PA (ROHL/) ROHLF C.  
Query Match 0.8%; Score 6; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1262

ID ADM14199 standard; peptide; 14 AA.  
DE HIV B cell epitope #57.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (LIPO/) LI P Q.  
PA (CHUY/) CHU Y.  
PA (QIU/) QIU J.  
Query Match 0.8%; Score 6; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1263  
ID ADO34385 standard; peptide; 14 AA.  
DE Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 162.  
PN W02004043403-A2.  
PD 27-MAY-2004.  
PA (UABR-) UAB RES FOUND.  
Query Match 0.8%; Score 6; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1264  
ID ADO34421 standard; peptide; 14 AA.  
DE Synthetic apolipoprotein-B mimicking peptide, SEQ ID No 198.  
PN W02004043403-A2.  
PD 27-MAY-2004.  
PA (UABR-) UAB RES FOUND.  
Query Match 0.8%; Score 6; DB 8; Length 14;  
Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
RESULT 1265  
ID AAG78745 standard; peptide; 15 AA.  
DE Human ribose phosphate glycine amide synthetase 12 N-terminus.  
PN W0200173065-A1.  
PD 04-OCT-2001.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 0.8%; Score 6; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1266  
ID ADE00866 standard; peptide; 15 AA.  
DE Human 193P1B1B protein peptide fragment 3857.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1267  
ID ADE00911 standard; peptide; 15 AA.  
DE Human 193P1B1B protein peptide fragment 3902.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1268  
ID ADE01040 standard; peptide; 15 AA.  
DE Human 193P1B1B protein peptide fragment 4031.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1269  
ID ADE00912 standard; peptide; 15 AA.  
DE Human 193P1B1B protein peptide fragment 3903.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1270  
ID ADE00664 standard; peptide; 15 AA.  
DE Human 193P1B1B protein peptide fragment 3655.  
PN W02003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1271

RESULT 1271  
ID ADE00810 standard; peptide; 15 AA.  
DE Human 193PIB1B protein peptide fragment 3801.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1272  
ID ADE00966 standard; peptide; 15 AA.  
DE Human 193PIB1B protein peptide fragment 3957.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1273  
ID ADE01108 standard; peptide; 15 AA.  
DE Human 193PIB1B protein peptide fragment 4099.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1274  
ID ADE01070 standard; peptide; 15 AA.  
DE Human 193PIB1B protein peptide fragment 4061.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1275  
ID ADE00825 standard; peptide; 15 AA.  
DE Human 193PIB1B protein peptide fragment 3816.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1276  
ID ADP53709 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #3903.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1277  
ID ADP53622 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #3816.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1278  
ID ADP53837 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #4031.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1279  
ID ADP53663 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #3857.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1280  
ID ADP53763 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #3957.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1281  
ID ADP53461 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #3655.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1282  
ID ADP53905 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #4099.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1283  
ID ADP53667 standard; peptide; 15 AA.  
DE Human 193PIB1B epitope #4061.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALITTA-EID P M.  
PA (FARI/) PARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1284  
ID ADP53607 standard; peptide; 15 AA.



DE Human 193P1E1B epitope #3801.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1285  
ID ADP53708 standard; peptide: 15 AA.  
DE Human 193P1E1B epitope #3902.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARI S M.  
PA (HUBE/) HUBERT R S.  
PA (GEMW/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
RESULT 1286  
ID AAR83658 standard; peptide: 17 AA.  
DE Insect haemolymph antibacterial polypeptide #8.  
PN WO9523513-A1.  
PD 08-SEP-1995.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 0.8%; Score 6; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 8.6e+02;  
RESULT 1287  
ID AAR74918 standard; peptide: 18 AA.  
DE Urea plasminogen activator residues 163-180.  
PN WO9309908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1288  
ID AAR9573 standard; peptide: 18 AA.  
DE Wasp venom Bhrx-1 subunit (b).N-terminal peptide.  
PN WO9616171-A1.  
PD 30-MAY-1996.  
PA (ZENE) ZENEGA LTD.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 0.8%; Score 6; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 9e+02;  
RESULT 1289  
ID AD129454 standard; peptide: 19 AA.  
DE ErbB ligand HB-EGF CCF/F motif peptide.  
PN WO2004005320-A2.  
PD 15-JAN-2004.  
PA (UMOR) UNIV MISSOURI.  
Query Match 0.8%; Score 6; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.5e+02;  
RESULT 1290  
ID AAR83657 standard; peptide: 20 AA.  
DE Insect haemolymph antibacterial polypeptide #7.  
PN WO9523513-A1.  
PD 08-SEP-1995.  
PA (SLOK) SLOAN KETTERING INST CANCER RES.  
Query Match 0.8%; Score 6; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1291  
ID ABU08144 standard; peptide: 20 AA.  
DE Human IL-1 RI signal peptide.  
PN GB2375604-A.  
PD 20-NOV-2002.  
PA (WARN) WARNER LAMBERT CO.  
Query Match 0.8%; Score 6; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;

RESULT 1292  
ID ADG17865 standard; peptide: 20 AA.  
DE Binding affinity measurement-related peptide Segid67.  
PN WO2003089662-A1.  
PD 30-OCT-2003.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 0.8%; Score 6; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1293  
ID ADK52540 standard; peptide: 20 AA.  
DE Fungal mycotoxin biosynthetic protein consensus sequence #2.  
PN EP1329521-A1.  
PD 23-JUL-2003.  
PA (EVIA/) EVIALIS T.  
Query Match 0.8%; Score 6; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1294  
ID ADN14077 standard; peptide: 20 AA.  
DE HIV helper T cell epitope #44.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (LIFC/) LI F Q.  
PA (CHUY/) CHU Y.  
PA (QIU/) QIU J.  
Query Match 0.8%; Score 6; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1295  
ID ADN14201 standard; peptide: 20 AA.  
DE HIV B cell epitope #59.  
PN US2003049253-A1.  
PD 13-MAR-2003.  
PA (LIFC/) LI F Q.  
PA (CHUY/) CHU Y.  
PA (QIU/) QIU J.  
Query Match 0.8%; Score 6; DB 7; Length 20;  
Best Local Similarity 100.0%; Pred. No. 9.9e+02;  
RESULT 1296  
ID AAB89179 standard; peptide: 21 AA.  
DE HIV gp120 protein binding peptide #272.  
PN WO200116182-A2.  
PD 08-MAR-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 0.8%; Score 6; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1297  
ID AAB89181 standard; peptide: 21 AA.  
DE HIV gp120 protein binding peptide #274.  
PN WO200116182-A2.  
PD 08-MAR-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 0.8%; Score 6; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1298  
ID AAB89180 standard; peptide: 21 AA.  
DE HIV gp120 protein binding peptide #273.  
PN WO200116182-A2.  
PD 08-MAR-2001.  
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
Query Match 0.8%; Score 6; DB 4; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1299  
ID AAU89796 standard; peptide: 21 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #1752.  
PN WO200172771-A2.  
PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
PA (NOVO) NOVO NORDISK AS.  
Query Match 0.8%; Score 6; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1300  
ID AAU89556 standard; peptide: 21 AA.  
DE Insulin/insulin-like growth factor receptor-binding peptide #1512.  
PN WO200172771-A2.

PD 04-OCT-2001.  
PA (DGIB-) DGI BIOTECHNOLOGIES LLC.  
Query Match 0.8%; Score 6; DB 5; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
RESULT 1301  
ID AAM18205 standard; protein; 22 AA.  
DE Peptide #4639 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1302  
ID AAM47407 standard; peptide; 22 AA.  
DE Peptide #57 for illustrating method of anticipating protein interaction.  
PN WO200167299-A1.  
PD 13-SEP-2001.  
PA (DNUC) DAICHI PHARM CO LTD.  
PA (FUIT) FUJITSU LTD.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1303  
ID ABB31987 standard; peptide; 22 AA.  
DE Peptide #4638 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1304  
ID ABB22530 standard; protein; 22 AA.  
DE Protein #4529 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1305  
ID AAM70365 standard; protein; 22 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30671.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1306  
ID AAM57939 standard; protein; 22 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30044.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1307  
ID ABB32060 standard; peptide; 22 AA.  
DE Human liver peptide, SEQ ID NO 30708.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1308  
ID AAM05822 standard; protein; 22 AA.  
DE Peptide #4504 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1309  
ID ABB28549 standard; protein; 22 AA.  
DE Novel human diagnostic protein #28540.

PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HXSE-) HYSECO INC.  
Query Match 0.8%; Score 6; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1310  
ID ABB40009 standard; peptide; 22 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29674.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1311  
ID AAO20901 standard; peptide; 22 AA.  
DE Swine fever envelope protein E2 fragment #5.  
PN WO200232453-A1.  
PD 25-APR-2002.  
PA (UYOI) UNIV QINGHUA.  
PA (BEIJ-) BEIJING FEIKAI BIOTECH CO LTD.  
Query Match 0.8%; Score 6; DB 5; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1312  
ID AAM19926 standard; protein; 23 AA.  
DE Peptide #6360 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1313  
ID ABB3934 standard; peptide; 23 AA.  
DE Peptide #7440 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1314  
ID AAM33553 standard; protein; 23 AA.  
DE Peptide #7590 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1315  
ID ABB24479 standard; protein; 23 AA.  
DE Protein #6478 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1316  
ID AAM73351 standard; protein; 23 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33657.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1317  
ID AAM60679 standard; protein; 23 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32784.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1318  
ID ABB55067 standard; peptide; 23 AA.  
DE Human liver peptide, SEQ ID NO 33715.

PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1319  
ID A0643304 standard; peptide: 23 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 32869.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 23;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
RESULT 1320  
ID A0693103 standard; peptide: 25 AA.  
DE CD4 anti-receptor peptide.  
PN W08090782-A.  
PD 19-OCT-1989.  
PA (USDC) US SEC OF COMMERCE.  
Query Match 0.8%; Score 6; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1321  
ID A0674927 standard; peptide: 25 AA.  
DE Urea plasmidogen activator residues 163-186.  
PN W05050908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1322  
ID A0671483 standard; peptide: 25 AA.  
DE *Escherichia chaffeensis* p28 protein N-terminal signal peptide.  
PN W0200032745-A2.  
PD 08-JUN-2000.  
PA (REBE-) RES DEV FOUND.  
Query Match 0.8%; Score 6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1323  
ID A0696113 standard; peptide: 25 AA.  
DE *S. pyogenes* hyperimmune system reactive antigen SPO0287.4.  
PN W02004078907-A2.  
PD 16-SEP-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 0.8%; Score 6; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
RESULT 1324  
ID A0684080 standard; peptide: 26 AA.  
DE *S. pyogenes* hyperimmune system reactive antigen SPO0287.4.  
PN W02004078907-A2.  
PD 16-SEP-2004.  
PA (INTE-) INTERCELL AG.  
Query Match 0.8%; Score 6; DB 8; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1325  
ID A0611853 standard; peptide: 27 AA.  
DE Bel natriuretic peptide.  
PN JPO3074400-A.  
PD 28-MAR-1991.  
PA (SMIB-) SMI BRYSTOL KK.  
Query Match 0.8%; Score 6; DB 2; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1326  
ID A0691306 standard; peptide: 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:482.  
PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONUICHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1327  
ID A0691315 standard; peptide: 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:491.

PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONUICHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1328  
ID A0691325 standard; peptide: 27 AA.  
DE Atrial-natriuretic peptide (ANP) SEQ ID NO:501.  
PN W0200069900-A2.  
PD 23-NOV-2000.  
PA (CONU-) CONUICHEM INC.  
Query Match 0.8%; Score 6; DB 4; Length 27;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1329  
ID A0626346 standard; peptide: 28 AA.  
DE Spacer oligopeptide D28.  
PN JPO4190791-A.  
PD 09-JUL-1992.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 28;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
RESULT 1330  
ID A0671663 standard; peptide: 29 AA.  
DE Modified urinary plasmidogen activator residues 159-188.  
PN JPO7039374-A.  
PD 10-FEB-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 29;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1331  
ID A0626347 standard; peptide: 30 AA.  
DE Spacer oligopeptide D30.  
PN JPO4190791-A.  
PD 09-JUL-1992.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1332  
ID A0642811 standard; peptide: 30 AA.  
DE U-PA (159-188).  
PN W09320194-A1.  
PD 14-OCT-1993.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1333  
ID A0672872 standard; peptide: 30 AA.  
DE Urokinase peptide fragment from amino acids 159-188.  
PN JPO7075580-A.  
PD 20-MAR-1995.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1334  
ID A0693589 standard; peptide: 30 AA.  
DE UK t-PA hybrid peptide CS19 residues 276-306.  
PN W09508908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1335  
ID A0693591 standard; peptide: 30 AA.  
DE UK t-PA hybrid peptide CS21 residues 276-306.  
PN W09508908-A1.  
PD 13-APR-1995.  
PA (SUMU) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1336  
ID A0676947 standard; peptide: 30 AA.  
DE UK t-PA hybrid peptide CS16 residues 276-306.  
PN W09508908-A1.

PD 13-APR-1995.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1337  
ID AAR76946 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS15 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1338  
ID AAR93592 standard; peptide; 30 AA.  
DE UK t-PA hybrid peptide CS12 residues 276-306.  
PN WO9509908-A1.  
PD 13-APR-1995.  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1339  
ID AAR71666 standard; peptide; 30 AA.  
DE Modified urinary plasminogen activator residues 159-188.  
PN JP07039374-A.  
PD 10-FEB-1995.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
RESULT 1340  
ID AAR72874 standard; peptide; 31 AA.  
DE t-PA peptide fragment from amino acids 276-306.  
PN JP07075580-A.  
PD 20-MAR-1995.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1341  
ID AAR79104 standard; peptide; 31 AA.  
DE Wild type tissue plasminogen activator residues 276-306.  
PN JP07039374-A.  
PD 10-FEB-1995.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1342  
ID AAM05988 standard; protein; 31 AA.  
DE Peptide #4670 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 31;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1343  
ID AAR24949 standard; peptide; 32 AA.  
DE Urokinase fragment.  
PN JP04144682-A.  
PD 19-MAY-1992.  
PA (SUMU ) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
RESULT 1344  
ID AAM16011 standard; protein; 33 AA.  
DE Peptide #2445 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1345  
ID AAB835004 standard; peptide; 33 AA.  
DE Peptide #2510 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1346  
ID AAM28512 standard; protein; 33 AA.  
DE Peptide #2549 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1347  
ID ABB20416 standard; protein; 33 AA.  
DE Protein #2415 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1348  
ID AAM68189 standard; protein; 33 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28495.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1349  
ID AAM00415 standard; protein; 33 AA.  
DE Human polypeptide SEQ ID NO 14307.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1350  
ID AAM55815 standard; protein; 33 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27920.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1351  
ID ABA49840 standard; peptide; 33 AA.  
DE Human liver peptide, SEQ ID NO 28488.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1352  
ID AAM03745 standard; protein; 33 AA.  
DE Peptide #2427 encoded by probe for measuring breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1353  
ID ABR72758 standard; peptide; 33 AA.  
DE Anticancer peptide derived from human thrombin.  
PN WO2003013569-A2.  
PD 20-FEB-2003.  
PA (TEXA ) UNIV TEXAS SYSTEM.  
Query Match 0.8%; Score 6; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1354  
ID ABR72759 standard; peptide; 33 AA.  
DE Anticancer peptide derived from human thrombin.  
PN WO2003013569-A2.  
PD 20-FEB-2003.  
PA (TEXA ) UNIV TEXAS SYSTEM.

Query Match 0.8%; Score 6; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
RESULT 1355  
ID AAR74068 standard; peptide; 35 AA.  
DE Superantigen peptide HIV Nef(31-65).  
PN WO9511975-A2.  
PD 04-MAY-1995.  
PA (UYFL) UNIV FLORIDA.  
Query Match 0.8%; Score 6; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1356  
ID AAY39987 standard; peptide; 35 AA.  
DE HIV Negative factor (Nef) protein residues 31-65.  
PN US968514-A.  
PD 19-OCT-1999.  
PA (UYFL) UNIV FLORIDA.  
Query Match 0.8%; Score 6; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1357  
ID ABU61264 standard; peptide; 35 AA.  
DE Human A domain from APOER2 #7.  
PN WO200288171-A2.  
PD 07-NOV-2002.  
PA (MAXI-) MAXIGEN INC.  
Query Match 0.8%; Score 6; DB 6; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1358  
ID ADP21486 standard; peptide; 35 AA.  
DE Human LDL receptor A domain peptide SegID 62.  
PN WO2004044011-A2.  
PD 27-MAY-2004.  
PA (AVID-) AVIDIA RES INST.  
Query Match 0.8%; Score 6; DB 8; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1359  
ID AA002449 standard; protein; 36 AA.  
DE Human polypeptide SEQ ID NO 16341.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1360  
ID AAR97691 standard; protein; 37 AA.  
DE Rat P865 MW domain-1.  
PN WO9617061-A1.  
PD 06-JUN-1996.  
PA (UYRQ) UNIV ROCKEFELLER.  
PA (DELB-) DELBRUECK CENT MOLECULAR MEDICINE MAX.  
Query Match 0.8%; Score 6; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1361  
ID AAW21577 standard; protein; 37 AA.  
DE Alzheimer's disease protein encoded by DNA from plasmid pGCS1243.  
PN WO9721807-A1.  
PD 19-JUN-1997.  
PA (KYOW) KYOWA HAKKO KOCYO KK.  
Query Match 0.8%; Score 6; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1362  
ID AAY48444 standard; protein; 37 AA.  
DE Human prostate cancer-associated protein 141.  
PN DE19811194-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 0.8%; Score 6; DB 2; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1363  
ID AAB21981 standard; peptide; 37 AA.  
DE F865/rae peptide containing a WW-domain #2.  
PN WO2004048621-A2.  
PD 24-AUG-2000.  
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

Query Match 0.8%; Score 6; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1364  
ID AAR83566 standard; protein; 37 AA.  
DE Colicin N 40-76 amino acid sequence SEQ ID NO:33.  
PN WO2003057708-A2.  
PD 17-JUL-2003.  
PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.  
Query Match 0.8%; Score 6; DB 6; Length 37;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
RESULT 1365  
ID AAR74067 standard; peptide; 38 AA.  
DE Superantigen peptide HIV Nef(1-38).  
PN WO9511975-A2.  
PD 04-MAY-1995.  
PA (UYFL) UNIV FLORIDA.  
Query Match 0.8%; Score 6; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1366  
ID AAY39972 standard; peptide; 38 AA.  
DE HIV Negative factor (Nef) protein residues 1-38.  
PN US968514-A.  
PD 19-OCT-1999.  
PA (UYFL) UNIV FLORIDA.  
Query Match 0.8%; Score 6; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1367  
ID AAB70442 standard; peptide; 38 AA.  
DE L. lactis signal peptide SP310 mutant amino acid sequence SEQ:55.  
PN WO20011060-A2.  
PD 15-FEB-2001.  
PA (BIOT-) BIOTEKNOLOGISK INST.  
Query Match 0.8%; Score 6; DB 4; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1368  
ID ABO58270 standard; protein; 38 AA.  
DE Human genome derived single exon protein #4504.  
PN US2003194704-A1.  
PD 16-OCT-2003.  
PA (PENNY) PENN S. G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 0.8%; Score 6; DB 8; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1369  
ID AAR64211 standard; peptide; 39 AA.  
DE Urinary plasminogen activator residues 150-188.  
PN JP06327473-A.  
PD 29-NOV-1994.  
PA (SUMU) SUMITOMO SEIVAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1370  
ID AA011683 standard; protein; 39 AA.  
DE Human polypeptide SEQ ID NO 25575.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1371  
ID AAB32936 standard; peptide; 39 AA.  
DE Human albumin-CD4 fusion protein junction peptide.  
PN WO200279232-A2.  
PD 10-OCT-2002.  
PA (LEXI-) LEXIGEN PHARM CORP.  
Query Match 0.8%; Score 6; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1372  
ID AAB32648 standard; peptide; 39 AA.  
DE Albumin-CD4 fusion protein junction peptide.  
PN WO200279415-A2.  
PD 10-OCT-2002.

PA (LEXI-) LEXIGEN PHARM CORP.  
Query Match 0.8%; Score 6; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1373  
ID ADF75022 standard; peptide; 39 AA.  
DE Human serum albumin-CD4 fusion protein junction sequence.  
PN US200316687-A1.  
PD 04-SEP-2003.  
PA (LEXI-) LEXIGEN PHARM CORP.  
Query Match 0.8%; Score 6; DB 7; Length 39;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
RESULT 1374  
ID AAF71494 standard; protein; 40 AA.  
DE Antigenic peptide cross-reactive with HTLV-III env protein 3'ORF.  
PN WO8702988-A.  
PD 21-MAY-1987.  
PA (HARD) HARVARD COLLEGE.  
Query Match 0.8%; Score 6; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1375  
ID AAY48263 standard; protein; 40 AA.  
DE Human prostate cancer-associated protein 49.  
PN DE1981193-A1.  
PD 16-SEP-1999.  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
Query Match 0.8%; Score 6; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1376  
ID AAR09340 standard; protein; 40 AA.  
DE Hepatitis GB virus protein sequence SEQ ID NO:467.  
PN US6051374-A.  
PD 18-APR-2000.  
PA (ABBQ) ABBOTT LAB.  
Query Match 0.8%; Score 6; DB 3; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1377  
ID AAE23150 standard; peptide; 40 AA.  
DE Influenza A virus subtype 16 haemagglutinin (HA) protein fragment #14.  
PN WO200224734-A2.  
PD 28-MAR-2002.  
PA (CHIR-) CHIRON SPA.  
Query Match 0.8%; Score 6; DB 5; Length 40;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1378  
ID AAR07101 standard; protein; 41 AA.  
DE Melanocyte-stimulating hormone inhibitor #6.  
PN EP389950-A.  
PD 03-OCT-1990.  
PA (LLOY) LLOYD CORP.  
Query Match 0.8%; Score 6; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1379  
ID AAW24762 standard; peptide; 42 AA.  
DE Adhesin Pcr44 N-terminal peptide.  
PN WO9716542-A1.  
PD 09-MAY-1997.  
PA (UYME) UNIV MELBOURNE.  
Query Match 0.8%; Score 6; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1380  
ID AAC02438 standard; protein; 42 AA.  
DE Human polypeptide SEQ ID NO 16330.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1381  
ID ABO60596 standard; protein; 42 AA.  
DE Human genome derived single exon protein #6830.  
PN US2003194704-A1.  
PD 16-OCT-2003.

PA (PENN/) PENN S G.  
PA (RANK/) RANK D R.  
PA (HANZ/) HANZEL D K.  
Query Match 0.8%; Score 6; DB 8; Length 42;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
RESULT 1382  
ID AAR58896 standard; protein; 43 AA.  
DE Human-223 cadherin-related molecule.  
PN WO9414960-A2.  
PD 07-JUL-1994.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1383  
ID AAR87135 standard; peptide; 43 AA.  
DE Protocadherin clone HUMAN-223.  
PN WO9600289-A1.  
PD 04-JAN-1996.  
PA (DOHE-) DOHENY EYE INST.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1384  
ID AAY21020 standard; protein; 43 AA.  
DE Human glial fibrillary acidic protein GFAP mutant fragment 29.  
PN WO9845322-A2.  
PD 15-OCT-1998.  
PA (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.  
PA (UYRO-) UNIV ROTTERDAM ERASMUS.  
PA (UYUT-) RIJKSUNIV UTRECHT.  
Query Match 0.8%; Score 6; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1385  
ID AAY32350 standard; peptide; 43 AA.  
DE Human C1qR EGF-2 peptide.  
PN WO9955839-A1.  
PD 04-NOV-1999.  
PA (REGC) UNIV CALIFORNIA.  
Query Match 0.8%; Score 6; DB 3; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1386  
ID ABG77431 standard; protein; 43 AA.  
DE Selected interacting domain (SID) polypeptide #242.  
PN WO200259255-A2.  
PD 01-AUG-2002.  
PA (HYBR-) HYBRIGENICS.  
Query Match 0.8%; Score 6; DB 5; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1387  
ID AAE30226 standard; peptide; 43 AA.  
DE Human LP288 YWTD island 2 repeat peptide #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 0.8%; Score 6; DB 6; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1388  
ID ADR51552 standard; protein; 43 AA.  
DE DR-binding receptor region of HB-EGF from humans.  
PN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1389  
ID ADR51550 standard; protein; 43 AA.  
DE DR-binding receptor region of HB-EGF from pigs.  
PN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 43;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1390  
ID AAC01303 standard; protein; 44 AA.

DE Human polypeptide SEQ ID NO 15195.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1391  
ID ABR51549 standard; protein; 44 AA.  
DE DT-binding receptor region of HB-EGF from rabbit.  
PN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1392  
ID ABR51551 standard; protein; 44 AA.  
DE DT-binding receptor region of HB-EGF from monkeys.  
PN WO2004069870-A2.  
PD 19-AUG-2004.  
PA (UYLE-) RIJKSUNIV LEIDEN.  
Query Match 0.8%; Score 6; DB 8; Length 44;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
RESULT 1393  
ID AAR64212 standard; peptide; 45 AA.  
DE Urinary plasminogen activator residues 159-203.  
PN JP0637473-A.  
PD 29-NOV-1994.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Query Match 0.8%; Score 6; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1394  
ID AAY08546 standard; protein; 45 AA.  
DE C-terminal alpha-CTD protein fragment FTSH\_HELPY.  
PN WO9925733-A2.  
PD 27-MAY-1999.  
PA (YISS) YISSUM RES & DEV CO.  
Query Match 0.8%; Score 6; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1395  
ID AAG2119 standard; protein; 45 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23559.  
PN EP033405-A2.  
PD 06-SEP-2000.  
Query Match 0.8%; Score 6; DB 3; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1396  
ID AAM1431 standard; protein; 45 AA.  
DE Peptide #665 encoded by probe for measuring cervical gene expression.  
PN WO200157278-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1397  
ID ABB33178 standard; peptide; 45 AA.  
DE Peptide #684 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1398  
ID AAM26641 standard; protein; 45 AA.  
DE Peptide #678 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1399  
ID ABB28006 standard; peptide; 45 AA.  
DE Human peptide #657 encoded by breast cell single exon nucleic acid probe.  
PN WO200157271-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1400  
ID ABB16643 standard; protein; 45 AA.  
DE Protein #642 encoded by probe for measuring heart cell gene expression.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1401  
ID AAM66362 standard; protein; 45 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26668.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1402  
ID AAM53974 standard; protein; 45 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26079.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1403  
ID AAG48028 standard; peptide; 45 AA.  
DE Human liver peptide, SEQ ID NO 26676.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1404  
ID AAM01963 standard; protein; 45 AA.  
DE Peptide #645 encoded by probe for measuring human breast gene expression.  
PN WO200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1405  
ID AAG36010 standard; peptide; 45 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 25675.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1406  
ID ADN05538 standard; protein; 45 AA.  
DE Antipeptidic protein sequence #935.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PA (GERTH) GENEVECH INC.  
Query Match 0.8%; Score 6; DB 8; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1407  
ID ABB03327 standard; protein; 46 AA.  
DE Human musculoskeletal system related polypeptide SEQ ID NO 1274.  
PN WO200155367-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1408  
ID AAO01399 standard; protein; 46 AA.  
DE Human polypeptide SEQ ID NO 15291.  
PN WO200164835-A2.  
PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1409  
ID AAC08005 standard; protein; 46 AA.  
DE Human polypeptide SEQ ID NO 21897.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1410  
ID ADH32592 standard; protein; 46 AA.  
DE Yeast smORF387-encoded polypeptide, SEQ ID NO:1050.  
PN WO200268693-A2.  
PD 06-SEP-2002.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 0.8%; Score 6; DB 5; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1411  
ID ABU12621 standard; protein; 46 AA.  
DE Novel human musculoskeletal system antigen #241.  
PN US2002147140-A1.  
PD 10-OCT-2002.  
PA (ROSE/) ROSEN C A.  
PA (ROBE/) ROSEN S M.  
PA (BARA/) BARASH S C.  
Query Match 0.8%; Score 6; DB 6; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1412  
ID ADJ28647 standard; protein; 46 AA.  
DE Human musculoskeletal system-associated protein - SEQ ID 1274.  
PN US2004009488-A1.  
PD 15-JAN-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 0.8%; Score 6; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1413  
ID ADS07325 standard; protein; 46 AA.  
DE Staphylococcus epidermis polypeptide seqid 6620.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BOSH/) BOSH D.  
Query Match 0.8%; Score 6; DB 8; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
RESULT 1414  
ID AAW28321 standard; protein; 47 AA.  
DE Staphylococcus aureus protein of unknown function.  
PN WO9730070-A1.  
PD 21-AUG-1997.  
PA (SMIX) SMITHKLINE BEECHAM CORP.  
Query Match 0.8%; Score 6; DB 2; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1415  
ID AAG18782 standard; protein; 47 AA.  
DE Zea mays protein fragment SEQ ID NO: 20328.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match 0.8%; Score 6; DB 3; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1416  
ID AAM47202 standard; peptide; 47 AA.  
DE Modular enzyme system related ACP-domain N-terminal peptide AVEA1\_3.  
PN WO200181564-A2.  
PD 01-NOV-2001.  
PA (ACTI-) ACTINODRUG PHARM GMBH.  
Query Match 0.8%; Score 6; DB 5; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1417  
ID ADP96929 standard; protein; 47 AA.  
DE Human 193P1E1B protein variant 1 fragment #2.  
PN WO2003050255-A2.  
PD 19-JUN-2003.  
PA (AGEN-) AGENSYS INC.  
Query Match 0.8%; Score 6; DB 7; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1418  
ID ADP49728 standard; peptide; 47 AA.  
DE Human 193P1E1Bv.1.  
PN US2004102407-A1.  
PD 27-MAY-2004.  
PA (RAIT/) RAITANO A B.  
PA (CHAL/) CHALLITA-EID P M.  
PA (FARI/) FARIS M.  
PA (HUBE/) HUBERT R S.  
PA (GEWM/) GE W.  
PA (JAKO/) JAKOBOVITS A.  
Query Match 0.8%; Score 6; DB 8; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1419  
ID AAB33113 standard; protein; 48 AA.  
DE Pinus radiata transcription factor protein sequence #240.  
PN WO200053724-A2.  
PD 14-SEP-2000.  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
Query Match 0.8%; Score 6; DB 3; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1420  
ID ABP43712 standard; protein; 48 AA.  
DE PRO566 protein.  
PN WO200231111-A2.  
PD 18-APR-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 0.8%; Score 6; DB 5; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1421  
ID AAE36818 standard; protein; 48 AA.  
DE Human HB-EGF domain.  
PN WO2003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOM-) BIOMOLECULAR RES INST LTD.  
PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match 0.8%; Score 6; DB 6; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1422  
ID ADN48881 standard; peptide; 48 AA.  
DE Heparin-binding epidermal-growth factor (HB-EGF) peptide.  
PN US6727077-B1.  
PD 27-APR-2004.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (GEOU) UNIV GEORGETOWN MEDICAL CENT.  
Query Match 0.8%; Score 6; DB 8; Length 48;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1423  
ID ABB38598 standard; peptide; 49 AA.  
DE Peptide #6104 encoded by human foetal liver single exon probe.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1424  
ID AAM32054 standard; protein; 49 AA.  
DE Peptide #6091 encoded by probe for measuring placental gene expression.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; Length 49;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
RESULT 1425  
ID AAM71762 standard; protein; 49 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32068.



PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 49;  
PRED. No. 2.2e+03;  
RESULT 1426  
ID AAM59226 standard; protein; 49 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 31331.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 49;  
PRED. No. 2.2e+03;  
RESULT 1427  
ID ABG53447 standard; peptide; 49 AA.  
DE Human liver peptide, SEQ ID No 32095.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 49;  
PRED. No. 2.2e+03;  
RESULT 1428  
ID ABG41576 standard; peptide; 49 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 31241.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 5; Length 49;  
PRED. No. 2.2e+03;  
RESULT 1429  
ID ADK14940 standard; protein; 49 AA.  
DE Urinary specific protein #46.  
PN W02003057839-A2.  
PD 17-JUL-2003.  
PA (DIAD-) DIADEXUS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 7; Length 49;  
PRED. No. 2.2e+03;  
RESULT 1430  
ID AAG04489 standard; protein; 50 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 535.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 3; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1431  
ID AAG37508 standard; protein; 50 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46130.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 3; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1432  
ID ABB22229 standard; protein; 50 AA.  
DE Protein #4228 encoded by probe for measuring heart cell gene expression.  
PN W0200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1433  
ID AAM70055 standard; protein; 50 AA.  
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30361.  
PN W0200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1434  
ID AAN40213 standard; protein; 50 AA.  
DE Propionibacterium acnes immunogenic protein #1109.  
PN W0200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.

Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1435  
ID AAM57648 standard; protein; 50 AA.  
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 29753.  
PN W0200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1436  
ID ABG51748 standard; peptide; 50 AA.  
DE Human liver peptide, SEQ ID No 30396.  
PN W0200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1437  
ID AAM05532 standard; protein; 50 AA.  
DE Peptide #4214 encoded by probe for measuring breast gene expression.  
PN W0200157270-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 4; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1438  
ID ABG39686 standard; peptide; 50 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 29351.  
PN W0200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 5; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1439  
ID ABM36732 standard; protein; 50 AA.  
DE Propionibacterium acnes predicted ORF-encoded polypeptide #1408.  
PN W02003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 6; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1440  
ID AAE36799 standard; protein; 50 AA.  
DE Human HB-EGF protein BGF-like domain.  
PN W02003014159-A1.  
PD 20-FEB-2003.  
PA (CSIR-) COMMONWEALTH SCI & IND RES ORG.  
PA (BIOM-) BIOMOLECULAR RES INST LTD.  
PA (HALT-) HALT INST MEDICAL RES WALTER & ELIZA.  
PA (LUDW-) LUDWIG INST CANCER RES.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 6; Length 50;  
PRED. No. 2.3e+03;  
RESULT 1441  
ID AAM67925 standard; protein; 51 AA.  
DE Fragment of human secreted protein encoded by gene 3.  
PN W09842738-A1.  
PD 01-OCT-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 2; Length 51;  
PRED. No. 2.3e+03;  
RESULT 1442  
ID AAG04468 standard; protein; 51 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 534.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Query Match  
Best Local Similarity 100.0%; Score 6; DB 3; Length 51;  
PRED. No. 2.3e+03;  
RESULT 1443  
ID AAG37507 standard; protein; 51 AA.  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 46129.  
PN EP1033405-A2.  
PD 06-SEP-2000.

```
Query Match 0.8%; Score 6; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1444
ID AAU53334 standard; protein; 51 AA.
DE Propionibacterium acnes immunogenic protein #14230.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1445
ID ABP11027 standard; protein; 51 AA.
DE Human OREF protein sequence SEQ ID NO:22036.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 0.8%; Score 6; DB 5; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1446
ID ABW49853 standard; protein; 51 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #14529.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
RESULT 1447
ID AAW21562 standard; protein; 52 AA.
DE LENO rat cholecystokinin-A receptor fragment, encoded by exon 1.
PN JP09065900-A.
PD 11-MAR-1997.
PA (SHO-) SHIONOGI & CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1448
ID AAR4514 standard; protein; 53 AA.
DE Plasmid pCDM8-D09 - D44 fragment D09.
PN WO9324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1449
ID AAW91699 standard; protein; 53 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:19292.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1450
ID AAM00082 standard; protein; 53 AA.
DE Sucrose transporter sequence #150.
PN WO200144476-A2.
PD 21-JUN-2001.
PA (BAI-) BASF PLANT SCI GMBH.
Query Match 0.8%; Score 6; DB 4; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
RESULT 1451
ID AAR64213 standard; peptide; 54 AA.
DE Urinary plasminogen activator residues 150-203.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1452
ID AAW46238 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #7134.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1453
ID AAW39328 standard; protein; 54 AA.
DE Propionibacterium acnes immunogenic protein #224.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1454
ID ABU02285 standard; protein; 54 AA.
DE S. pneumoniae type 4 strain protein from coding region #1863.
PN WO00277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1455
ID ABW42757 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7433.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1456
ID ABW35847 standard; protein; 54 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #523.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1457
ID AAR45145 standard; protein; 55 AA.
DE Plasmid pCDM8-D09 - D44 fragment D11.
PN WO9324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1458
ID AAR45146 standard; protein; 56 AA.
DE Plasmid pCDM8-D09 - D44 fragment D(1+11).
PN WO9324624-A1.
PD 09-DEC-1993.
PA (SUMU-) SUMITOMO PHARM CO LTD.
Query Match 0.8%; Score 6; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1459
ID AAR64210 standard; peptide; 56 AA.
DE Tissue plasminogen activator residues 266-321.
PN JP06327473-A.
PD 29-NOV-1994.
PA (SUMU-) SUMITOMO SEIYAKU KK.
Query Match 0.8%; Score 6; DB 2; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1460
ID AAG21118 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23558.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1461
ID AAG55284 standard; protein; 56 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 70861.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 0.8%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
RESULT 1462
```

ID AAM14482 standard; protein, 56 AA.  
 DE Peptide #916 encoded by probe for measuring cervical gene expression.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1463  
 ID ABB13430 standard; peptide, 56 AA.  
 DE Peptide #936 encoded by human foetal liver single exon probe.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1464  
 ID AAM26895 standard; protein, 56 AA.  
 DE Peptide #932 encoded by probe for measuring placental gene expression.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1465  
 ID ABB28255 standard; peptide, 56 AA.  
 DE Human peptide #906 encoded by breast cell single exon nucleic acid probe.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1466  
 ID ABB18869 standard; protein, 56 AA.  
 DE Protein #88 encoded by probe for measuring heart cell gene expression.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1467  
 ID AAM66609 standard; protein, 56 AA.  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 26915.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1468  
 ID AAM54215 standard; protein, 56 AA.  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 26320.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1469  
 ID AAG48277 standard; peptide, 56 AA.  
 DE Human liver peptide, SEQ ID NO 26925.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1470  
 ID AAM02209 standard; protein, 56 AA.  
 DE Peptide #891 encoded by probe for measuring human breast gene expression.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 4; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1471  
 ID ABB05146 standard; protein, 56 AA.

DE Human ORFX protein sequence SEQ ID NO:10274.  
 PN WO200192523-A2.  
 PD 06-DEC-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 0.8%; Score 6; DB 5; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1472  
 ID ABB09848 standard; protein, 56 AA.  
 DE Human ORFX protein sequence SEQ ID NO:19678.  
 PN WO200192523-A2.  
 PD 06-DEC-2001.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 0.8%; Score 6; DB 5; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1473  
 ID AAG36261 standard; peptide, 56 AA.  
 DE Human peptide encoded by genome-derived single exon probe SEQ ID 25926.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Query Match 0.8%; Score 6; DB 5; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1474  
 ID ABB05586 standard; protein, 56 AA.  
 DE M. tuberculosis and M. leprae marker protein #237.  
 PN WO200274903-A2.  
 PD 26-SEP-2002.  
 PA (INSP) INST PASTEUR.  
 Query Match 0.8%; Score 6; DB 5; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1475  
 ID ADN47344 standard; protein, 56 AA.  
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1222.  
 PN WO2004022736-A1.  
 PD 18-MAR-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Query Match 0.8%; Score 6; DB 8; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 RESULT 1476  
 ID AAG10655 standard; protein, 57 AA.  
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 9063.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Query Match 0.8%; Score 6; DB 3; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 RESULT 1477  
 ID AAR45147 standard; protein, 58 AA.  
 DE Plasmid pCDM8-D09 - D44 fragment D(14).  
 PN WO9324624-A1.  
 PD 09-DEC-1993.  
 PA (SMTU) SUMITOMO PHARM CO LTD.  
 Query Match 0.8%; Score 6; DB 2; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 RESULT 1478  
 ID AAO1116 standard; protein, 58 AA.  
 DE Human polypeptide SEQ ID NO 25008.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 0.8%; Score 6; DB 4; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 RESULT 1479  
 ID AAO02406 standard; protein, 58 AA.  
 DE Human polypeptide SEQ ID NO 16298.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC.  
 Query Match 0.8%; Score 6; DB 4; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 RESULT 1480  
 ID AAB41904 standard; protein, 59 AA.  
 DE Human ORFX ORF1668 polypeptide sequence SEQ ID NO:3336.  
 PN WO200058473-A2.

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PD 05-OCT-2000.
PA (CURA-) COPAGEN CORP.
Query Match 0.8%; Score 6; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1481
ID AAB90620 standard; protein; 59 AA.
DE Human secreted protein, SEQ ID NO: 163.
PN WO200121658-A1.
PD 29-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1482
ID AAG99892 standard; peptide; 59 AA.
DE ERA binding domain polypeptide SEQ ID NO 334.
PN WO200153458-A2.
PD 26-JUL-2001.
PA (SMIX) SMITHKLINE BEECHAM CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1483
ID AAM96307 standard; protein; 59 AA.
DE Human reproductive system related antigen SEQ ID NO: 4965.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1484
ID AAO11933 standard; protein; 59 AA.
DE Human polypeptide SEQ ID NO 25825.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1485
ID AAU64191 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #25087.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1486
ID AAU43121 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #4017.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1487
ID AAU55216 standard; protein; 59 AA.
DE Propionibacterium acnes immunogenic protein #26112.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1488
ID AABM1735 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #26411.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1489
ID AABM39640 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4316.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1490
ID AABM60710 standard; protein; 59 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #25386.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1491
ID ABB70853 standard; protein; 60 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39351.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1492
ID ABB41719 standard; peptide; 60 AA.
DE Peptide #9225 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1493
ID AAM35515 standard; protein; 60 AA.
DE Peptide #9552 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1494
ID AAM75403 standard; protein; 60 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 35709.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1495
ID AAU52361 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #13257.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1496
ID AAU63335 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #24231.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1497
ID AAU61570 standard; protein; 60 AA.
DE Propionibacterium acnes immunogenic protein #22466.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 0.8%; Score 6; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
RESULT 1498
ID AAM62593 standard; protein; 60 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 34698.
PN WO200157275-A2.
PD 09-AUG-2001.
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PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1499  
ID ABG57158 standard; peptide; 60 AA  
DE Human liver peptide; SEQ ID NO 35806.  
PN WC200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 4; length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
RESULT 1500  
ID ABG44990 standard; peptide; 60 AA.  
DE Human peptide encoded by genome-derived single exon probe SEQ ID 34655.  
PN WC200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 0.8%; Score 6; DB 5; length 60;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;

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## OM protein - protein search, using sw model

Run on: July 12, 2005, 17:19:03 ; Search time 44 Seconds  
(without alignments)  
1574.456 Million cell updates/sec

Title: US-10-063-546-38  
Perfect score: 720  
Sequence: 1 MELGWTQLGLTFRLQLLIS.....LSTAFKVLPEKDWIERNMK 720

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database :

PIR 79: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	178	24.7	181	2 T08805	hypothetical prote
2	232	1.2	232	2 T070372	hypothetical prote
3	9	1.2	276	2 T29125	ketoacyl reductase
4	9	1.2	730	1 BMH01	procollagen C-endo
5	9	1.2	823	1 A58788	procollagen C-endo
6	9	1.2	986	1 B58788	procollagen C-endo
7	9	1.2	991	2 I49540	procollagen C-endo
8	9	1.2	1464	2 S58984	development protei
9	9	1.2	2531	2 T31070	notch homolog - se
10	9	1.1	114	2 S00996	Ig kappa chain pre
11	11	1.1	158	2 G70323	conserved hypochet
12	8	1.1	235	2 D42696	thrombin (EC 3.4.2
13	8	1.1	235	2 H42696	thrombin (EC 3.4.2
14	8	1.1	236	2 C42696	thrombin (EC 3.4.2
15	8	1.1	240	2 AB0338	probable membrane
16	8	1.1	395	2 T25020	hypothetical prote
17	8	1.1	395	2 A82283	vibriobactin-speci
18	8	1.1	407	1 KPB07	coagulation factor
19	8	1.1	486	2 T38174	probable GCSL/GUO3
20	8	1.1	737	2 AG2156	hypothetical prote
21	8	1.1	1019	2 A38738	coagulation factor
22	8	1.1	1070	2 T31069	collid-BMP-1 like
23	7	1.0	59	2 B89983	hypothetical prote
24	7	1.0	75	2 B86487	unknown protein [i
25	7	1.0	91	2 B96528	protein F27315.6 [
26	7	1.0	114	2 D72600	hypothetical prote
27	7	1.0	143	2 A85072	hypothetical prote
28	7	1.0	167	2 S05364	hypothetical prote
29	7	1.0	168	2 D86534	CT066 hypothetical

30	7	1.0	168	2 D72089	CT066 hypothetical
31	7	1.0	171	2 B81580	conserved hypochet
32	7	1.0	173	2 T45501	hypothetical prote
33	7	1.0	178	2 F86271	protein Fl6A14.6 [
34	7	1.0	191	2 G75299	telurium resistanc
35	7	1.0	193	2 G64241	hypothetical prote
36	7	1.0	196	2 UC4257	beta A4-crystallin
37	7	1.0	201	1 S16262	auxin-binding prot
38	7	1.0	209	2 S27494	nods protein - Bra
39	7	1.0	211	2 AC0268	probable exported
40	7	1.0	212	2 AE0652	probable outer mem
41	7	1.0	212	2 S07797	acid protein precu
42	7	1.0	212	2 C85706	probable outer mem
43	7	1.0	212	2 D90848	probable outer mem
44	7	1.0	213	2 B86828	hypothetical prote
45	7	1.0	215	2 T50589	probable Tetr-fam1
46	7	1.0	227	2 D69296	conserved hypochet
47	7	1.0	231	2 A86592	low calcium respon
48	7	1.0	231	2 H72031	type III secretion
49	7	1.0	232	2 C83139	outer membrane pro
50	7	1.0	235	2 E42696	thrombin (EC 3.4.2
51	7	1.0	236	2 F84273	hypothetical prote
52	7	1.0	239	2 G42696	thrombin (EC 3.4.2
53	7	1.0	239	2 B82123	chemotaxis protein
54	7	1.0	243	2 A56338	venom proteinase (
55	7	1.0	247	2 G86011	glycerophosphodies
56	7	1.0	247	2 G91165	glycerophosphodies
57	7	1.0	250	2 A10206	probable chaperone
58	7	1.0	255	2 S07553	hypothetical prote
59	7	1.0	259	2 A12835	N-acetylaminogly-L
60	7	1.0	259	2 D97613	hypothetical prote
61	7	1.0	260	2 A36402	corticotropic / 11
62	7	1.0	263	2 S05433	corticotropic / 11
63	7	1.0	265	2 E70520	hypothetical prote
64	7	1.0	270	2 S04380	opacity protein P.
65	7	1.0	271	2 T50620	hypothetical prote
66	7	1.0	307	2 B82343	D-isomer specific
67	7	1.0	312	2 S67052	hypothetical prote
68	7	1.0	315	2 A87249	conserved hypochet
69	7	1.0	333	2 A84055	transcription regu
70	7	1.0	336	2 G87202	probable membrane
71	7	1.0	337	2 D72690	hypothetical prote
72	7	1.0	339	2 AG2041	queuine tRNA-ribos
73	7	1.0	349	2 C72630	hypothetical prote
74	7	1.0	350	2 T25172	MSS2 protein - Yea
75	7	1.0	351	2 S67649	hypothetical prote
76	7	1.0	355	2 T13831	NADH2 dehydrogenas
77	7	1.0	355	2 T13830	NADH2 dehydrogenas
78	7	1.0	355	2 T14016	NADH2 dehydrogenas
79	7	1.0	355	2 T14009	NADH2 dehydrogenas
80	7	1.0	355	2 T14012	NADH2 dehydrogenas
81	7	1.0	355	2 T14011	NADH2 dehydrogenas
82	7	1.0	355	2 T11737	NADH2 dehydrogenas
83	7	1.0	355	2 T13989	NADH2 dehydrogenas
84	7	1.0	355	2 T14010	NADH2 dehydrogenas
85	7	1.0	355	2 T14013	NADH2 dehydrogenas
86	7	1.0	355	2 T11752	NADH2 dehydrogenas
87	7	1.0	355	2 T11760	NADH2 dehydrogenas
88	7	1.0	355	2 T14013	NADH2 dehydrogenas
89	7	1.0	355	2 T11733	NADH2 dehydrogenas
90	7	1.0	355	2 T11762	NADH2 dehydrogenas
91	7	1.0	355	2 T14014	NADH2 dehydrogenas
92	7	1.0	355	2 T11754	NADH2 dehydrogenas
93	7	1.0	355	2 T13988	NADH2 dehydrogenas
94	7	1.0	355	2 T14008	NADH2 dehydrogenas
95	7	1.0	355	2 T11739	NADH2 dehydrogenas
96	7	1.0	355	2 T13977	NADH2 dehydrogenas
97	7	1.0	355	2 T13894	NADH2 dehydrogenas
98	7	1.0	355	2 T12118	NADH2 dehydrogenas
99	7	1.0	355	2 T14028	NADH2 dehydrogenas
100	7	1.0	355	2 T14048	NADH2 dehydrogenas
101	7	1.0	355	2 T11603	NADH2 dehydrogenas
102	7	1.0	355	2 T11604	NADH2 dehydrogenas

103	7	1.0	355	2	T11602	NADH2 dehydrogenas	176	6	0.8	27	2	A33431	aerial natriuretic
104	7	1.0	355	2	T11601	NADH2 dehydrogenas	177	6	0.8	35	2	D82224	hypothetical prote
105	7	1.0	355	2	T12109	NADH2 dehydrogenas	178	6	0.8	40	2	E82433	hypothetical prote
106	7	1.0	355	2	T12107	NADH2 dehydrogenas	179	6	0.8	48	2	G81543	hypothetical prote
107	7	1.0	355	2	T12119	NADH2 dehydrogenas	180	6	0.8	53	2	G82813	hypothetical prote
108	7	1.0	355	2	A48358	ORF355 - Bradyrhiz	181	6	0.8	54	2	A95210	conserved hypotet
109	7	1.0	355	2	A28700	mandelate racemase	182	6	0.8	54	2	H81814	probable small sec
110	7	1.0	372	2	A83260	hypothetical prote	183	6	0.8	55	1	FECLCU	ferredoxin 244Fe-4
111	7	1.0	375	2	A81227	conserved hypotet	184	6	0.8	55	2	T07197	hypothetical prote
112	7	1.0	375	2	F81999	probable integral	185	6	0.8	56	2	E87173	conserved hypotet
113	7	1.0	387	1	S75050	IMP dehydrogenase	186	6	0.8	57	2	S66318	protein kinase AK5
114	7	1.0	387	2	AC1813	hypothetical prote	187	6	0.8	57	2	S66316	hypothetical prote
115	7	1.0	398	2	E83438	probable transport	188	6	0.8	59	2	A83209	hypothetical prote
116	7	1.0	437	2	F69383	coenzyme F390 synt	189	6	0.8	62	2	G59147	comotoxin Im5.1 pr
117	7	1.0	437	2	J50237	hypothetical 48K p	190	6	0.8	64	2	T08457	probable outer env
118	7	1.0	439	2	T49189	kinasin heavy chai	191	6	0.8	64	2	H75204	ferredoxin PAB3048
119	7	1.0	459	2	T08594	probable sulfate a	192	6	0.8	66	2	D98068	degenerate transpo
120	7	1.0	461	2	D70561	hypothetical prote	193	6	0.8	67	2	AC1954	hypothetical prote
121	7	1.0	472	2	T27755	hypothetical prote	194	6	0.8	68	2	T00189	hypothetical prote
122	7	1.0	479	2	H90042	hypothetical prote	195	6	0.8	68	2	A95993	hypothetical prote
123	7	1.0	489	2	S69027	ammonium transport	196	6	0.8	69	2	AE2949	hypothetical prote
124	7	1.0	492	2	T23349	hypothetical prote	197	6	0.8	70	1	R5EC31	ribosomal protein
125	7	1.0	492	2	S46225	ammonium transport	198	6	0.8	70	2	G91236	50S ribosomal subu
126	7	1.0	493	2	A33809	cartilage matrix p	199	6	0.8	70	2	G86083	hypothetical prote
127	7	1.0	494	1	A23079	lymphocyte surfac	200	6	0.8	70	2	G82588	hypothetical prote
128	7	1.0	497	2	S43609	roIA protein - Str	201	6	0.8	71	2	I60082	CD4 receptor - hum
129	7	1.0	497	2	H70168	hypothetical prote	202	6	0.8	71	2	H86751	prophage p12 prote
130	7	1.0	505	2	C90569	hypothetical prote	203	6	0.8	73	2	H83204	conserved hypotet
131	7	1.0	529	2	T18595	hypothetical prote	204	6	0.8	73	2	F97136	hypothetical prote
132	7	1.0	532	2	A72694	hypothetical prote	205	6	0.8	75	2	J01429	hypothetical 8.1K
133	7	1.0	544	2	S06602	modulo antigen - f	206	6	0.8	75	2	D82592	hypothetical prote
134	7	1.0	553	2	D95071	metallo-beta-lacta	207	6	0.8	77	2	T06954	hypothetical prote
135	7	1.0	553	2	B97939	conserved hypotet	208	6	0.8	77	2	AC2101	lipoprotein (Impor
136	7	1.0	556	2	S02154	NADH2 dehydrogenas	209	6	0.8	78	2	A42506	conserved hypotet
137	7	1.0	561	2	C75543	6-aminohexanoate-c	210	6	0.8	79	2	D69309	hypothetical prote
138	7	1.0	580	2	D84772	probable sugar tra	211	6	0.8	80	2	E97949	hypothetical prote
139	7	1.0	581	2	T38864	probable regulator	212	6	0.8	84	2	S27152	ribosomal protein
140	7	1.0	582	2	F71431	hypothetical prote	213	6	0.8	85	2	G64217	auxin-induced prot
141	7	1.0	583	2	T25690	hypothetical prote	214	6	0.8	85	2	T12211	hypothetical prote
142	7	1.0	585	2	T18736	hypothetical prote	215	6	0.8	86	2	T02494	hypothetical prote
143	7	1.0	617	2	S10511	chrombin (EC 3.4.2	216	6	0.8	86	2	E90660	damage-inducible p
144	7	1.0	617	2	D90487	maltoase ABC transp	217	6	0.8	86	2	C85511	DNA-damage-inducib
145	7	1.0	618	2	A35827	chrombin (EC 3.4.2	218	6	0.8	86	2	C64747	hypothetical prote
146	7	1.0	622	1	TBRU	chrombin (EC 3.4.2	219	6	0.8	87	2	T10462	hypothetical prote
147	7	1.0	625	1	TBBO	probable serine/th	220	6	0.8	87	2	T50008	hypothetical prote
148	7	1.0	658	2	T04831	hypothetical prote	221	6	0.8	88	2	B82860	hypothetical prote
149	7	1.0	678	2	D87607	hypothetical prote	222	6	0.8	88	2	C97251	probable membrane
150	7	1.0	684	2	H96646	hypothetical prote	223	6	0.8	88	2	AB1901	hypothetical prote
151	7	1.0	684	2	T02149	hypothetical prote	224	6	0.8	91	2	C81922	hypothetical prote
152	7	1.0	707	2	JC2218	procollagen C-endo	225	6	0.8	91	2	AE0710	probable exported
153	7	1.0	708	2	T43109	cytoleysin B transp	226	6	0.8	92	2	F36905	conserved hypotet
154	7	1.0	746	2	C95110	competence protein	227	6	0.8	94	2	T44722	probable transcrip
155	7	1.0	783	2	B83232	conserved hypotet	228	6	0.8	95	2	C83517	hypothetical prote
156	7	1.0	790	2	G02678	cadherin-14 huma	229	6	0.8	98	2	B82483	hypothetical prote
157	7	1.0	791	2	H96839	hypothetical prote	230	6	0.8	98	2	T74483	hypothetical prote
158	7	1.0	826	2	T06036	hypothetical prote	231	6	0.8	98	2	S03386	antigen (clone 22)
159	7	1.0	833	2	S50225	potassium transpor	232	6	0.8	99	2	S44658	ZK353.2 protein -
160	7	1.0	841	2	T38703	hypothetical prote	233	6	0.8	100	2	C71012	hypothetical prote
161	7	1.0	856	2	T16543	hypothetical prote	234	6	0.8	102	2	D84024	transcription regu
162	7	1.0	859	2	S66827	alumininum resistan	235	6	0.8	104	2	F45681	transposase - Bact
163	7	1.0	903	2	E86221	protein T01H3.2 (I	236	6	0.8	104	2	F45681	orf 61.2 - phage T
164	7	1.0	980	2	T24336	hypothetical prote	237	6	0.8	105	2	C69068	divalent cation to
165	7	1.0	995	2	A88483	protein COSD1.1 (	238	6	0.8	106	2	D90392	conserved hypotet
166	7	1.0	1048	2	T31653	hypothetical prote	239	6	0.8	107	2	G71517	probable L21 ribos
167	7	1.0	1100	2	JC8033	leukocyte formin p	240	6	0.8	108	2	G84532	similar to glibere
168	7	1.0	1240	2	T04833	hypothetical prote	241	6	0.8	108	2	A28667	hypothetical prote
169	7	1.0	1346	2	T17412	polypeptide syntas	242	6	0.8	109	2	B53281	tetracenomycin-bio
170	7	1.0	1522	2	S48904	probable purine nu	243	6	0.8	109	2	T73985	hypothetical prote
171	7	1.0	1742	2	T49451	kinasin-like prote	244	6	0.8	109	2	T44129	hypothetical prote
172	7	1.0	1822	2	T50207	probable protein t	245	6	0.8	113	2	T45195	hypothetical prote
173	7	1.0	2605	2	T18552	safamycin Mx1 syn	246	6	0.8	114	2	T26771	hypothetical prote
174	7	1.0	2907	2	A57278	fibrillin-2 precur	247	6	0.8	115	2	H72705	hypothetical prote
175	7	1.0	2918	2	A54105	fibrillin-2 precur	248	6	0.8	116	2	D96530	probable ribosomal



249	6	0.8	117	2	I51573	gene wnt-2 protein
250	6	0.8	117	2	H90021	50S ribosomal prot
251	6	0.8	117	2	C72511	hypothetical prote
252	6	0.8	118	2	H71564	hypothetical prote
253	6	0.8	118	2	T14660	hypothetical prote
254	6	0.8	118	2	JC5793	elongin B - fruit
255	6	0.8	119	2	F70941	hypothetical prote
256	6	0.8	122	2	H64217	ribosomal protein
257	6	0.8	122	2	S62831	ribosomal protein
258	6	0.8	123	2	E71163	hypothetical prote
259	6	0.8	123	2	S72389	hypothetical prote
260	6	0.8	123	2	S75382	hypothetical prote
261	6	0.8	124	1	KNIV71	nonstructural prot
262	6	0.8	124	2	AB1163	conserved hypotnet
263	6	0.8	124	2	F81942	probable regulator
264	6	0.8	126	2	T47297	hypothetical prote
265	6	0.8	127	2	T14956	hypothetical prote
266	6	0.8	127	2	F69377	mo/ybdenum-pterin-
267	6	0.8	127	2	T05261	cold-regulated pro
268	6	0.8	129	2	T06188	probable DNA-direc
269	6	0.8	129	2	S52792	Ig kappa chain V r
270	6	0.8	129	2	C69488	LSU ribosomal prot
271	6	0.8	129	2	E75602	hypothetical prote
272	6	0.8	130	2	S57896	polyketide synthas
273	6	0.8	130	2	T35906	probable quinone b
274	6	0.8	130	2	B83992	hypothetical prote
275	6	0.8	131	2	T49455	hypothetical prote
276	6	0.8	131	2	T29078	hypothetical prote
277	6	0.8	132	2	T50416	40S ribosomal prot
278	6	0.8	132	2	H87626	hypothetical prote
279	6	0.8	133	2	E71062	hypothetical prote
280	6	0.8	133	2	F81748	conserved hypotnet
281	6	0.8	133	2	H81191	hypothetical prote
282	6	0.8	134	2	E71945	hypothetical prote
283	6	0.8	134	2	E64561	conserved hypotnet
284	6	0.8	134	2	B72651	hypothetical prote
285	6	0.8	136	2	E69376	hypothetical prote
286	6	0.8	136	2	E80394	ferric uptake regu
287	6	0.8	137	2	A83852	hypothetical prote
288	6	0.8	138	2	D83824	transcription regu
289	6	0.8	138	2	T29558	hypothetical prote
290	6	0.8	139	2	G90414	conserved hypotnet
291	6	0.8	140	2	E81659	conserved hypotnet
292	6	0.8	141	2	T33271	hypothetical prote
293	6	0.8	141	2	S55247	hemoglobin alpha-A
294	6	0.8	141	2	T39720	ORF10 - Agrobacter
295	6	0.8	141	2	G72651	hypothetical prote
296	6	0.8	143	2	S50549	hypothetical prote
297	6	0.8	143	2	B72627	hypothetical prote
298	6	0.8	144	2	T49457	hypothetical prote
299	6	0.8	145	2	C64447	hypothetical prote
300	6	0.8	145	2	F84251	hypothetical prote
301	6	0.8	146	2	H64340	hypothetical prote
302	6	0.8	147	2	S01655	alpha-amy/ase/tryp
303	6	0.8	147	2	T35980	probable pepide t
304	6	0.8	149	2	T35846	probable integrat
305	6	0.8	149	2	T49200	hypothetical prote
306	6	0.8	150	2	AC1720	transcription regu
307	6	0.8	151	2	C71503	probable rRNA meth
308	6	0.8	151	2	B87624	transcription regu
309	6	0.8	151	2	A97008	transcription regu
310	6	0.8	152	2	D98270	hypothetical prote
311	6	0.8	153	2	T06564	hypothetical prote
312	6	0.8	153	2	C98238	alpha-amy/ase/tryp
313	6	0.8	153	2	AB3047	hypothetical 16.4k
314	6	0.8	153	2	AB1907	conserved hypotnet
315	6	0.8	154	2	E83634	hypothetical prote
316	6	0.8	155	2	B90143	hypothetical prote
317	6	0.8	155	2	A82884	conserved hypotnet
318	6	0.8	156	2	G69233	N-terminal acetyl
319	6	0.8	157	2	T8321	ORF MSV160 hypothe
320	6	0.8	158	2	D62499	hypothetical prote
321	6	0.8	159	2	B70635	hypothetical prote
322	6	0.8	159	2	A72709	hypothetical prote
323	6	0.8	159	2	D86743	hypothetical prote
324	6	0.8	159	2	D86286	Similar to gb - Ar
325	6	0.8	160	2	H55545	ARA-III adhesin -
326	6	0.8	160	2	T35987	probable ribosome-
327	6	0.8	160	2	AC0835	Sera (tmRNA)-bindi
328	6	0.8	160	2	AE0135	Sera-binding prote
329	6	0.8	160	2	T48148	hypothetical prote
330	6	0.8	161	2	T31531	hypothetical prote
331	6	0.8	161	2	E90372	conserved hypotnet
332	6	0.8	162	2	H75071	transcription regu
333	6	0.8	162	2	C97657	peaxb protein [lipo
334	6	0.8	162	2	AC2881	DNA-binding protei
335	6	0.8	162	2	H70803	probable transcrip
336	6	0.8	162	2	AB1950	hypothetical prote
337	6	0.8	162	2	H71093	hypothetical prote
338	6	0.8	163	2	B97290	3-isopropylmalate
339	6	0.8	164	2	A45512	cold-regulated pro
340	6	0.8	164	2	UC4675	transcription fact
341	6	0.8	165	2	AB0851	hypothetical prote
342	6	0.8	165	2	S70217	sipe protein - Sal
343	6	0.8	165	2	A57357	sica protein - Sal
344	6	0.8	165	2	H86948	probable transcrip
345	6	0.8	166	2	I39546	hypothetical prote
346	6	0.8	167	2	E71391	NADH2 dehydrogenas
347	6	0.8	167	2	AD0601	DNA protection dur
348	6	0.8	167	2	B90740	global regulator p
349	6	0.8	167	2	A46401	DNA-binding protei
350	6	0.8	167	2	D85590	global regulator.
351	6	0.8	167	2	AG0306	probable DNA-bind
352	6	0.8	167	2	E71391	hypothetical prote
353	6	0.8	168	2	A69708	signal peptidase I
354	6	0.8	169	2	A88489	nitrare reductase
355	6	0.8	170	2	A88638	protein P58F6.3 [i
356	6	0.8	171	2	S76982	hypothetical prote
357	6	0.8	171	2	T41924	hypothetical prote
358	6	0.8	172	2	AG3532	D-lactate dehydrat
359	6	0.8	172	2	G82151	peptidoglycan-asso
360	6	0.8	172	2	G69087	conserved hypotnet
361	6	0.8	172	2	AE2283	hypothetical prote
362	6	0.8	172	2	D71136	hypothetical prote
363	6	0.8	173	2	H70113	ribosomal protein
364	6	0.8	174	2	E69038	heat shock protein
365	6	0.8	175	2	T07877	self-pruning prote
366	6	0.8	175	2	AC3014	MuTr/nudix family
367	6	0.8	175	2	G86458	unknown protein.
368	6	0.8	176	2	A34630	DNA-binding protei
369	6	0.8	176	2	AE0866	conserved hypotnet
370	6	0.8	177	2	S45878	hypothetical prote
371	6	0.8	177	2	E95222	conserved hypotnet
372	6	0.8	177	2	D75309	protein-tyrosine p
373	6	0.8	177	2	E98086	conserved hypotnet
374	6	0.8	178	2	A93637	probable NADH2 deh
375	6	0.8	178	2	B42845	3-hydroxybutyrate
376	6	0.8	178	2	H84789	hypothetical prote
377	6	0.8	178	2	A86836	hypothetical prote
378	6	0.8	178	2	S26481	calcium-binding pr
379	6	0.8	179	2	G75452	ribonuclease H - D
380	6	0.8	179	2	G90003	ATP synthase delta
381	6	0.8	180	2	PC1305	genome polypotein
382	6	0.8	180	2	PC1304	genome polypotein
383	6	0.8	180	2	PC1303	genome polypotein
384	6	0.8	180	2	T23339	hypothetical prote
385	6	0.8	182	2	T33915	meiotic recombinat
386	6	0.8	182	2	A72361	hypothetical prote
387	6	0.8	183	2	E69432	hypothetical prote
388	6	0.8	183	2	T07677	plastil-specific pr
389	6	0.8	184	2	T09609	uropolakin II - hum
390	6	0.8	184	2	A54135	uropolakin II precu
391	6	0.8	184	2	UC7839	uropolakin II prote
392	6	0.8	184	2	E87506	hypothetical prote
393	6	0.8	185	2	F70479	flavodoxin - Aquif
394	6	0.8	185	2	B81732	general stress pro

395	6	0.8	185	2	E71469	probable general s
396	6	0.8	185	2	A49713	uroplakin II precu
397	6	0.8	186	1	R5B98E	ribosomal protein
398	6	0.8	186	2	T41601	hypothetical prote
399	6	0.8	187	2	G75022	hypothetical prote
400	6	0.8	187	2	B83084	probable transcrip
401	6	0.8	188	2	S70680	bpiu protein - Bor
402	6	0.8	189	1	XMECFD	3-octaprenyl-4-hyd
403	6	0.8	189	2	AB0801	probable decarboxy
404	6	0.8	189	2	C91028	3-octaprenyl-4-hyd
405	6	0.8	189	2	D85872	3-octaprenyl-4-hyd
406	6	0.8	189	2	D71658	3-octaprenyl-4-hyd
407	6	0.8	189	2	T51064	hypothetical prote
408	6	0.8	189	2	AB0361	probable iron-sulp
409	6	0.8	190	2	AB0338	probable 3-octapre
410	6	0.8	191	2	A97800	hypothetical prote
411	6	0.8	191	2	C64574	hypothetical prote
412	6	0.8	192	2	M45836	MHC class II histo
413	6	0.8	192	2	H72099	phenylacrylate dec
414	6	0.8	192	2	H86523	phenylacrylate dec
415	6	0.8	192	2	E75021	probable transcrip
416	6	0.8	193	2	T30325	hypothetical prote
417	6	0.8	194	1	HSN110	histone H1-0 - hum
418	6	0.8	194	2	C82041	general secretion
419	6	0.8	196	2	D86190	decarboxylase (imp
420	6	0.8	196	2	AE3096	phenylacrylic acid
421	6	0.8	196	2	AC3629	3-octaprenyl-4-hyd
422	6	0.8	197	1	R5WUL9	ribosomal protein
423	6	0.8	197	2	E95411	probable decarboxy
424	6	0.8	197	2	B70761	probable lipoprote
425	6	0.8	197	2	D87309	hypothetical prote
426	6	0.8	197	2	H75188	hypothetical prote
427	6	0.8	198	2	E81391	probable transcrip
428	6	0.8	198	2	AC1890	hypothetical prote
429	6	0.8	199	2	G75575	glutathione transf
430	6	0.8	199	2	G75575	hypothetical prote
431	6	0.8	200	2	B95349	probable decarboxy
432	6	0.8	201	2	C36885	bo-t-type ubiquitin
433	6	0.8	201	2	AD2419	SOS function regul
434	6	0.8	201	2	C69271	hypothetical prote
435	6	0.8	202	2	H81731	CDP-diacylglycerol
436	6	0.8	202	2	C71469	probable glycerol-
437	6	0.8	202	2	T37025	probable sigma fac
438	6	0.8	202	2	AD2197	hypothetical prote
439	6	0.8	202	2	D72573	hypothetical prote
440	6	0.8	203	2	S74809	lexa protein - Syn
441	6	0.8	203	2	AH0223	probable glycosida
442	6	0.8	204	2	C38129	bo-t-type ubiquitin
443	6	0.8	204	2	S03246	net protein (clone
444	6	0.8	204	2	G71172	hypothetical prote
445	6	0.8	205	1	XMBSTI	regulatory protein
446	6	0.8	205	1	ASLJH3	net protein - huma
447	6	0.8	205	2	D85764	probable oxidoredu
448	6	0.8	205	2	G64914	dimethylsulfoxide
449	6	0.8	205	2	G90915	probable oxidoredu
450	6	0.8	205	2	T01744	ribosomal protein
451	6	0.8	205	2	S43467	net protein - huma
452	6	0.8	205	2	D69036	conserved hypotet
453	6	0.8	205	2	C83325	maf protein VC0418
454	6	0.8	205	2	UC7975	HIV accessory prot
455	6	0.8	206	1	ASLJ12	net protein - huma
456	6	0.8	206	1	ASLJFV	net protein - huma
457	6	0.8	206	1	ASLJVL	net protein - huma
458	6	0.8	206	2	A86609	glycerol-3-P phosp
459	6	0.8	206	2	B72016	CDP-diacylglycerol
460	6	0.8	206	2	S03245	net protein (clone
461	6	0.8	206	2	S33986	net protein - huma
462	6	0.8	206	2	S03244	net protein (clone
463	6	0.8	206	2	A39268	heparin-binding pr
464	6	0.8	208	1	A38432	heparin-binding EG
465	6	0.8	208	1	A41914	diphtheria toxin re
466	6	0.8	208	1	A41636	GTP-binding protei
467	6	0.8	208	2	E64357	ribosomal protein
468	6	0.8	208	2	D87565	conserved hypotet
469	6	0.8	209	2	A99460	conserved hypotet
470	6	0.8	209	2	C87521	hypothetical prote
471	6	0.8	209	2	T07779	dehydratin homolog C
472	6	0.8	210	2	G95858	probable 3-octapre
473	6	0.8	210	2	D84238	hypothetical prote
474	6	0.8	210	2	H75361	leu/phe-tRNA-prote
475	6	0.8	211	1	ZKEP74	transcription regu
476	6	0.8	211	2	T47580	ribosomal protein
477	6	0.8	211	2	S45464	hypothetical prote
478	6	0.8	212	1	QOLJZR	net protein - huma
479	6	0.8	212	1	S37973	DNA-directed RNA p
480	6	0.8	214	2	D46681	glutathione transf
481	6	0.8	214	2	E46681	glutathione transf
482	6	0.8	214	2	T14920	hypothetical prote
483	6	0.8	215	2	C46681	glutathione transf
484	6	0.8	215	2	AD0455	thiamine-phosphate
485	6	0.8	215	2	T45885	hypothetical prote
486	6	0.8	215	2	T16383	hypothetical prote
487	6	0.8	216	1	C64081	L-fuculose-phospha
488	6	0.8	216	2	D86564	yege family (impor
489	6	0.8	216	2	G72060	yege family - Chla
490	6	0.8	216	2	G72509	hypothetical prote
491	6	0.8	217	2	D82407	outer membrane pro
492	6	0.8	218	2	F85571	probable carboxyla
493	6	0.8	218	2	H90720	probable carboxyla
494	6	0.8	218	2	F64806	ypgj protein - Bsc
495	6	0.8	218	2	B64595	endonuclease III -
496	6	0.8	218	2	C71918	endonuclease III -
497	6	0.8	218	2	A70601	hypothetical prote
498	6	0.8	218	2	T50440	hypothetical prote
499	6	0.8	218	2	AG3301	conserved hypotet
500	6	0.8	218	2	H87666	hypothetical prote
501	6	0.8	218	2	E75389	hypothetical prote
502	6	0.8	218	2	G69374	hypothetical prote
503	6	0.8	218	2	A13612	hypothetical cyto
504	6	0.8	220	2	S20581	14-3-3 protein hom
505	6	0.8	220	2	T26991	hypothetical prote
506	6	0.8	221	2	B70890	hypothetical prote
507	6	0.8	221	2	A11232	oligopeptide ABC t
508	6	0.8	222	2	AC1495	ribulose-5-phospha
509	6	0.8	222	2	T35145	glutamate transpor
510	6	0.8	222	2	AH0991	cell division ARP-
511	6	0.8	222	2	AB1408	hypothetical prote
512	6	0.8	222	2	AG1166	Ribulose-5-Phospha
513	6	0.8	223	2	C81397	phosphoribosylform
514	6	0.8	223	2	T34828	potassium uptake p
515	6	0.8	223	2	D75040	hypothetical prote
516	6	0.8	223	2	T31703	hypothetical prote
517	6	0.8	224	1	R5SP11	ribosomal protein
518	6	0.8	224	2	C86571	L4 ribosomal prote
519	6	0.8	224	2	H72055	ribosomal protein
520	6	0.8	224	2	C81417	probable transcrip
521	6	0.8	224	2	T71101	hypothetical prote
522	6	0.8	225	2	B97580	hypothetical prote
523	6	0.8	225	2	AH2800	conserved hypotet
524	6	0.8	225	2	T29632	hypothetical prote
525	6	0.8	226	2	A35968	tox regulon trans
526	6	0.8	227	2	T22144	hypothetical prote
527	6	0.8	227	2	A87361	flagellar hook ass
528	6	0.8	227	2	T41133	hypothetical prote
529	6	0.8	228	2	AB0438	conserved hypotet
530	6	0.8	228	2	B82087	probable smp prote
531	6	0.8	229	2	S70599	cycochrome-c oxida
532	6	0.8	229	2	S14207	cycochrome-c oxida
533	6	0.8	229	2	C90912	probable antilemi
534	6	0.8	229	2	P90972	antiterminator (im
535	6	0.8	229	2	C85820	antiterminator (im
536	6	0.8	229	2	T48348	lysine decarboxyla
537	6	0.8	230	1	NM1V16	nonstructural prot
538	6	0.8	230	1	NM1V45	nonstructural prot
539	6	0.8	230	1	NM1V46	nonstructural prot
540	6	0.8	230	1	NM1V47	nonstructural prot

541	6	0.8	230	1	MNIVA8	nonstructural prot	614	6	0.8	257	2	T00064	MERS protein - mou
542	6	0.8	230	2	A45575	nonstructural prot	615	6	0.8	257	2	T00780	myb-related protei
543	6	0.8	230	2	G70504	probable cmk prote	616	6	0.8	257	2	T33392	hypothetical prote
544	6	0.8	231	2	S57271	14-3-3 protein hom	617	6	0.8	258	2	T07389	14-3-3 protein lft
545	6	0.8	231	2	D49934	phosphoglycolate p	618	6	0.8	258	2	T04131	14-3-3 protein, is
546	6	0.8	231	2	B69858	hypothetical prote	619	6	0.8	258	2	AF0016	probable biotin bi
547	6	0.8	231	2	AI3283	transcription regu	620	6	0.8	258	2	AH2615	hypothetical prote
548	6	0.8	232	2	AG2525	hypothetical prote	621	6	0.8	258	2	G86764	hypothetical prote
549	6	0.8	233	2	I55654	MHC class II prote	622	6	0.8	258	2	T31647	hypothetical prote
550	6	0.8	233	2	C82360	cell division ATP-	623	6	0.8	259	1	A47237	14-3-3 protein hom
551	6	0.8	233	2	A72786	hypothetical transp	624	6	0.8	259	2	B69113	cell division inh
552	6	0.8	233	2	H75359	hypothetical prote	625	6	0.8	259	2	G97397	ubiquitinone/menqu
553	6	0.8	234	2	S61309	nitrate reductase	626	6	0.8	259	2	D81083	conserved hypochet
554	6	0.8	234	2	T07686	transcription fact	627	6	0.8	259	2	D81659	conserved hypochet
555	6	0.8	234	2	F95952	probable membrane-	628	6	0.8	260	1	S30927	14-3-3 protein hom
556	6	0.8	234	2	C97001	ABC transporter, A	629	6	0.8	260	2	T07388	14-3-3 protein lft
557	6	0.8	235	2	B98108	response regulator	630	6	0.8	260	2	T02051	14-3-3 protein hom
558	6	0.8	235	2	E95243	response regulator	631	6	0.8	260	2	S20580	14-3-3 protein hom
559	6	0.8	235	2	C75030	hypothetical prote	632	6	0.8	260	2	D69299	hypothetical prote
560	6	0.8	236	2	AH3230	hypothetical prote	633	6	0.8	260	2	T51079	related to chitina
561	6	0.8	236	2	E42600	probable octopine	634	6	0.8	261	1	S18911	14-3-3 protein hom
562	6	0.8	236	2	T10417	p25 protein - Orgy	635	6	0.8	261	2	S52110	sepiapterin reduct
563	6	0.8	236	2	T02432	ethylene-responsiv	636	6	0.8	261	2	A71192	probable glucose 1
564	6	0.8	237	2	E97712	transcription acti	637	6	0.8	261	2	S52899	14-3-3 protein hom
565	6	0.8	237	2	C70157	hypothetical prote	638	6	0.8	261	2	H83442	probable enoyl-CoA
566	6	0.8	238	2	I71907	MHC H2-IE-beta cel	639	6	0.8	261	2	H70100	conserved hypochet
567	6	0.8	238	2	T14629	hypothetical prote	640	6	0.8	261	2	D64166	hypothetical prote
568	6	0.8	239	2	A72623	hypothetical prote	641	6	0.8	262	2	H71390	cytochrome-c oxida
569	6	0.8	239	2	D81351	hypothetical prote	642	6	0.8	262	2	T04406	14-3-3b protein -
570	6	0.8	240	2	T24239	hypothetical prote	643	6	0.8	262	2	S57276	14-3-3 protein hom
571	6	0.8	241	2	I48657	I-E(b-beta) protei	644	6	0.8	262	2	T47002	hypothetical prote
572	6	0.8	241	2	T23823	hypothetical prote	645	6	0.8	262	2	AH0238	probable phosphate
573	6	0.8	241	2	H81536	hypothetical prote	646	6	0.8	262	2	T22148	hypothetical prote
574	6	0.8	242	2	B82815	conserved hypochet	647	6	0.8	263	2	F87043	BCF subfamily sigm
575	6	0.8	243	2	TX0162	lectin I - furze	648	6	0.8	263	2	T26031	hypothetical prote
576	6	0.8	244	2	C95901	probable short cha	649	6	0.8	263	2	T18930	hypothetical prote
577	6	0.8	244	2	S76160	hypothetical prote	650	6	0.8	264	1	HLMSB1	H-2 class II histo
578	6	0.8	245	2	S28827	chlorophyll a/b-bi	651	6	0.8	264	1	HLMSB	H-2 class II histo
579	6	0.8	246	1	S56439	ammonium transp	652	6	0.8	264	1	D64368	cell division inh
580	6	0.8	246	2	T51631	probable transcrip	653	6	0.8	264	2	A30529	H-2 class II histo
581	6	0.8	246	2	AP1054	cy8Q protein [limp	654	6	0.8	264	2	I56056	MHC E-beta-E - mou
582	6	0.8	246	2	H86118	ammonium transp	655	6	0.8	264	2	A81668	conserved hypochet
583	6	0.8	246	2	H91277	ammonium transp	656	6	0.8	264	2	E71509	hypothetical prote
584	6	0.8	247	2	JT0555	MHC class II histo	657	6	0.8	264	2	T13116	protein gp30 - pha
585	6	0.8	247	2	S23474	rod-core linker po	658	6	0.8	264	2	D71037	hypothetical prote
586	6	0.8	247	2	H90419	hypothetical prote	659	6	0.8	265	2	T30346	NADH2 dehydrogenas
587	6	0.8	248	2	S53727	14-3-3 protein hom	660	6	0.8	265	2	T12599	NADH2 dehydrogenas
588	6	0.8	249	2	F87153	probable pseudouri	661	6	0.8	265	2	T12597	NADH2 dehydrogenas
589	6	0.8	249	2	H72200	conserved hypochet	662	6	0.8	265	2	T12601	hypothetical prote
590	6	0.8	250	2	T06338	probable vacuolar	663	6	0.8	266	2	D83210	hypothetical prote
591	6	0.8	250	2	S58362	nucleolar protein	664	6	0.8	266	2	T40318	hypothetical prote
592	6	0.8	250	2	S61626	hypothetical prote	665	6	0.8	266	2	AB3571	nickel transport A
593	6	0.8	250	2	T46912	hypothetical prote	666	6	0.8	267	2	H85090	14-3-3-like protei
594	6	0.8	250	2	H95161	conserved hypochet	667	6	0.8	267	2	C86472	probable 14-3-3 pr
595	6	0.8	250	2	G98027	conserved hypochet	668	6	0.8	267	2	S40006	trypsin (EC 3.4.21
596	6	0.8	250	2	E84708	probable signal pe	669	6	0.8	267	2	A98129	hypothetical prote
597	6	0.8	251	2	S47970	14-3-3 protein hom	670	6	0.8	267	2	AE3158	hypothetical prote
598	6	0.8	252	2	F84728	probable CCR4-asso	671	6	0.8	267	2	H90368	hypothetical prote
599	6	0.8	253	1	DLDO1A	discoidin I chain	672	6	0.8	267	2	G84862	probable clathrin
600	6	0.8	253	1	DLDO1C	discoidin I chain	673	6	0.8	268	2	H87708	exodeoxyribonuclea
601	6	0.8	253	2	AE0809	conserved hypochet	674	6	0.8	268	2	A64123	transcription fact
602	6	0.8	253	2	E64025	hypothetical prote	675	6	0.8	268	2	S11324	hypothetical prote
603	6	0.8	254	2	T07387	14-3-3 protein lft	676	6	0.8	268	2	T04965	hypothetical prote
604	6	0.8	254	2	S55375	14-3-3 protein - p	677	6	0.8	268	2	T40606	hypothetical prote
605	6	0.8	254	2	T07103	14-3-3 protein hom	678	6	0.8	269	2	T36639	probable substrate
606	6	0.8	255	2	T04127	14-3-3 protein, is	679	6	0.8	269	2	AG3538	ubiquitinone/menqu
607	6	0.8	255	2	T02050	GPI4-c protein hom	680	6	0.8	269	2	AE0466	probable haloacid
608	6	0.8	256	2	T04153	trypsin (EC 3.4.21	681	6	0.8	270	2	AB1580	conserved hypochet
609	6	0.8	256	2	T10109	amidease yead [limp	682	6	0.8	270	2	F69362	conserved hypochet
610	6	0.8	256	2	T44452	probable pseudouri	683	6	0.8	271	2	A85552	probable carboxyla
611	6	0.8	256	2	D70565	probable membrane	684	6	0.8	271	2	P90701	probable carboxyla
612	6	0.8	256	2	A10267	hypothetical prote	685	6	0.8	271	2	G64783	probable carboxyla
613	6	0.8	256	2	G71121		686	6	0.8	271	2		

687	6	0.8	272	2	B75293	760	6	0.8	295	2	F83142	probable transcrip
688	6	0.8	272	2	AG2819	761	6	0.8	295	2	T32202	hypothetical prote
689	6	0.8	272	2	G97597	762	6	0.8	297	2	ABC transporter, m	
690	6	0.8	273	2	D81878	763	6	0.8	297	2	T46590	probable regulator
691	6	0.8	273	2	H81140	764	6	0.8	297	2	S55063	conserved hypotnet
692	6	0.8	273	2	T49994	765	6	0.8	297	2	H90154	hypothetical prote
693	6	0.8	273	2	F82999	766	6	0.8	297	2	D83157	probable transcrip
694	6	0.8	273	2	A86280	767	6	0.8	297	2	T27525	hypothetical prote
695	6	0.8	273	2	A13630	768	6	0.8	298	2	AH0947	probable sugar kin
696	6	0.8	273	2	AC3573	769	6	0.8	298	2	C55223	minor tail protein
697	6	0.8	273	2	G83403	770	6	0.8	298	2	A28260	chromosomal protei
698	6	0.8	273	2	C95924	771	6	0.8	299	2	AE0269	conserved hypotnet
699	6	0.8	274	2	G86977	772	6	0.8	299	2	A87530	phosphorylaae fami
700	6	0.8	274	2	H83707	773	6	0.8	299	2	S30861	hypothetical prote
701	6	0.8	274	2	D96840	774	6	0.8	300	1	S40827	probable sugar kin
702	6	0.8	274	2	H70247	775	6	0.8	300	2	F91229	probable kinase [i
703	6	0.8	275	2	S40007	776	6	0.8	300	2	E86076	probable kinase yi
704	6	0.8	275	2	S40005	777	6	0.8	301	2	AD0660	probable transcrip
705	6	0.8	275	2	E70693	778	6	0.8	301	2	E86486	protein F2809.4 [i
706	6	0.8	275	2	G83522	779	6	0.8	302	2	S69188	probable flavonol
707	6	0.8	276	2	JE0218	780	6	0.8	302	2	AF3306	dipeptide transpor
708	6	0.8	276	2	E84373	781	6	0.8	302	2	E84421	probable phosphati
709	6	0.8	278	2	AE0210	782	6	0.8	302	2	B70888	hypothetical prote
710	6	0.8	278	2	AD0146	783	6	0.8	302	2	PC4287	protein kinase (EC
711	6	0.8	279	1	S74824	784	6	0.8	303	2	D83082	probable permease
712	6	0.8	279	2	C70458	785	6	0.8	303	2	S77278	lipic acid synthe
713	6	0.8	279	2	B70328	786	6	0.8	303	2	T36509	probable molybdopt
714	6	0.8	280	2	T36066	787	6	0.8	303	2	B72218	hypothetical prote
715	6	0.8	280	2	B84498	788	6	0.8	304	2	F83987	heat-shock protein
716	6	0.8	280	2	H72504	789	6	0.8	304	2	D72316	ribosomal large su
717	6	0.8	281	2	T43945	790	6	0.8	304	2	A96642	hypothetical prote
718	6	0.8	281	2	T05522	791	6	0.8	304	2	S75441	hypothetical prote
719	6	0.8	281	2	JE0418	792	6	0.8	305	2	T23022	hypothetical prote
720	6	0.8	282	2	AB1728	793	6	0.8	305	2	T20585	hypothetical prote
721	6	0.8	282	2	AC1054	794	6	0.8	306	2	A48652	transfer protein t
722	6	0.8	284	2	D81075	795	6	0.8	306	2	B83723	hypothetical prote
723	6	0.8	284	2	S75817	796	6	0.8	307	2	H70214	antigen, P35 homol
724	6	0.8	284	2	T24479	797	6	0.8	307	2	S55596	hypothetical prote
725	6	0.8	284	2	F81431	798	6	0.8	308	2	I40166	aspartate carbamoy
726	6	0.8	285	2	B83588	799	6	0.8	308	2	S77938	ENNA-LP protein -
727	6	0.8	285	2	F70194	800	6	0.8	308	2	T05297	hypothetical prote
728	6	0.8	285	2	AH0200	801	6	0.8	308	2	E90670	probable transcrip
729	6	0.8	286	2	E97720	802	6	0.8	309	2	B84550	hypothetical prote
730	6	0.8	286	2	A71722	803	6	0.8	310	2	AE8398	N-acetyl-gamma-glu
731	6	0.8	286	2	B83343	804	6	0.8	311	2	G90407	homoserine kinase
732	6	0.8	286	2	E91277	805	6	0.8	312	2	F82889	holliday junction
733	6	0.8	286	2	E86118	806	6	0.8	312	2	T45834	hypothetical prote
734	6	0.8	286	2	S56436	807	6	0.8	313	2	A12202	hypothetical prote
735	6	0.8	287	2	E75202	808	6	0.8	314	2	C69286	hypothetical prote
736	6	0.8	287	2	S03787	809	6	0.8	314	2	E96759	probable tumor-rel
737	6	0.8	287	2	AF0970	810	6	0.8	314	2	D97318	ABC-type MDR trans
738	6	0.8	287	2	F65165	811	6	0.8	316	2	E70664	hypothetical prote
739	6	0.8	287	2	H86040	812	6	0.8	316	2	B97086	hypothetical prote
740	6	0.8	287	2	G91193	813	6	0.8	317	1	E87185	3',5'-cyclic-nucle
741	6	0.8	287	2	E69778	814	6	0.8	317	2	F82672	ATP sulfurylase, s
742	6	0.8	288	2	G64102	815	6	0.8	317	2	S72871	hypothetical prote
743	6	0.8	288	2	T22721	816	6	0.8	318	1	F70536	3',5'-cyclic-nucle
744	6	0.8	290	1	D47468	817	6	0.8	318	2	C71168	hypothetical prote
745	6	0.8	290	2	E70141	818	6	0.8	319	2	AC2536	hypothetical prote
746	6	0.8	290	2	T24747	819	6	0.8	320	2	T10281	hypothetical prote
747	6	0.8	290	2	D71546	820	6	0.8	321	2	F97122	exopolysphatase
748	6	0.8	290	2	F81700	821	6	0.8	321	2	T27463	hypothetical prote
749	6	0.8	291	2	S05508	822	6	0.8	321	2	G27347	hypothetical prote
750	6	0.8	291	2	A97387	823	6	0.8	321	2	F81030	ABC transporter, p
751	6	0.8	291	2	AB2605	824	6	0.8	321	2	F81976	probable ferric en
752	6	0.8	292	2	S54533	825	6	0.8	321	2	A69088	conserved hypotnet
753	6	0.8	292	2	T34529	826	6	0.8	322	2	G72421	ion (Iii) ABC tran
754	6	0.8	292	2	T52257	827	6	0.8	322	2	E64238	hypothetical prote
755	6	0.8	292	2	H70513	828	6	0.8	322	2	E70306	conserved hypotnet
756	6	0.8	293	1	D69300	829	6	0.8	322	2	AF2725	transcription regu
757	6	0.8	293	2	T41928	830	6	0.8	322	2	B97507	probable transcrip
758	6	0.8	293	2	T31618	831	6	0.8	323	2	T22492	hypothetical prote
759	6	0.8	293	2	B75570	832	6	0.8	323	2	T47447	sulfotransferase-1

833	6	0.8	323	2	E83464	6	0.8	344	2	C75203	6	0.8	hypothetical prote
834	6	0.8	324	2	T07832	6	0.8	345	2	T17065	6	0.8	NADH2 dehydrogenas
835	6	0.8	324	2	F66788	6	0.8	345	2	JC1174	6	0.8	antidase (EC 3.5.1.
836	6	0.8	325	1	A45470	6	0.8	345	2	S73729	6	0.8	M307 homolog H08
837	6	0.8	325	2	T1610	6	0.8	345	2	A98251	6	0.8	hypothetical prote
838	6	0.8	325	2	T07833	6	0.8	345	2	AB3035	6	0.8	conserved hypotnet
839	6	0.8	325	2	T57009	6	0.8	346	2	UC7523	6	0.8	catabolite control
840	6	0.8	325	2	G90040	6	0.8	346	2	C96739	6	0.8	hypothetical prote
841	6	0.8	325	2	T23426	6	0.8	346	2	D42087	6	0.8	al-pheromone recep
842	6	0.8	326	2	T03928	6	0.8	346	2	S64693	6	0.8	pheromone receptor
843	6	0.8	326	2	F66407	6	0.8	346	2	T46914	6	0.8	hypothetical prote
844	6	0.8	326	2	A84452	6	0.8	347	2	T22655	6	0.8	hypothetical prote
845	6	0.8	326	2	A11732	6	0.8	348	2	D84798	6	0.8	probable mitochond
846	6	0.8	326	2	S49937	6	0.8	348	2	D84922	6	0.8	probable sugar tra
847	6	0.8	327	2	AB1822	6	0.8	348	2	T31681	6	0.8	bacs protein - Bac
848	6	0.8	327	2	T19529	6	0.8	348	2	F96997	6	0.8	uncharacterized co
849	6	0.8	328	2	T27911	6	0.8	350	2	T25366	6	0.8	hypothetical prote
850	6	0.8	328	2	T50104	6	0.8	351	2	G96923	6	0.8	NADH-dependent fla
851	6	0.8	328	2	B95307	6	0.8	351	2	T01845	6	0.8	hypothetical prote
852	6	0.8	328	2	B95404	6	0.8	352	2	A39042	6	0.8	faty-acid synthas
853	6	0.8	329	2	T74448	6	0.8	352	2	E83519	6	0.8	quinolinate synthe
854	6	0.8	329	2	C97264	6	0.8	353	2	S74379	6	0.8	probable ATPase -
855	6	0.8	329	2	AD1170	6	0.8	353	2	F84252	6	0.8	phycocyanin alpha
856	6	0.8	329	2	AP1527	6	0.8	353	2	H71223	6	0.8	probable dolichol-
857	6	0.8	329	2	T09897	6	0.8	354	2	C81986	6	0.8	probable O-6-alogl
858	6	0.8	329	2	H85520	6	0.8	354	2	C81040	6	0.8	O-6-sialoglycoprotei
859	6	0.8	330	2	G88115	6	0.8	355	2	C86592	6	0.8	antipeptidase P [
860	6	0.8	330	2	F72428	6	0.8	355	2	B72032	6	0.8	proline dipeptidas
861	6	0.8	330	2	A85074	6	0.8	356	2	T36961	6	0.8	probable zinc-cont
862	6	0.8	330	2	B97941	6	0.8	356	2	H84934	6	0.8	UUP-N-acetylmutra
863	6	0.8	331	2	S70212	6	0.8	356	2	H72214	6	0.8	hypothetical prote
864	6	0.8	331	2	B87359	6	0.8	356	2	AC1888	6	0.8	hypothetical prote
865	6	0.8	331	2	E82170	6	0.8	357	2	E64233	6	0.8	membrane transport
866	6	0.8	332	2	T47703	6	0.8	358	2	JQ0586	6	0.8	hypothetical prote
867	6	0.8	332	2	A1355	6	0.8	358	2	T36443	6	0.8	nucleosaprid prote
868	6	0.8	332	2	AB1726	6	0.8	359	2	T29647	6	0.8	probable penicilli
869	6	0.8	333	1	H64400	6	0.8	359	2	D83255	6	0.8	hypothetical prote
870	6	0.8	333	2	A84523	6	0.8	360	2	D83255	6	0.8	3-isopropylmalate
871	6	0.8	333	2	A41881	6	0.8	361	1	SYEBKR	6	0.8	choisimate synthas
872	6	0.8	334	2	T19637	6	0.8	361	1	SYECCR	6	0.8	choisimate synthas
873	6	0.8	334	2	B87545	6	0.8	361	2	AF0804	6	0.8	choisimate synthas
874	6	0.8	334	2	AB3414	6	0.8	361	2	E91030	6	0.8	choisimate synthas
875	6	0.8	335	2	G70369	6	0.8	361	2	F85874	6	0.8	choisimate synthas
876	6	0.8	335	2	F96999	6	0.8	361	2	F82115	6	0.8	choisimate synthas
877	6	0.8	335	2	H81677	6	0.8	361	2	JC6314	6	0.8	major porin protei
878	6	0.8	335	2	H91191	6	0.8	361	2	A43510	6	0.8	basic membrane pro
879	6	0.8	335	2	A86039	6	0.8	362	2	D72734	6	0.8	probable histidine
880	6	0.8	335	2	AB2193	6	0.8	362	2	G84526	6	0.8	hypothetical prote
881	6	0.8	335	2	T33457	6	0.8	362	2	AB2393	6	0.8	glycosyltransferas
882	6	0.8	335	2	E71215	6	0.8	364	2	H70776	6	0.8	hypothetical prote
883	6	0.8	336	2	S61299	6	0.8	365	1	A44974	6	0.8	ferredoxin-NADP re
884	6	0.8	336	2	C81073	6	0.8	365	2	T23220	6	0.8	hypothetical prote
885	6	0.8	336	2	B81869	6	0.8	366	1	UN0146	6	0.8	translatation releas
886	6	0.8	336	2	A97305	6	0.8	366	2	A64950	6	0.8	membrane-bound pen
887	6	0.8	337	2	AH0972	6	0.8	366	2	C85800	6	0.8	probable cytochrom
888	6	0.8	339	2	AD0009	6	0.8	366	2	G90951	6	0.8	probable cytochrom
889	6	0.8	339	2	T46731	6	0.8	366	2	JB0105	6	0.8	testicular serine
890	6	0.8	339	2	B55962	6	0.8	366	2	F87508	6	0.8	GTP-binding protei
891	6	0.8	339	2	E82211	6	0.8	367	2	S68680	6	0.8	stres-activated p
892	6	0.8	339	2	G82113	6	0.8	367	2	JB0104	6	0.8	testicular serine
893	6	0.8	339	2	F97121	6	0.8	367	2	H83088	6	0.8	membrane-bound lyl
894	6	0.8	340	2	T35394	6	0.8	368	2	G85587	6	0.8	hypothetical prote
895	6	0.8	340	2	T14774	6	0.8	368	2	F90737	6	0.8	hypothetical prote
896	6	0.8	341	2	T33221	6	0.8	368	2	H64815	6	0.8	YJNR protein - Bac
897	6	0.8	341	2	AB1394	6	0.8	369	1	RDSPXX	6	0.8	ferredoxin-NADP re
898	6	0.8	341	2	AB1769	6	0.8	369	2	F81674	6	0.8	conserved hypotnet
899	6	0.8	342	2	H86893	6	0.8	369	2	S37314	6	0.8	cycH protei
900	6	0.8	342	2	A10043	6	0.8	369	2	H82404	6	0.8	hypothetical prote
901	6	0.8	342	2	AP1398	6	0.8	370	2	F95363	6	0.8	probable serine-py
902	6	0.8	342	2	AC1774	6	0.8	370	2	C96979	6	0.8	similar to spore g
903	6	0.8	342	2	C86811	6	0.8	370	2	AF1432	6	0.8	recf protei
904	6	0.8	343	2	G72218	6	0.8	370	2	H72748	6	0.8	probable glycerol
905	6	0.8	344	1	S49978	6	0.8	370	2	T33382	6	0.8	hypothetical prote

979	6	0.8	371	2	C70237	hypothetical prote
980	6	0.8	371	2	T18558	probable mitochond
981	6	0.8	372	1	A5510	chorismate synthas
982	6	0.8	372	1	D69442	conserved hypotnet
983	6	0.8	372	2	S18953	fix23-1 protein -
984	6	0.8	372	2	T09612	secreted glycoprot
985	6	0.8	373	2	A82398	maltose/maltodextr
986	6	0.8	373	2	G90398	hypothetical prote
987	6	0.8	373	2	E72216	alanine-tRNA ligas
988	6	0.8	374	2	D90338	hypothetical prote
989	6	0.8	374	2	G89846	hypothetical prote
990	6	0.8	375	2	S17253	alcohol dehydrogen
991	6	0.8	375	2	D82585	imidazolesglycerolp
992	6	0.8	375	2	A83802	NAD biosynthesis n
993	6	0.8	375	2	C90746	probable enzyme [i
994	6	0.8	375	2	G85596	probable enzyme yb
995	6	0.8	375	2	C64824	probable RNA methy
996	6	0.8	376	1	F64705	conserved hypotnet
997	6	0.8	376	2	F71815	hypothetical prote
998	6	0.8	376	2	AD1915	hypothetical prote
999	6	0.8	377	2	G85975	hypothetical prote
1000	6	0.8	379	2	T32778	hypothetical prote
1001	6	0.8	379	2	T21417	hypothetical prote
1002	6	0.8	380	2	A55259	hypothetical prote
1003	6	0.8	380	2	T43016	DNA mismatch repai
1004	6	0.8	380	2	G86656	ABC transporter pe
1005	6	0.8	380	2	A12185	hypothetical prote
1006	6	0.8	381	2	A43769	fodrin alpha chain
1007	6	0.8	381	2	S65212	hypothetical prote
1008	6	0.8	381	2	T34692	probable transmemb
1009	6	0.8	382	2	E8249	mmp protein VC1037
1010	6	0.8	382	2	G86791	hypothetical prote
1011	6	0.8	382	2	T38092	hypothetical prote
1012	6	0.8	382	2	A13175	conserved hypotnet
1013	6	0.8	383	1	A25978	alcohol dehydrogen
1014	6	0.8	383	2	S32975	gene BCR2 protein
1015	6	0.8	383	2	B83205	hypothetical prote
1016	6	0.8	383	2	T23041	hypothetical prote
1017	6	0.8	383	2	A71139	hypothetical prote
1018	6	0.8	384	2	G91130	N-acetylglactosam
1019	6	0.8	385	2	T52483	hypothetical prote
1020	6	0.8	385	2	T47535	hypothetical prote
1021	6	0.8	385	2	T51127	G6P synthase [lmp
1022	6	0.8	385	2	A82651	hypothetical prote
1023	6	0.8	385	2	D97433	polyamine transpor
1024	6	0.8	386	1	S22315	smbNP-associated p
1025	6	0.8	386	2	H71511	probable 2-compone
1026	6	0.8	386	2	T09598	cyclin 4, D-type -
1027	6	0.8	387	2	H71708	pol (A) POLYMERASE
1028	6	0.8	387	2	T38876	probable ribosomal
1029	6	0.8	387	2	F82815	voltage-gated pota
1030	6	0.8	387	2	C86640	multidrug efflux t
1031	6	0.8	387	2	S00867	colicin N - Escher
1032	6	0.8	387	2	T47013	hypothetical prote
1033	6	0.8	387	2	E83679	multidrug-efflux t
1034	6	0.8	387	2	E97028	probable amidohydr
1035	6	0.8	387	2	AD0237	probable membrane
1036	6	0.8	387	2	A86322	F6a14.9 protein -
1037	6	0.8	388	2	H83714	alanine racemase B
1038	6	0.8	388	2	AG2663	mmp protein [lmpor
1039	6	0.8	389	2	B86017	probable 3-oxoacyl
1040	6	0.8	389	2	B91171	probable 3-oxoacyl
1041	6	0.8	389	2	C83202	alginatase biosynthe
1042	6	0.8	390	2	F97445	mmp protein homolo
1043	6	0.8	390	2	A83384	N-acetylneuramoyl-L
1044	6	0.8	391	2	F83269	fatty-acid oxidati
1045	6	0.8	391	2	B70625	protein T20D3.3 [i
1046	6	0.8	392	2	B70625	probable PPE prote
1047	6	0.8	392	2	F83610	probable fatty acyl
1048	6	0.8	392	2	AB1505	hietidyl-tRNA synt
1049	6	0.8	392	2	S72984	hypothetical prote
1050	6	0.8	392	2	T34095	zinc finger protei
1051	6	0.8	393	2	AB0035	cystathionine beta
1052	6	0.8	393	2	AB1146	hietidyl-tRNA synt
1053	6	0.8	393	2	F91195	probable integrase
1054	6	0.8	393	2	G86042	probable integrase
1055	6	0.8	393	2	A55859	regulatory prote
1056	6	0.8	393	2	D96577	hypothetical prote
1057	6	0.8	393	2	E97309	probable amidohydr
1058	6	0.8	394	2	US0600	t-plasminogen acti
1059	6	0.8	394	2	T44463	integrase int [lmp
1060	6	0.8	394	2	S26431	intermediate filam
1061	6	0.8	394	2	S39739	efflux protein hom
1062	6	0.8	395	1	Q0ECPR	hypothetical 45.2K
1063	6	0.8	395	2	F69148	hypothetical prote
1064	6	0.8	395	2	T00574	probable protein k
1065	6	0.8	395	2	A40270	cyclin E - human
1066	6	0.8	395	2	A91129	hypothetical prote
1067	6	0.8	395	2	H85973	hypothetical prote
1068	6	0.8	395	2	AB3543	succinyl-diaminopi
1069	6	0.8	395	2	A95860	hypothetical prote
1070	6	0.8	395	2	B83313	probable type II s
1071	6	0.8	396	2	AB2309	hypothetical prote
1072	6	0.8	397	2	A82108	flagellar hook-ans
1073	6	0.8	397	2	AB1142	penicillin-binding
1074	6	0.8	398	2	C81729	Mrx/TnaB/TyRO perm
1075	6	0.8	398	2	D83506	conserved hypotnet
1076	6	0.8	398	2	AH1500	penicillin-binding
1077	6	0.8	399	2	F82657	beta-ketocyl-[ACP
1078	6	0.8	399	2	A31137	hemocyanin - giant
1079	6	0.8	399	2	F89893	hypothetical prote
1080	6	0.8	400	1	JC1428	ketol-acid reducto
1081	6	0.8	400	2	G64104	pantothenate metab
1082	6	0.8	400	2	F86887	hypothetical prote
1083	6	0.8	400	2	T04460	protein kinase AMB
1084	6	0.8	401	2	T25031	hypothetical prote
1085	6	0.8	402	2	AD1417	drug-efflux transp
1086	6	0.8	402	2	AF1792	ectin Cl - sea ur
1087	6	0.8	402	2	S71137	endospem specific
1088	6	0.8	402	2	T04348	hypothetical prote
1089	6	0.8	403	1	C83881	homeotic protein 1
1090	6	0.8	403	1	S23802	probable high-affi
1091	6	0.8	403	1	S01828	cytokeratin 19 - m
1092	6	0.8	403	2	T00028	hypothetical prote
1093	6	0.8	403	2	T45580	hypothetical prote
1094	6	0.8	403	2	T27948	hypothetical prote
1095	6	0.8	404	2	UC5171	D-galactose-bindin
1096	6	0.8	404	2	T40532	ketol-acid reducto
1097	6	0.8	404	2	G01507	LIM domain transcr
1098	6	0.8	404	2	A55444	integral membrane
1099	6	0.8	404	2	B46189	orf within vasococ
1100	6	0.8	405	1	T00089	ABC transporter rg
1101	6	0.8	405	2	AH2995	conserved hypotnet
1102	6	0.8	405	2	AB0793	probable MR-MLR-fa
1103	6	0.8	406	1	I58187	homeotic protein 1
1104	6	0.8	406	1	I48186	homeotic protein 1
1105	6	0.8	406	1	I48637	homeotic protein 1
1106	6	0.8	406	1	I50375	homeotic protein 1
1107	6	0.8	406	1	G70639	hypothetical prote
1108	6	0.8	406	2	B89942	conserved hypotnet
1109	6	0.8	407	2	AC2721	MFS permease [lmpo
1110	6	0.8	407	2	G97502	probable mfs trans
1111	6	0.8	408	2	B95214	hypothetical prote
1112	6	0.8	408	2	H98250	hypothetical prote
1113	6	0.8	409	2	UC1378	arylalialyphospha
1114	6	0.8	409	2	C95042	hypothetical prote
1115	6	0.8	410	2	T34717	probable transmemb
1116	6	0.8	410	2	S68515	probable arginine
1117	6	0.8	410	2	D84785	hypothetical prote
1118	6	0.8	410	2	S38228	hypothetical prote
1119	6	0.8	411	2	H95048	3-oxoacyl-(acyl)-ca
1120	6	0.8	411	2	PC2061	genome polyprotein
1121	6	0.8	411	2	AE3485	florfenicol resist
1122	6	0.8	411	2	S40064	3-deoxy-manno-octu
1123	6	0.8	412	2	H70915	probable pgk prote
1124	6	0.8	412	2	H75484	hypothetical prote

1125	6	0.8	413	2	T43170	probable triacylgly	1198	6	0.8	431	2	T00698	methionyl aminope
1126	6	0.8	413	2	S61305	cycH protein - Par	1199	6	0.8	431	2	JS0599	t-plasminogen acti
1127	6	0.8	413	2	A82726	conserved hypotnet	1200	6	0.8	431	2	F86179	hypothetical prote
1128	6	0.8	413	2	T26915	hypothetical prote	1201	6	0.8	432	1	RMQ074	T-cell surface gly
1129	6	0.8	414	2	H70667	probable oxidoredu	1202	6	0.8	432	1	RMQ074	T-cell surface gly
1130	6	0.8	414	2	F97919	3-oxoacyl-l-acyl-ca	1203	6	0.8	432	2	E71442	probable asparagin
1131	6	0.8	414	2	E90572	hypothetical prote	1204	6	0.8	432	2	E89954	conserved hypotnet
1132	6	0.8	414	2	E87316	periplasmic phosph	1205	6	0.8	433	1	JN0560	u-plasminogen acti
1133	6	0.8	414	2	E87292	pentapeptide repes	1206	6	0.8	433	1	UKBAY	u-plasminogen acti
1134	6	0.8	414	2	A29835	SalI protein - Bsc	1207	6	0.8	433	2	D75480	UP-N-acetylmuramo
1135	6	0.8	414	2	A10277	probable phage-rel	1208	6	0.8	434	2	A86305	FeII, 5 protein - A
1136	6	0.8	415	2	TE8144	corticotropin-rel	1209	6	0.8	435	2	H82501	nicotinate phospho
1137	6	0.8	415	2	D81909	probable integral	1210	6	0.8	435	2	T47737	hypothetical prote
1138	6	0.8	415	2	D81107	conserved hypotnet	1211	6	0.8	435	2	AB1786	cellobiose phospho
1139	6	0.8	415	2	T49072	hypothetical prote	1212	6	0.8	435	2	E83362	probable 2-ketoglu
1140	6	0.8	416	1	SC0673	calreticulin precu	1213	6	0.8	436	2	G97701	polynucleotide ade
1141	6	0.8	416	1	ACCH3N	nicotinic acetylch	1214	6	0.8	436	2	JC5599	cholecystokinin-A
1142	6	0.8	416	1	D11277	cytosine-tRNA liga	1215	6	0.8	436	2	S74385	hypothetical prote
1143	6	0.8	417	2	D98078	conserved hypotnet	1216	6	0.8	436	2	F48399	hypothetical prote
1144	6	0.8	417	2	G98200	sarcosine oxidase	1217	6	0.8	436	2	F86486	protein F2809.3 [1
1145	6	0.8	417	2	AB3086	sarcosine oxidase	1218	6	0.8	436	2	G97186	diverged glycosylt
1146	6	0.8	417	2	AB3056	sarcosine oxidase	1219	6	0.8	437	2	S34959	NADH2 dehydrogenas
1147	6	0.8	417	2	T05207	hypothetical prote	1220	6	0.8	437	2	A55682	keratin 13, type I
1148	6	0.8	417	2	A97063	NAD(FAD)-dependent	1221	6	0.8	438	1	S11225	transcription fact
1149	6	0.8	418	2	H97437	cyclopropane-fatty	1222	6	0.8	438	2	JC1179	transfoming prote
1150	6	0.8	418	2	AC2656	cyclopropane-fatty	1223	6	0.8	438	2	AF3215	ABC transporter, m
1151	6	0.8	418	2	E96765	hypothetical prote	1224	6	0.8	438	2	AH2285	hypothetical prote
1152	6	0.8	418	2	H83126	probable secretion	1225	6	0.8	439	1	TVC2WC	transforming prote
1153	6	0.8	419	2	C64813	probable protein k	1226	6	0.8	439	1	TVMS	transforming prote
1154	6	0.8	419	2	D86785	diaminopimelate de	1227	6	0.8	439	1	T25494	probable cytochrom
1155	6	0.8	419	2	JC4123	pregnancy-specific	1228	6	0.8	440	1	A05875	transcription fact
1156	6	0.8	419	2	S75647	glutamate N-acetyl	1229	6	0.8	440	1	Q08YRY	TYA protein - yeas
1157	6	0.8	419	2	B89788	hypothetical prote	1230	6	0.8	440	2	S43113	phosphorylpruvate hy
1158	6	0.8	419	2	P83673	PTS system, galact	1231	6	0.8	440	2	I48291	transcription fact
1159	6	0.8	420	2	B98288	hypothetical prote	1232	6	0.8	440	2	I50213	protein-tyrosine-p
1160	6	0.8	420	2	B95100	conserved hypotnet	1233	6	0.8	440	2	S57044	TYA protein - yeas
1161	6	0.8	420	2	D97968	conserved hypotnet	1234	6	0.8	440	2	A22671	TYA protein - yeas
1162	6	0.8	421	2	B84702	hypothetical prote	1235	6	0.8	440	2	S57046	TYA protein - yeas
1163	6	0.8	422	2	H82236	iron-containing al	1236	6	0.8	440	2	S69837	TYA protein - yeas
1164	6	0.8	422	2	P89805	xanthine permease	1237	6	0.8	440	2	S45866	TYA protein - yeas
1165	6	0.8	423	2	A13309	tRNA adenyllyltrans	1238	6	0.8	440	2	S69964	TYA protein - yeas
1166	6	0.8	423	2	A99230	sarcosine oxidase	1239	6	0.8	440	2	S50947	TYA protein - yeas
1167	6	0.8	423	2	AH1407	PTS system galacti	1240	6	0.8	440	2	S51894	TYA protein - yeas
1168	6	0.8	423	2	AH1763	PTS system galacti	1241	6	0.8	440	2	S69840	TYA protein - yeas
1169	6	0.8	423	2	T31342	ragd protein - Bra	1242	6	0.8	440	2	S69985	TYA protein - yeas
1170	6	0.8	424	2	C64362	aconitate hydratase	1243	6	0.8	440	2	S69971	TYA protein - yeas
1171	6	0.8	424	2	T35355	probable secreted	1244	6	0.8	440	2	S69976	TYA protein - yeas
1172	6	0.8	424	2	AD2017	cell wall-binding	1245	6	0.8	440	2	S53588	TYA protein - yeas
1173	6	0.8	424	2	AB1933	probable malate de	1246	6	0.8	440	2	S70228	TYA protein - yeas
1174	6	0.8	426	2	C61173	malate oxidoreduct	1247	6	0.8	440	2	S53553	TYA protein - yeas
1175	6	0.8	426	2	T52285	setine/threonine-8	1248	6	0.8	440	2	S51249	TYA protein YDB557
1176	6	0.8	426	2	E70058	ubiquinol-cytochro	1249	6	0.8	440	2	S61577	TYA protein - yeas
1177	6	0.8	427	2	S55905	phosphotransferase	1250	6	0.8	440	2	S40909	TYA protein - yeas
1178	6	0.8	427	2	G69067	N-ethylmaleline ch	1251	6	0.8	440	2	D69596	branched-chain aml
1179	6	0.8	427	2	T29376	hypothetical prote	1252	6	0.8	440	2	D64186	conserved hypotnet
1180	6	0.8	427	2	A86493	polymorphic outer	1253	6	0.8	440	2	C97620	probable proteinas
1181	6	0.8	428	1	TYHUEK	transforming prote	1254	6	0.8	441	1	A53988	transcription fact
1182	6	0.8	428	2	D70989	probable oxidoredu	1255	6	0.8	441	1	TVCHTE	transcription fact
1183	6	0.8	428	2	D70343	glycine hydroxymet	1256	6	0.8	441	1	TVHDET	transcription fact
1184	6	0.8	428	2	JN0692	cholecystokinin cy	1257	6	0.8	441	2	C38575	glucuronate 2-dehydr
1185	6	0.8	428	2	P85485	flavoprotein, elec	1258	6	0.8	441	2	E84264	isochoformate synt
1186	6	0.8	428	2	F90634	flavoprotein [lipo	1259	6	0.8	442	1	UKPG	u-plasminogen acti
1187	6	0.8	428	2	C64725	fixC protein - Bsc	1260	6	0.8	442	2	G84465	probable cytochrom
1188	6	0.8	428	2	B75133	cytochrome-c3 hydr	1261	6	0.8	443	2	G59102	hypothetical prote
1189	6	0.8	428	2	T06290	hypothetical prote	1262	6	0.8	443	2	F30010	NADH2 dehydrogenas
1190	6	0.8	428	2	G56273	protein-histidine	1263	6	0.8	443	2	I39538	alpha-amylase - Ae
1191	6	0.8	429	2	E70979	carbon dioxide-fix	1264	6	0.8	444	2	A42685	cholecystokinin re
1192	6	0.8	429	2	JC4965	ellI protein - mou	1265	6	0.8	444	2	H71243	probable helicase
1193	6	0.8	429	2	C64199	hypothetical prote	1266	6	0.8	445	2	T26752	hypothetical prote
1194	6	0.8	429	2	A70949	hypothetical prote	1267	6	0.8	446	2	E75075	hybrid cluster 14F
1195	6	0.8	430	2	F87472	FMN oxidoreductase	1268	6	0.8	446	2	F86815	hypothetical prote
1196	6	0.8	431	1	UKHU	u-plasminogen acti	1269	6	0.8	446	2	T07907	hydroxyproline-ric
1197	6	0.8	431	2	F84077	homoserine dehydro	1270	6	0.8	446	2	A75209	DNA repair protein

1271	6	0.8	447	2	C66233	hypothetical prote
1272	6	0.8	448	2	A81919	hypothetical prote
1273	6	0.8	449	2	AC1019	probable xanthine/
1274	6	0.8	449	2	T23126	hypothetical prote
1275	6	0.8	450	2	C87463	hypothetical prote
1276	6	0.8	450	2	T08701	hypothetical prote
1277	6	0.8	451	2	A85836	PTS system galacti
1278	6	0.8	451	2	C64976	galC protein - Bac
1279	6	0.8	451	2	G90990	PTS system galacti
1280	6	0.8	451	2	T36217	plasmid transfer p
1281	6	0.8	452	2	I49595	cytokerin 15 - m
1282	6	0.8	454	1	C69214	zinc metalloprotei
1283	6	0.8	454	1	F75580	probable sugar tra
1284	6	0.8	455	2	B90619	NADH dehydrogenase
1285	6	0.8	455	2	S50725	hypothetical prote
1286	6	0.8	456	1	KRMU5	keratin 15, type I
1287	6	0.8	456	2	T40386	hypothetical prote
1288	6	0.8	456	2	H85022	hypothetical prote
1289	6	0.8	456	2	T05612	hypothetical prote
1290	6	0.8	456	2	S47924	MG1 protein - yea
1291	6	0.8	457	2	AC1056	murain peptidase lig
1292	6	0.8	457	2	B86121	probable ligase Yj
1293	6	0.8	457	2	B91280	probable ligase [i
1294	6	0.8	457	2	S66459	UDP-N-acetylmurama
1295	6	0.8	457	2	AH0898	PTS system, galact
1296	6	0.8	457	2	B83643	potasssium uptake p
1297	6	0.8	458	1	B82268	conserved hypotet
1298	6	0.8	458	1	RHMUT4	T-cell surface gly
1299	6	0.8	458	2	B90621	NADH dehydrogenase
1300	6	0.8	458	2	B90625	NADH dehydrogenase
1301	6	0.8	458	2	B90615	NADH dehydrogenase
1302	6	0.8	458	2	B90617	NADH dehydrogenase
1303	6	0.8	458	2	T11176	NADH2 dehydrogenas
1304	6	0.8	458	2	T11528	NADH2 dehydrogenas
1305	6	0.8	458	2	B99613	NADH dehydrogenase
1306	6	0.8	458	2	B90627	NADH dehydrogenase
1307	6	0.8	458	2	B90623	NADH dehydrogenase
1308	6	0.8	458	2	B97324	sugar/Na <sup>+</sup> (H <sup>+</sup> ) s1mp
1309	6	0.8	459	2	S10196	NADH2 dehydrogenas
1310	6	0.8	459	2	T11411	NADH2 dehydrogenas
1311	6	0.8	459	2	T11189	NADH2 dehydrogenas
1312	6	0.8	459	2	T11256	NADH2 dehydrogenas
1313	6	0.8	459	2	T11084	NADH2 dehydrogenas
1314	6	0.8	459	2	AEO679	probable membrane
1315	6	0.8	459	2	G90080	Na <sup>+</sup> /H <sup>+</sup> antiporter
1316	6	0.8	459	2	G81187	probable transmemb
1317	6	0.8	459	2	F81914	hypothetical prote
1318	6	0.8	459	2	T24742	hypothetical prote
1319	6	0.8	459	2	D86256	hypothetical prote
1320	6	0.8	460	2	T24248	keratin, type II -
1321	6	0.8	461	2	A43782	probable carboxype
1322	6	0.8	461	2	C86935	probable transmemb
1323	6	0.8	461	2	D81418	hypothetical prote
1324	6	0.8	462	2	T00621	hypothetical prote
1325	6	0.8	462	2	T28699	probable phosphoty
1326	6	0.8	463	2	S72992	peptidyl prolyl ci
1327	6	0.8	463	2	T39621	glutathione-disulf
1328	6	0.8	464	2	AG3774	glutathione-disulf
1329	6	0.8	464	2	E97554	probable CoA-depen
1330	6	0.8	464	2	AF0761	hypothetical prote
1331	6	0.8	464	2	C83328	transferring prote
1332	6	0.8	465	2	S03325	probable tata bind
1333	6	0.8	465	2	T40697	conserved hypotet
1334	6	0.8	466	2	C64690	sensory kinase Bae
1335	6	0.8	467	2	E64974	hypothetical prote
1336	6	0.8	468	2	A12956	ethanolamine utili
1337	6	0.8	469	2	AE1220	glycosyltransferas
1338	6	0.8	470	2	B90481	hypothetical prote
1339	6	0.8	470	2	D85111	hypothetical prote
1340	6	0.8	470	2	T31049	hypothetical prote
1341	6	0.8	470	2	T31049	hypothetical prote
1342	6	0.8	470	2	T45272	noix protein - Rnl
1343	6	0.8	471	2	S35019	
1344	6	0.8	471	2	E83173	hypothetical prote
1345	6	0.8	471	2	A84741	probable myrosinas
1346	6	0.8	472	2	T47436	protein kinase-lik
1347	6	0.8	472	2	E98020	hypothetical prote
1348	6	0.8	472	2	T51559	probable flavonol
1349	6	0.8	473	2	E86955	conserved hypotet
1350	6	0.8	473	2	G70975	hypothetical prote
1351	6	0.8	474	2	S30227	transposase - C1os
1352	6	0.8	474	2	H82564	3-isopropylmalate
1353	6	0.8	474	2	T20694	hypothetical prote
1354	6	0.8	475	2	A70318	aldenhyde dehydroge
1355	6	0.8	476	2	T47606	UMP synthase - Ara
1356	6	0.8	476	2	S46440	bifunctional UMP s
1357	6	0.8	477	1	A33639	t-plaaminogen acti
1358	6	0.8	477	1	JS0597	t-plaaminogen acti
1359	6	0.8	477	2	JS0598	hypothetical prote
1360	6	0.8	477	2	T46304	aldenhyde dehydroge
1361	6	0.8	478	2	E90495	translation elonga
1362	6	0.8	478	2	S36183	translation elonga
1363	6	0.8	478	2	UQ2240	TYA protein - yea
1364	6	0.8	478	2	S52602	hypothetical prote
1365	6	0.8	478	2	T25899	related to aldenhyd
1366	6	0.8	479	2	T51919	lipopolysaccharide
1367	6	0.8	479	2	D72354	sefine/threonine p
1368	6	0.8	479	2	S48705	protein kinase hom
1369	6	0.8	480	2	T04849	lipopolysaccharide
1370	6	0.8	480	2	B35843	probable non-proce
1371	6	0.8	482	2	E97012	altronate oxidore
1372	6	0.8	483	2	A85723	tagaturonate reduc
1373	6	0.8	483	2	D64906	altronate oxidore
1374	6	0.8	483	2	H90894	gag-myc polypotei
1375	6	0.8	484	1	TVMVFT	hypothetical prote
1376	6	0.8	484	2	D89781	hypothetical prote
1377	6	0.8	484	2	T33492	transcription fact
1378	6	0.8	485	1	TVCHET	transcription fact
1379	6	0.8	485	2	AD0041	glutamy1-tRNA (Gln)
1380	6	0.8	485	2	B69795	probable phox prot
1381	6	0.8	485	2	A70706	probable cytochrom
1382	6	0.8	486	2	T32401	glutamy1-tRNA (Gln
1383	6	0.8	486	2	T51582	coenzyme F420-guin
1384	6	0.8	487	2	H69477	hypothetical prote
1385	6	0.8	487	2	E98326	transcription fact
1386	6	0.8	488	1	TYFVES	hypothetical prote
1387	6	0.8	488	2	F95875	hypothetical prote
1388	6	0.8	489	2	JC4787	shaw protein - Cal
1389	6	0.8	490	2	D70008	nicotinate phospho
1390	6	0.8	490	2	G70108	hypothetical prote
1391	6	0.8	491	2	AT0068	udp-N-acetylmurama
1392	6	0.8	491	2	D97311	amino acid transpo
1393	6	0.8	492	2	AG1838	hypothetical prote
1394	6	0.8	492	2	G71112	catalase (EC 1.11.
1395	6	0.8	492	2	S41288	genome polypotein
1396	6	0.8	492	2	C63316	protein T10022.7 [
1397	6	0.8	493	2	T51453	serine/threonine s
1398	6	0.8	493	2	A85441	cytochrome P450-1i
1399	6	0.8	495	2	S60589	acetylcholine rece
1400	6	0.8	495	2	G82371	FlxG-related prote
1401	6	0.8	496	2	T11376	cytochrome-c oxida
1402	6	0.8	496	2	H70668	acid-coa ligase, p
1403	6	0.8	496	2	G87546	proline/lysine-ric
1404	6	0.8	496	2	T17908	serine protease,
1405	6	0.8	497	2	B81728	acetyl-CoA acetyl
1406	6	0.8	497	2	S27785	phosphoprotein pho
1407	6	0.8	498	1	S52570	probable succinate
1408	6	0.8	498	2	B95893	potassium channel
1409	6	0.8	498	2	A41359	nitrogenase (EC 1.
1410	6	0.8	499	1	B29042	phosphoprotein pho
1411	6	0.8	499	1	A55346	nicotinic acetylch
1412	6	0.8	499	2	A24572	glutelin 2 precurs
1413	6	0.8	499	2	B34332	glutelin type I pr
1414	6	0.8	499	2	S06350	glutelin precursor
1415	6	0.8	499	2	A27033	hypothetical prote
1416	6	0.8	499	2	H87460	



1417	6	0.8	499	2	T47879	hypothetical prote
1418	6	0.8	522	1	S22571	integrase-like pro
1419	6	0.8	500	1	A44001	gag polyprotein -
1420	6	0.8	501	2	C82414	aminopeptidase VCA
1421	6	0.8	502	2	T35743	ribosomal protein
1422	6	0.8	502	2	A37040	nicotinic acetylch
1423	6	0.8	502	2	T19876	lipoprotein lipa -
1424	6	0.8	503	2	T46852	anthranilate synth
1425	6	0.8	503	2	A53956	nicotinic acetylch
1426	6	0.8	503	2	A54868	nuclear respirator
1427	6	0.8	504	2	AB2843	hydrolyase [impor
1428	6	0.8	504	2	C86428	hypothetical prote
1429	6	0.8	505	1	FWYCA	H+-transporting tw
1430	6	0.8	506	2	G31090	H+-transporting tw
1431	6	0.8	506	2	AE1807	ATP synthase chain
1432	6	0.8	506	2	D82081	UDP-N-acetylmuram
1433	6	0.8	506	2	T41623	probable protein k
1434	6	0.8	507	1	A39072	steroid 17alpha-mo
1435	6	0.8	507	2	T51658	terminal deoxynuc
1436	6	0.8	507	2	T07012	acetyl-CoA carboxy
1437	6	0.8	507	2	C96988	probable membrane
1438	6	0.8	508	1	UPBSHS	histidine ammonia-
1439	6	0.8	508	2	E70764	probable cobI prot
1440	6	0.8	509	2	E80504	hypothetical prote
1441	6	0.8	509	2	S45631	DNA primase chain
1442	6	0.8	509	2	A13300	sugar transport AT
1443	6	0.8	510	2	T29642	hypothetical prote
1444	6	0.8	511	2	A54676	antiquitin - human
1445	6	0.8	512	2	S04672	H+-transporting tw
1446	6	0.8	512	2	A05196	hypothetical prote
1447	6	0.8	512	2	B69146	glutathione-regula
1448	6	0.8	512	2	B69024	conserved hypotet
1449	6	0.8	513	2	F83162	nitrate reductase
1450	6	0.8	513	2	A81850	probable integrase
1451	6	0.8	513	2	CG1092	oxalate/formate an
1452	6	0.8	513	2	H69735	endo-1,4-beta-xyla
1453	6	0.8	514	2	A10671	respiratory nitrat
1454	6	0.8	514	2	C70446	hypothetical prote
1455	6	0.8	515	2	T43152	hypothetical prote
1456	6	0.8	515	2	B81318	probable two-domai
1457	6	0.8	516	2	T48238	hypothetical prote
1458	6	0.8	517	2	F86921	probable acyl CoA
1459	6	0.8	517	2	D90073	hypothetical prote
1460	6	0.8	517	2	T27927	hypothetical prote
1461	6	0.8	518	2	D64244	H+-transporting tw
1462	6	0.8	518	2	C70887	probable Propionyl
1463	6	0.8	520	2	H95884	probable regulator
1464	6	0.8	522	2	S51557	cytochrome P450, 3
1465	6	0.8	523	2	B95922	hypothetical nucle
1466	6	0.8	523	2	A53196	orphan hormone nuc
1467	6	0.8	523	2	S68517	nuclear hormone re
1468	6	0.8	525	2	A70735	probable guaA prot
1469	6	0.8	525	2	G71317	hypothetical prote
1470	6	0.8	525	2	T34178	hypothetical prote
1471	6	0.8	526	1	T45058	phosphoprotein pho
1472	6	0.8	526	2	A81135	phosphoribosylam
1473	6	0.8	527	2	A42032	epidermal growth f
1474	6	0.8	528	2	CG5527	regulator for prp
1475	6	0.8	528	2	H90676	regulator for prp
1476	6	0.8	529	2	C86958	probable GMP synth
1477	6	0.8	529	2	A95423	probable ABC trans
1478	6	0.8	529	2	T27922	hypothetical prote
1479	6	0.8	530	2	H81865	purH bifunctional
1480	6	0.8	530	2	T12031	hypothetical prote
1481	6	0.8	530	2	UC7983	peptidoglycan reco
1482	6	0.8	530	2	T28212	hypothetical prote
1483	6	0.8	530	2	C82442	probable peptide A
1484	6	0.8	531	2	AD0666	conserved hypotet
1485	6	0.8	531	2	T05644	hypothetical prote
1486	6	0.8	531	2	T52462	hypothetical prote
1487	6	0.8	531	2	T28222	hypothetical prote
1488	6	0.8	533	2	B26446	vire2 protein - Ag
1489	6	0.8	533	2	S73755	adhesin PI precurs

1490	6	0.8	534	2	D71698	Cytochrome-c oxida
1491	6	0.8	535	2	C96618	probable squalene
1492	6	0.8	536	2	T38210	scd2 protein - fis
1493	6	0.8	536	2	AG1482	hypothetical prote
1494	6	0.8	536	2	AB3038	conserved hypotet
1495	6	0.8	538	2	G83653	oligopeptide ABC t
1496	6	0.8	538	2	T40992	hypothetical prote
1497	6	0.8	539	2	G95405	hypothetical prote
1498	6	0.8	540	1	OXECLD	L-aspartate oxidas
1499	6	0.8	540	1	H91058	guinolinate synthe
1500	6	0.8	540	2	AB0830	L-aspartate oxidas

## ALIGNMENTS

RESULT 1  
 T08805  
 Hypothetical protein DKFZp586H2123.1 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
 C/Accession: T08805  
 R:Angorge, W.; Wikner, U.; Mewes, H.W.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove  
 submitted to the Protein Sequence Database, May 1999  
 A/Reference number: Z16472  
 A/Accession: T08805  
 A/Molecule type: mRNA  
 A/Residues: 1-181 <ANS>  
 A/Cross-references: UNIPROT:Q9Y432; EMBL:AL050214  
 A/Experimental source: adult uterus; clone DKFZp586H2123  
 C/Genetics:  
 A/Note: DKFZp586H2123.1

Query Match 24.7%; Score 178; DB 2; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-182; Indels 0; Gaps 0;  
 Matches 178; Conservative 0; Mismatches 0;

Qy	543	ISATILHPNDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITTVAGWN	602
Db	4	ISATILHPNDPILLDADIAILKLLDKARISTRVQPICLAASRDLSFQESHITTVAGWN	63
Qy	603	VLADVRSFGKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTDNMFCAWEPAPSDICT	662
Db	64	VLADVRSFGKNDTLRSQVSVVDSLLCEQHEDHGIPVSVTDNMFCAWEPAPSDICT	123
Qy	663	AETGCIAAVSFPGASPEPRWHLMGVSWSYDKTSRSLSTAFKXVLPFQDIERNMK	720
Db	124	AETGCIAAVSFPGASPEPRWHLMGVSWSYDKTSRSLSTAFKXVLPFQDIERNMK	181

## RESULT 2

E70372  
 Hypothetical protein ag\_836 - Aquifex aeolicus  
 C/Species: Aquifex aeolicus  
 C/Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C/Accession: E70372  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove  
 V.  
 Nature 392, 353-358, 1998  
 A/Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A/Reference number: A70300; MUID:98196666; PMID:9537320  
 A/Accession: E70372  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-232 <AGP>  
 A/Cross-references: UNIPROT:O67008; GB:AE000709; MID:G2983373; PID:AA06970.1; PID:G2983  
 A/Experimental source: strain VFS  
 C/Genetics:  
 A/Gene: ag\_836

Query Match 1.2%; Score 9; DB 2; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 0.45;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96  
|||||  
DB 23 FENCKSCRN 31

## RESULT 3

T29125  
ketocycl1 reductase homolog - Streptomyces coelicolor  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T29125  
R/Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A/Reference number: 217215  
A/Accession: T29125  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-276 <PAR>  
A/Cross-references: UNIPROT:O86553; EMBL:AL031350; PIDN:CAA20507.1  
C/Genetics:  
A/Note: SCIF2.16c  
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 1.2%; Score 9; DB 2; Length 276;  
Best Local Similarity 100.0%; Pred. No. 0.53;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 670 AVSFGGRAS 678  
|||||  
DB 225 AVSFGGRAS 233

## RESULT 4

BMH1  
Procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human  
N/Alternate names: bone morphogenic protein 1 (BMP1)  
C/Species: Homo sapiens (man)  
C/Date: 16-Sep-1992 #sequence\_revision 03-Aug-1995 #text\_change 18-Jun-1999  
C/Accession: A37278; B58788  
R/Woroney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Witters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1988  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Residues: 1-730 <MOZ>  
A/Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500  
C/Genetics:  
A/Gene: GDB:BMP1  
A/Cross-references: GDB:125203; OMIM:112264  
A/Map position: 8p21-8p21

C/Function:  
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
C/Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology;  
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1  
F.1-22/Domain: signal sequence #status predicted <SIG>  
F.23-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>  
F.130-321/Domain: ascatin homology <AST>  
F.1322-431/Domain: C1r/C1s repeat homology <C1R1>  
F.1435-544/Domain: C1r/C1s repeat homology <C1R2>  
F.551-587/Domain: EGF homology <EGF>  
F.591-700/Domain: C1r/C1s repeat homology <C1R3>  
F.91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F.163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
F.213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted  
F.213/Active site: Glu #status predicted  
F.565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2%; Score 9; DB 1; Length 730;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
|||||  
DB 377 YDYVEVRDG 385

## RESULT 5

A58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human  
N/Alternate names: bone morphogenic protein splice form BMP-1/HIS  
C/Species: Homo sapiens (man)  
C/Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 18-Jun-1999  
C/Accession: A37278; A58788  
R/Woroney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Witters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1988  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Residues: 1-702; 'EKRPALQPPRGPRHQLKFRVQKRNTPQ' <MOZ>  
A/Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500  
R/Takahara, K.; Lyons, G.E.; Greenspan, D.S.  
J. Biol. Chem. 269, 32572-32578, 1994  
A/Title: Bone morphogenic protein-1 and a mammalian tollold homologue (MT1d) are encoded

A/Reference number: A58788; MUID:95096114; PMID:7798260  
A/Accession: A58788  
A/Molecule type: mRNA  
A/Residues: 703-823 <TAK>  
A/Cross-references: GB:J35278; NID:G619423; PIDN:AA41703.1; PID:G619424  
C/Genetics:  
A/Gene: GDB:BMP1; BMP-1  
A/Cross-references: GDB:125203; OMIM:112264  
A/Map position: 8p21-8p21

C/Function:  
A/Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
C/Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology;  
C/Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; g1  
F.1-22/Domain: signal sequence #status predicted <SIG>  
F.23-823/Product: procollagen C-endopeptidase splice form HIS #status predicted <MAT>  
F.130-321/Domain: C1r/C1s repeat homology <C1R1>  
F.1322-431/Domain: C1r/C1s repeat homology <C1R2>  
F.551-587/Domain: EGF homology <EGF>  
F.591-700/Domain: C1r/C1s repeat homology <C1R3>  
F.738-752/Region: histidine-rich  
F.91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F.163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
F.213,217,223,272/Binding site: zinc (His, His, Tyr) #status predicted  
F.213/Active site: Glu #status predicted  
F.565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2%; Score 9; DB 1; Length 823;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
|||||  
DB 377 YDYVEVRDG 385

## RESULT 6

B58788  
procollagen C-endopeptidase (EC 3.4.24.19) precursor, tollold-like splice form - human  
N/Alternate names: bone morphogenic protein 1, tollold-like splice form  
C/Species: Homo sapiens (man)  
C/Date: 28-Mar-1998 #sequence\_revision 09-Apr-1998 #text\_change 09-Jul-2004  
C/Accession: A37278; B58788  
R/Woroney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Witters, M.J.; Kriz, R.W.; Hew  
Science 242, 1528-1534, 1988  
A/Title: Novel regulators of bone formation: molecular clones and activities.  
A/Reference number: A37278; MUID:89072730; PMID:3201241  
A/Accession: A37278  
A/Molecule type: mRNA  
A/Cross-references: GB:M22488; NID:G179499; PIDN:AA51833.1; PID:G179500  
A/Map position: 8p21-8p21

A:Cross-references: UNIPROT:P13197; GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500  
 R:Yakahara, K.; Lyons, G.E.; Greenpan, D.S.  
 J. Biol. Chem. 269, 32572-32578, 1994  
 A:Title: Bone morphogenetic protein-1 and a mammalian tollid homologue (mTld) are encoded  
 A:Reference number: A58788; MUID:95096114; PMID:7798260  
 A:Accession: B58788  
 A:Molecule type: mRNA  
 A:Residues: 703-966 <TR>  
 A:Cross-references: GB:L35279; NID:g619860; PIDN:AA41710.1; PID:g619861  
 C:Genetics:  
 A:Gene: GDB:BMP1; BMP-1  
 A:Cross-references: GDB:125203; OMTM:112264  
 A:Map position: Bp21-8p21  
 C:Function:  
 A:Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type  
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; E  
 C:Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; gl  
 F:1-22/Domains: signal sequence #status predicted <SIG>  
 F:123-986/Product: procollagen C-endopeptidase tollid-like splice form #status predicted  
 F:130-331/Domains: ascatin homology <AST>  
 F:132-431/Domains: C1r/C1s repeat homology <C1R1>  
 F:1435-544/Domains: C1r/C1s repeat homology <C1R2>  
 F:1551-587/Domains: EGF homology <EG1>  
 F:1591-700/Domains: EGF homology <C1R3>  
 F:1707-742/Domains: C1r/C1s repeat homology <EG2>  
 F:1747-856/Domains: C1r/C1s repeat homology <C1R4>  
 F:1860-973/Domains: C1r/C1s repeat homology <C1R5>  
 F:91,147,332,363,599/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:163-319,185-205,322-348,375-387,435-461,488-510,551-563,559-572,574-587,591-617,644-66  
 F:123,217,423,272/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:214/Active site: Glu #status predicted  
 F:565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted

Query Match 1.2% Score 9; DB 1; Length 986;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
 |||||  
 Db 377 YDYVEVRDG 385

RESULT 7  
 149540  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: 149540  
 R:Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.  
 Dev. Biol. 163, 175-183, 1994  
 A:Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rel  
 A:Reference number: 149540; MUID:94223942; PMID:8174772  
 A:Accession: 149540  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-991 <RES>  
 A:Cross-references: UNIPROT:P98063; GB:L24755; NID:g439606; PIDN:AA37306.1; PID:g439607  
 C:Genetics:  
 A:Gene: BMP-1  
 C:Superfamily: procollagen C-endopeptidase; ascatin homology; C1r/C1s repeat homology; E  
 C:Keywords: hydrolyase; metalloproteinase; zinc  
 F:135-336/Domains: ascatin homology <AST>  
 F:156-592/Domains: EGF homology <EG1>  
 F:1596-705/Domains: C1r/C1s repeat homology <C1R>  
 F:1712-747/Domains: EGF homology <EG2>  
 F:218,222,228,277/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:219/Active site: Glu #status predicted

Query Match 1.2% Score 9; DB 2; Length 991;  
 Best Local Similarity 100.0%; Pred. No. 1.7;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187

Db 382 YDYVEVRDG 390  

RESULT 8  
 558984  
 A:Title: The tolkin gene is a tollid/BMP-1 homologue that is essential for Drosophila d  
 development protein tolkin (EC 3.4.24.-) - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: 558984  
 R:Finelli, A.L.; Xie, T.; Bossie, C.A.; Blackman, R.K.; Padgett, R.W.  
 Genetics 141, 271-281, 1995  
 A:Title: The tolkin gene is a tollid/BMP-1 homologue that is essential for Drosophila d  
 A:Reference number: 558984; MUID:96042912; PMID:8536976  
 A:Accession: 558984  
 A:Molecule type: mRNA  
 A:Residues: 1-1466 <FIN>  
 A:Cross-references: UNIPROT:Q24132; EMBL:U34777; NID:g1002985; PIDN:AA47015.1; PID:g100  
 A:Note: the authors did not translate the codon for residue 722  
 C:Genetics:  
 A:Gene: tolkin  
 A:Cross-references: FlyBase:FBgn0004885  
 C:Keywords: hydrolyase; metalloproteinase; zinc  
 F:523-722/Domains: ascatin homology <AST>  
 F:958-993/Domains: EGF homology <EGF>  
 F:1118-1153/Domains: EGF homology <EGF1>  
 F:614,618,624,673/Binding site: zinc (His, His, His, Tyr) #status predicted  
 F:615/Active site: Glu #status predicted

Query Match 1.2% Score 9; DB 2; Length 1464;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  

Db 897 YDYVEVRDG 905

RESULT 9  
 T31070  
 C:Species: Lytechinus variegatus (variegated urchin)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
 C:Accession: T31070  
 R:Sherwood, D.R.; McClay, D.R.  
 Development 124, 3363-3374, 1997  
 A:Title: Identification and localization of a sea urchin Notch homologue: insights into v  
 A:Reference number: Z20966; MUID:97454256; PMID:9310331  
 A:Accession: T31070  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2531 <SHE>  
 A:Cross-references: EMBL:AF00634; NID:g2570350; PID:g2570351; PIDN:AA582088.1  
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 1.2% Score 9; DB 2; Length 2531;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 260 CACIAGYTG 268  

Db 537 CACIAGYTG 545

RESULT 10  
 S00996  
 IG kappa chain precursor V region (A10) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Jul-1999  
 C:Accession: S00996  
 R:Strandinger, B.; Thiebe, R.; Huber, C.; Osterholzer, E.; Zachau, H.G.  
 Biol. Chem. Hoppe-Seyler 369, 601-607, 1988  
 A:Title: Two unusual human immunoglobulin V-kappa genes.

A:Reference number: S00996; MUID:89134397; PMID:2852016  
 A:Accession: S00996  
 A:Molecule type: DNA  
 A:Residues: 1-114 <STR>  
 A:Cross-references: EMBL:W2750; NID:q185914; PIDN:AAAS8912.1; PID:q553479  
 A:Note: this sequence was determined from the germ-line gene  
 C:Genetics:  
 A:Intron: 16/1  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-114/Product: Ig kappa chain V region #status predicted <MAT>  
 F:42-107/Diulfide bonds: #status predicted

Query Match 1.1%; Score 8; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSLH 215  
 DB 46 QSIGSSLH 53

RESULT 11  
 G70323  
 conserved hypothetical protein aq\_260 - Aquifex aeolicus  
 C:Species: Aquifex aeolicus  
 C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C:Accession: G70323  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
 Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Accession: G70323  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-158 <AQF>  
 A:Cross-references: UNIPROT:Q66619; GB:AE000681; NID:g2982963; PIDN:AAC06588.1; PID:g298  
 A:Experimental source: strain VFS  
 C:Genetics:  
 A:Gene: aq\_260  
 C:Superfamily: nus operon 15K protein

Query Match 1.1%; Score 8; DB 2; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 3.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GREVVGY 64  
 DB 114 GREVVGY 121

RESULT 12  
 D42696  
 thrombin (EC 3.4.21.5) B chain - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C:Accession: D42696  
 R:Bantfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: D42696  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <BAN>  
 A:Cross-references: UNIPROT:Q91001; GB:M81391  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650  
 DB 158 VTDMNPCA 164

RESULT 13  
 H42696  
 thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)  
 C:Species: Acipenser transmontanus (white sturgeon)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C:Accession: H42696  
 R:Bantfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: H42696  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-235 <BAN>  
 A:Cross-references: UNIPROT:Q90244; GB:M81399  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650  
 DB 157 VTDMNPCA 164

RESULT 14  
 C42696  
 thrombin (EC 3.4.21.5) B chain - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C:Accession: C42696  
 R:Bantfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A:Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A:Reference number: A42696; MUID:92212913; PMID:1557383  
 A:Accession: C42696  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: mRNA  
 A:Residues: 1-236 <BAN>  
 A:Cross-references: UNIPROT:Q28731; GB:M81396  
 C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C:Keywords: hydrolase; serine proteinase  
 F:1-227/Domain: trypsin homology (fragment) <TRY>

Query Match 1.1%; Score 8; DB 2; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 5.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 643 VTDMNPCA 650  
 DB 158 VTDMNPCA 165

RESULT 15  
 AB0338  
 Probable membrane protein dead [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AB0338  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,

Wed Jul 13 11:59:53 2005

Nature 413, 523-527, 2001  
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; MUID:21470413; PMID:1156360  
 A;Accession: AB0338  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-240 <KUR>  
 A;Cross-references: UNIPROT:Q8ZD23; GB:AL590842; PTDN:CAC93009.1; PID:G15980748; GSPDB:C  
 C;Genetics:  
 A;Gene: dedd  
 C;Superfamily: dedd protein

Query Match 1.1%; Score 8; DB 2; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 5.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 SKOKLQSA 387  
 |||||  
 Db 212 SKOKLQSA 219

Search completed: July 12, 2005, 17:23:21  
 Job time : 63 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 12, 2005, 17:20:13 ; Search time 176 Seconds  
(without alignments)  
2094.869 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720  
Sequence: 1 MELGCWTOGLTFLQLLLS.....LSTAFKVLPRKMIERNKK 720

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1500 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	720	2 Q6UXH9	Q6UXH9 homo sapien
2	563	78.2	720	2 Q6N062	Q6N062 homo sapien
3	446	61.9	737	2 Q96JW2	Q96JW2 homo sapien
4	386	53.6	417	2 Q71R92	Q71R92 homo sapien
5	178	24.7	181	2 Q9Y432	Q9Y432 homo sapien
6	61	8.5	720	2 Q8K2B8	Q8K2B8 mus muscu
7	41	5.7	720	2 Q8K2B8	Q8K2B8 mus muscu
8	24	3.3	722	2 Q6DIV5	Q6DIV5 xenopus tro
9	9	1.2	232	2 Q91WZ0	Q91WZ0 rattus norv
10	9	1.2	232	1 Y836_AQUAE	Y836_AQUAE aquifex aeo
11	9	1.2	276	2 Q86553	Q86553 streptomyce
12	9	1.2	593	2 Q6PJN5	Q6PJN5 homo sapien
13	9	1.2	639	1 BMPH_STRPU	BMPH_STRPU strongyloce
14	9	1.2	691	2 Q57658	Q57658 gallus gall
15	9	1.2	775	2 Q6P550	Q6P550 mus muscu
16	9	1.2	860	2 Q7QAH1	Q7QAH1 anopheles g
17	9	1.2	923	1 NRPI_BRARE	NRPI_BRARE brachydanio
18	9	1.2	923	2 Q69DB8	Q69DB8 brachydanio
19	9	1.2	986	1 BMP1_HUMAN	BMP1_HUMAN homo sapien
20	9	1.2	991	1 BMP1_MOUSE	BMP1_MOUSE mus muscu
21	9	1.2	991	1 Q6NZM2	Q6NZM2 mus muscu
22	9	1.2	1015	2 Q9Y6L7	Q9Y6L7 homo sapien
23	9	1.2	1078	2 Q9UQ00	Q9UQ00 homo sapien
24	9	1.2	1464	2 Q23995	Q23995 drosophila
25	9	1.2	1464	2 Q24132	Q24132 drosophila
26	9	1.2	1464	2 Q9VC47	Q9VC47 drosophila
27	9	1.2	2531	2 Q16004	Q16004 lytechinus
28	8	1.1	81	2 Q79204	Q79204 human immun
29	8	1.1	133	2 Q6LTX4	Q6LTX4 human immun
30	8	1.1	136	2 Q8CEX5	Q8CEX5 mus muscu
31	8	1.1	152	2 Q924X1	Q924X1 mus muscu

32	8	1.1	158	1 Y260_AQUAE	Y260_AQUAE aquifex aeo
33	8	1.1	235	2 Q90244	Q90244 acipenser t
34	8	1.1	235	2 Q28731	Q28731 oryctolagus
35	8	1.1	240	2 Q668X3	Q668X3 yersinia ps
36	8	1.1	240	2 Q8ZD23	Q8ZD23 yersinia ps
37	8	1.1	242	2 Q8D0T9	Q8D0T9 yersinia ps
38	8	1.1	360	1 MTSB_LACLC	MTSB_LACLC lactococcus
39	8	1.1	367	2 Q9XUN6	Q9XUN6 caenorhabdi
40	8	1.1	385	2 Q90WS2	Q90WS2 elaphe sp.
41	8	1.1	395	1 VIBC_VIBCH	VIBC_VIBCH vibrio chol
42	8	1.1	407	1 FA7_BOVIN	FA7_BOVIN bos taurus
43	8	1.1	411	2 Q6TUT3	Q6TUT3 oryza sativ
44	8	1.1	413	2 Q7X370	Q7X370 uncultured
45	8	1.1	456	1 YDBH_SCHPO	YDBH_SCHPO schizosacch
46	8	1.1	556	2 Q7UX12	Q7UX12 rhodospirell
47	8	1.1	559	2 Q62KX6	Q62KX6 burkholderi
48	8	1.1	569	2 Q63TF6	Q63TF6 burkholderi
49	8	1.1	607	2 Q91001	Q91001 gallus gall
50	8	1.1	608	2 Q9PTW7	Q9PTW7 struthio ca
51	8	1.1	611	2 Q94HU9	Q94HU9 oryza sativ
52	8	1.1	611	2 Q7XG00	Q7XG00 oryza sativ
53	8	1.1	719	2 Q9PVY2	Q9PVY2 triakis scy
54	8	1.1	737	2 Q8YTB7	Q8YTB7 anabaena sp
55	8	1.1	740	1 CATB_STRRE	CATB_STRRE streptomyce
56	8	1.1	752	2 Q42374	Q42374 brachydanio
57	8	1.1	764	2 Q8XTM0	Q8XTM0 ralestonia s
58	8	1.1	963	2 Q44393	Q44393 pisaster oc
59	8	1.1	1019	1 LFC_CARRO	LFC_CARRO carcinocor
60	8	1.1	1019	2 P28175	P28175 tachyples
61	8	1.1	1019	2 Q8T5S1	Q8T5S1 tachyples
62	8	1.1	1070	2 Q91972	Q91972 aplysia cal
63	8	1.1	1083	2 Q26423	Q26423 carcinocor
64	8	1.1	1238	2 Q9N614	Q9N614 drosophila
65	8	1.1	1238	2 Q9VCDB	Q9VCDB drosophila
66	8	1.1	1316	2 Q96JU7	Q96JU7 homo sapien
67	7	1.0	36	2 Q7UD51	Q7UD51 rhodospirell
68	7	1.0	37	2 Q8F0D9	Q8F0D9 leptospira
69	7	1.0	47	2 Q75GQ9	Q75GQ9 oryza sativ
70	7	1.0	50	2 Q626D5	Q626D5 oryza sativ
71	7	1.0	54	2 Q8N087	Q8N087 corynebacte
72	7	1.0	55	2 Q768X9	Q768X9 uncultured
73	7	1.0	59	2 Q931M9	Q931M9 staphylococ
74	7	1.0	59	2 Q99SV1	Q99SV1 staphylococ
75	7	1.0	59	2 Q7A0F7	Q7A0F7 staphylococ
76	7	1.0	59	2 Q6G7Z5	Q6G7Z5 staphylococ
77	7	1.0	59	2 Q6GFB7	Q6GFB7 staphylococ
78	7	1.0	61	2 Q8GRP5	Q8GRP5 arabidopsis
79	7	1.0	61	2 Q8GRP6	Q8GRP6 arabidopsis
80	7	1.0	61	2 Q8GZP3	Q8GZP3 arabidopsis
81	7	1.0	61	2 Q8GZP4	Q8GZP4 arabidopsis
82	7	1.0	61	2 Q8GZP5	Q8GZP5 arabidopsis
83	7	1.0	61	2 Q8GZP7	Q8GZP7 arabidopsis
84	7	1.0	61	2 Q8GZP8	Q8GZP8 arabidopsis
85	7	1.0	61	2 Q8GZP9	Q8GZP9 arabidopsis
86	7	1.0	62	2 Q7P1Z1	Q7P1Z1 anopheles g
87	7	1.0	67	2 Q9EMT6	Q9EMT6 amaseta moo
88	7	1.0	81	2 Q79303	Q79303 human immun
89	7	1.0	82	2 Q790D16	Q790D16 human immun
90	7	1.0	86	2 Q7X3H3	Q7X3H3 chlorella x
91	7	1.0	91	2 Q9M9B7	Q9M9B7 suid herpes
92	7	1.0	106	2 Q87074	Q87074 suid herpes
93	7	1.0	108	2 Q62QF8	Q62QF8 bacillus li
94	7	1.0	109	2 Q666A7	Q666A7 caenorhabdi
95	7	1.0	112	2 P91967	P91967 trichinella
96	7	1.0	114	2 Q9YCI9	Q9YCI9 aeropyrum p
97	7	1.0	120	2 Q816A0	Q816A0 aplysia cal
98	7	1.0	123	2 Q6W1F1	Q6W1F1 rhizobium s
99	7	1.0	124	2 Q7WC39	Q7WC39 bordetella

105	1.0	124	2	081G20	081g20 bacillus ce	178	7	1.0	211	2	08ZEh2	08zeH2 yersinia pe
106	1.0	124	2	08G3X3	08g3x3 bifidobacte	179	7	1.0	211	2	08d4T7	08d4T7 erwina car
107	1.0	126	2	06N0G5	06ng05 arabidopsis	180	7	1.0	212	1	0MPW_ECOLI	P13364 escherichia
108	1.0	129	2	08TF53	08tf53 vibrio para	181	7	1.0	212	1	0MPW_SALTI	08z762 salmonella
109	1.0	132	2	08MG97	08mg97 apatania zo	182	7	1.0	212	1	0MPW_SALTY	08zp50 salmonella
110	1.0	132	2	09LI58	09li58 streptomyce	183	7	1.0	212	2	0708A2	07g8a2 anopheles g
111	1.0	136	2	06SA41	06sa41 metathizium	184	7	1.0	212	2	08XC86	08xc86 escherichia
112	1.0	141	2	06A6E6	06a6e6 propionibac	185	7	1.0	213	2	09CF55	09cf55 lactococcus
113	1.0	143	2	09S9X5	09s9x5 arabidopsi	186	7	1.0	214	2	08TK02	08tk02 vibrio para
114	1.0	144	2	08MG98	08mg98 moropsych	187	7	1.0	215	2	074TX0	074tx0 yersinia pe
115	1.0	146	2	06R6N1	06r6n1 sus scrofa	188	7	1.0	215	2	08D0J8	08d0j8 yersinia pe
116	1.0	146	2	07S0S0	07s0s0 bartigiola	189	7	1.0	215	2	09RKP8	09rkp8 streptomyce
117	1.0	146	2	07S0F3	07s0f3 rhopalomyia	190	7	1.0	221	2	09SS24	09ss24 dirosophila
118	1.0	146	2	07S0F4	07s0f4 rhopalomyia	191	7	1.0	221	2	09VYW7	09vwy7 dirosophila
119	1.0	146	2	07S0F5	07s0f5 rhopalomyia	192	7	1.0	222	2	087IA9	087ia9 neurospora
120	1.0	146	2	07S0F6	07s0f6 rhopalomyia	193	7	1.0	222	2	06ESR8	06esr8 oryza sativ
121	1.0	146	2	07S0F7	07s0f7 rhopalomyia	194	7	1.0	222	2	08KOM4	08kqm4 saccharopol
122	1.0	146	2	07S0F8	07s0f8 rhopalomyia	195	7	1.0	223	2	07Z7Z4	07z7z4 inocybe sie
123	1.0	146	2	07S0F9	07s0f9 rhopalomyia	196	7	1.0	225	2	08MOX1	08mox1 synodiactyl
124	1.0	146	2	07S0G0	07s0g0 rhopalomyia	197	7	1.0	225	2	08WSL0	08ws10 oryza sativ
125	1.0	146	2	07S0G1	07s0g1 rhopalomyia	198	7	1.0	225	2	07XH60	07xh60 oryza sativ
126	1.0	146	2	07S0G2	07s0g2 rhopalomyia	199	7	1.0	226	2	06J2M1	06j2m1 bacillus ce
127	1.0	146	2	07S0G3	07s0g3 rhopalomyia	200	7	1.0	226	2	0816L1	0816l1 bacillus ce
128	1.0	146	2	07S0G4	07s0g4 rhopalomyia	201	7	1.0	226	2	08IKC5	08ikc5 bacillus an
129	1.0	146	2	07S0G5	07s0g5 rhopalomyia	202	7	1.0	226	2	06HC61	06hc61 bacillus th
130	1.0	146	2	06YTF3	06ytf3 oryza sativ	203	7	1.0	227	2	02S6T5	02s6t5 archaeoglob
131	1.0	147	2	06TMY5	06tmy5 symbiobacte	204	7	1.0	227	2	07Z8D8	07z8d8 inocybe ada
132	1.0	154	2	050211	050211 mycobacteri	205	7	1.0	227	2	088QI8	088qi8 pseudomonas
133	1.0	156	2	06EU04	06eu04 oryza sativ	206	7	1.0	228	2	07Z8Z5	07z8z5 inocybe che
134	1.0	156	2	08BPF6	08bpf6 xanthomonas	207	7	1.0	228	2	0889S0	0889s0 pseudomonas
135	1.0	157	2	09SW21	09sw21 anthonomus	208	7	1.0	231	2	07NB38	07nb38 mycoplasma
136	1.0	158	2	09AV48	09av48 oryza sativ	209	7	1.0	231	2	09Z7Y5	09z7y5 chlamydia p
137	1.0	158	2	06S4W6	06s4w6 oryza sativ	210	7	1.0	232	2	09HWM1	09hwm1 pseudomonas
138	1.0	163	2	07S1L20	07s1l20 oryza sativ	211	7	1.0	233	2	07Z8Z4	07z8z4 inocybe che
139	1.0	164	2	09G6K6	09g6k6 homo sapien	212	7	1.0	235	2	08LDZ5	08ldz5 arabidopsis
140	1.0	164	2	YPA2_ASCIM	P23375 ascobolus i	213	7	1.0	235	2	08VY63	08vy63 arabidopsis
141	1.0	168	2	08DUF0	08duf0 synecococc	214	7	1.0	235	2	06YTS3	06yts3 oryza sativ
142	1.0	168	2	09Z8U3	09z8j3 chlamydia p	215	7	1.0	235	2	0910U4	0910u4 gecko gecko
143	1.0	169	2	08TNK8	08tnk8 vibrio para	216	7	1.0	236	2	09HQG1	09hqg1 halobacteri
144	1.0	170	2	084RT8	084rt8 chamaemelum	217	7	1.0	237	2	07ZWL3	07zwl3 xenopus lae
145	1.0	170	2	084SG4	084sg4 chamaemelum	218	7	1.0	238	2	07Z7Z1	07z7z1 inocybe ste
146	1.0	171	2	09R0P0	09r0p0 vibrio chol	219	7	1.0	238	2	08CW43	08cw43 escherichia
147	1.0	171	2	09K279	09k279 chlamydia p	220	7	1.0	239	2	09KQD6	09kqd6 vibrio chol
148	1.0	172	2	09CLY6	09cly6 pasteurella	221	7	1.0	239	2	0912I8	0912i8 oncorhynch
149	1.0	172	2	09DFD1	09dfd1 oncorhynch	222	7	1.0	240	2	089IB3	089ib3 bradyrhizob
150	1.0	175	2	07NK23	07nk23 gloeobacter	223	7	1.0	241	2	08FRK8	08frk8 corynebacte
151	1.0	176	2	09PUC7	09puc7 gallus galli	224	7	1.0	242	2	07Z9K7	07z9k7 desulfovibx
152	1.0	178	2	09ILMH2	09ilmh2 arabidopsis	225	7	1.0	243	2	07MAI3	07mai3 megabombus
153	1.0	181	2	08TNZ6	08tnz6 vibrio para	226	7	1.0	244	2	07X990	07x990 oryza sativ
154	1.0	185	2	09KMW2	09kwm2 salmonella	227	7	1.0	244	2	06DIS2	06dis2 xenopus tro
155	1.0	186	2	06BL42	06bl42 debaryomyce	228	7	1.0	247	2	08FCQ3	08fcq3 escherichia
156	1.0	187	2	084SJO	084sjo matricaria	229	7	1.0	247	2	08X6U7	08x6u7 escherichia
157	1.0	187	2	06WTT3	06wt3 mycoplasma	230	7	1.0	247	2	083PUB	083pub shigella fl
158	1.0	189	2	084SJI	084sji matricaria	231	7	1.0	248	2	049138	049138 arabidopsis
159	1.0	190	2	YRI5_GLOVI	07nh22 gloeobacter	232	7	1.0	249	2	06IEB3	06ieb3 retus norv
160	1.0	190	2	06BSX0	06bsx0 debaryomyce	233	7	1.0	249	2	08C1O8	08c1o8 mus muscu
161	1.0	191	1	MAF_BACAN	081ld6 bacillus an	234	7	1.0	250	2	08ZFK6	08zfk6 yersinia pe
162	1.0	191	2	06J3Y9	06j3y9 bacillus ce	235	7	1.0	253	2	089UG6	089ug6 bradyrhizob
163	1.0	191	2	09R5A2	09r5a2 deinococcus	236	7	1.0	254	2	074WV1	074wv1 nanoarchaeu
164	1.0	191	2	06HD71	06hd71 bacillus th	237	7	1.0	254	2	06N3W7	06n3w7 rhodospseudo
165	1.0	193	1	Y3I7_MYCGE	P47617 mycoplasma	238	7	1.0	255	1	V29K_PEBV	P14850 pea early b
166	1.0	195	2	06AMIS	06amis desulfotale	239	7	1.0	255	2	09Y7A9	09y7a9 metathizium
167	1.0	196	1	CRBD_CHICK	P49152 gallus galli	240	7	1.0	255	2	084700	084700 pea early b
168	1.0	198	2	08XR75	08xrt75 ralscinia s	241	7	1.0	259	2	069EZ7	069ez7 homo sapien
169	1.0	201	1	ABPI_MAIZE	P13689 sus mayas (m	242	7	1.0	259	2	08UDJ2	08udj2 agrobacteri
170	1.0	202	2	06ZS58	06zsp8 homo sapien	243	7	1.0	260	1	COLI_RANRI	P22923 r corticotr
171	1.0	203	2	07Z2X1	07z2x1 bacillus ce	244	7	1.0	263	1	COLI_RANCA	P11885 r corticotr
172	1.0	204	2	08JIS7	08jis7 xenopus lae	245	7	1.0	263	2	06LJ06	06lj06 photobacter
173	1.0	208	2	09Z3I5	09z3i5 breadyrhizob	246	7	1.0	265	2	007812	007812 mycobacteri
174	1.0	209	1	NODS_BRAVA	P26026 breadyrhizob	247	7	1.0	265	2	068AV7	068av7 uncultured
175	1.0	210	2	07SC67	07sc67 aebhya goes	248	7	1.0	265	2	007181	007181 mycobacteri
176	1.0	211	2	06ESR9	06esr9 oryza sativ	249	7	1.0	266	2	07U190	07u190 mycobacteri
177	1.0	211	2	066AK7	066ak7 yersinia ps	250	7	1.0	266	2	081916	081916 biotoma trop



251	7	1.0	266	2	06JYE6	06JYE6 elasmosteeth	324	7	1.0	355	2	047485	047485 carabus cia
252	7	1.0	266	2	073QA7	073QA7 treponema d	325	7	1.0	355	2	047486	047486 carabus sic
253	7	1.0	266	2	09QU80	09QU80 te vitru. o	326	7	1.0	355	2	047487	047487 carabus lat
254	7	1.0	268	2	09XY56	09XY56 ctenecephal	327	7	1.0	355	2	078724	078724 carabus bla
255	7	1.0	268	2	06N9D3	06N9D3 rhodopsophal	328	7	1.0	355	2	078725	078725 carabus tit
256	7	1.0	271	2	09NPM7	09NPM7 homo sapien	329	7	1.0	355	2	079586	079586 carabus aut
257	7	1.0	272	2	051013	051013 neisseria g	330	7	1.0	355	2	099052	099052 carabus por
258	7	1.0	273	2	083DW2	083DW2 coxiella bu	331	7	1.0	355	2	099053	099053 carabus por
259	7	1.0	278	2	084C08	084C08 pseudomonas	332	7	1.0	355	2	099054	099054 carabus por
260	7	1.0	280	2	087X78	087X78 pseudomonas	333	7	1.0	355	2	092098	092098 carabus mar
261	7	1.0	281	2	08U4H8	08U4H8 pyrococcus	334	7	1.0	355	2	092100	092100 carabus wag
262	7	1.0	281	2	06JYN8	06JYN8 ralsstonia ha	335	7	1.0	355	2	092101	092101 carabus lep
263	7	1.0	282	2	08UXE9	08UXE9 rosellinia	336	7	1.0	355	2	092102	092102 carabus lud
264	7	1.0	284	2	096089	096089 haemaphysal	337	7	1.0	355	2	092103	092103 carabus bor
265	7	1.0	286	2	09H7G9	09H7G9 homo sapien	338	7	1.0	355	2	037388	037388 carabus geh
266	7	1.0	291	1	PCAR_PSEBU	05154 pseudomonas	339	7	1.0	355	2	037389	037389 carabus geh
267	7	1.0	291	1	09R9T0	09R9T0 pseudomonas	340	7	1.0	355	2	037428	037428 carabus fru
268	7	1.0	291	2	08BN41	08BN41 pseudomonas	341	7	1.0	355	2	037441	037441 carabus van
269	7	1.0	292	2	054441	054441 bacillus ps	342	7	1.0	355	2	037443	037443 carabus bla
270	7	1.0	294	1	PEPM_MYTEB	056839 mytilus edu	343	7	1.0	355	2	037444	037444 carabus bla
271	7	1.0	295	2	069E28	069E28 homo sapien	344	7	1.0	355	2	037445	037445 carabus bla
272	7	1.0	295	2	06DDJ3	06DDJ3 erwinia car	345	7	1.0	355	2	037446	037446 carabus bla
273	7	1.0	299	2	08T8D9	08T8D9 trypanosoma	346	7	1.0	355	2	037447	037447 carabus bla
274	7	1.0	299	2	07PM47	07PM47 anopheles g	347	7	1.0	355	2	037448	037448 carabus bla
275	7	1.0	300	2	08IN70	08IN70 drosophila	348	7	1.0	355	2	037449	037449 carabus bla
276	7	1.0	301	2	07ZSX7	07ZSX7 figu rubrip	349	7	1.0	355	2	037453	037453 carabus bla
277	7	1.0	303	1	LEPC_XANAC	08PP43 xanthomonas	350	7	1.0	355	2	037454	037454 carabus bla
278	7	1.0	303	2	074ZD4	074ZD4 ashbya goss	351	7	1.0	355	2	037457	037457 carabus bla
279	7	1.0	303	2	06VQ99	06VQ99 tetradodon n	352	7	1.0	355	2	037459	037459 carabus bla
280	7	1.0	304	2	08XXF6	08XXF6 ralsstonia s	353	7	1.0	355	2	037465	037465 carabus por
281	7	1.0	305	1	LEPC_RALSO	09HL16 ralsstonia s	354	7	1.0	355	2	037518	037518 carabus mae
282	7	1.0	306	2	08L5B0	08L5B0 cryza sativ	355	7	1.0	355	2	037542	037542 carabus sac
283	7	1.0	307	2	07Q528	07Q528 anopheles g	356	7	1.0	355	2	085A26	085A26 carabus sac
284	7	1.0	307	2	09KV69	09KV69 vibrio chol	357	7	1.0	355	2	085BA4	085BA4 carabus cha
285	7	1.0	308	1	T2RC_MOUSE	059532 mus musculu	358	7	1.0	355	2	085GL4	085GL4 carabus sma
286	7	1.0	308	2	07M704	07M704 mus musculu	359	7	1.0	355	2	085GL5	085GL5 carabus sma
287	7	1.0	312	2	012125	012125 baccharomyc	360	7	1.0	355	2	085GL6	085GL6 carabus kub
288	7	1.0	314	2	06FUP3	06FUP3 candida gla	361	7	1.0	355	2	085GL7	085GL7 carabus for
289	7	1.0	315	1	Y001_CAUCR	09AC59 caulobacter	362	7	1.0	355	2	085GL8	085GL8 carabus jan
290	7	1.0	315	2	055Z30	055Z30 streptomyce	363	7	1.0	355	2	085GL9	085GL9 carabus osa
291	7	1.0	317	2	09KMA7	09KMA7 agrobacteri	364	7	1.0	355	2	085GM0	085GM0 carabus nan
292	7	1.0	318	2	06CP66	06CP66 Kluyveromyc	365	7	1.0	355	2	085GM1	085GM1 carabus kas
293	7	1.0	321	2	067LFP	067LFP symbiobacte	366	7	1.0	355	2	085GM2	085GM2 carabus rem
294	7	1.0	324	2	090Z55	090Z55 acophilalmu	367	7	1.0	355	2	085GM3	085GM3 carabus alp
295	7	1.0	329	2	08U2M3	08U2M3 pyrococcus	368	7	1.0	355	2	085GM4	085GM4 carabus wag
296	7	1.0	329	2	089MG1	089MG1 bradyrhizob	369	7	1.0	355	2	085GM5	085GM5 carabus lam
297	7	1.0	330	2	030523	030523 vibrio shil	370	7	1.0	355	2	085GM6	085GM6 carabus dra
298	7	1.0	332	2	08NX19	08NX19 staphylococ	371	7	1.0	355	2	085GM7	085GM7 carabus ben
299	7	1.0	333	2	09K7W7	09K7W7 bacillus ha	372	7	1.0	355	2	085GM8	085GM8 carabus wen
300	7	1.0	336	2	069510	069510 mycobacteri	373	7	1.0	355	2	085GM9	085GM9 carabus gan
301	7	1.0	336	2	08PR42	08PR42 xanthomonas	374	7	1.0	355	2	085GN0	085GN0 carabus lam
302	7	1.0	336	2	06MS16	06MS16 mycoplasma	375	7	1.0	355	2	085GN1	085GN1 carabus cra
303	7	1.0	336	2	07WL07	07WL07 bordetella	376	7	1.0	355	2	085GN2	085GN2 carabus cra
304	7	1.0	337	2	09YDH3	09YDH3 aetopyrum p	377	7	1.0	355	2	085GN3	085GN3 carabus vir
305	7	1.0	338	2	08PE85	08PE85 xanthomonas	378	7	1.0	355	2	085GN4	085GN4 carabus vir
306	7	1.0	342	2	07XE33	07XE33 cryza sativ	379	7	1.0	355	2	085GN5	085GN5 carabus sun
307	7	1.0	343	2	07VVI3	07VVI3 bordetella	380	7	1.0	355	2	085GN6	085GN6 carabus bus
308	7	1.0	343	2	06D7G2	06D7G2 vibrio vuln	381	7	1.0	355	2	085GN7	085GN7 carabus erv
309	7	1.0	344	2	084QA9	084QA9 cryza sativ	382	7	1.0	355	2	085GN8	085GN8 carabus bur
310	7	1.0	344	2	092M18	092M18 rhizobium m	383	7	1.0	355	2	085GN9	085GN9 carabus tal
311	7	1.0	345	2	07W7L8	07W7L8 bordetella	384	7	1.0	355	2	085G64	085G64 carabus pun
312	7	1.0	346	2	06JY16	06JY16 eupolemus s	385	7	1.0	355	2	085G65	085G65 carabus mul
313	7	1.0	347	2	06EZC2	06EZC2 escherichia	386	7	1.0	355	2	085G66	085G66 carabus imp
314	7	1.0	347	2	07P022	07P022 chromobacte	387	7	1.0	355	2	085G67	085G67 carabus hem
315	7	1.0	348	1	RTCA_PYRAE	08484 pyrobaculum	388	7	1.0	355	2	085G68	085G68 carabus mul
316	7	1.0	349	2	09YBV1	09YBV1 aetopyrum p	389	7	1.0	355	2	085G69	085G69 carabus mul
317	7	1.0	349	2	06NDF7	06NDF7 rhodospseudo	390	7	1.0	355	2	085G70	085G70 carabus syr
318	7	1.0	350	2	018122	018122 caenorhabdi	391	7	1.0	355	2	085G71	085G71 carabus pio
319	7	1.0	351	1	MS82_YEAST	040990 baccharomyc	392	7	1.0	355	2	085G72	085G72 carabus pio
320	7	1.0	352	2	08GC90	08GC90 mus musculu	393	7	1.0	355	2	085G75	085G75 carabus tor
321	7	1.0	354	2	099Q08	099Q08 bradyrhizob	394	7	1.0	355	2	085G76	085G76 carabus ere
322	7	1.0	354	2	099Q80	099Q80 bradyrhizob	395	7	1.0	355	2	085G77	085G77 carabus nor
323	7	1.0	355	2	047484	047484 carabus vir	396	7	1.0	355	2	085G78	085G78 carabus nor

397	1.0	355	2	085GT9	085GT9 carabus tor	470	7	1.0	355	2	09MR78	09mr78 carabus por
398	7	355	2	085GU0	085GU0 carabus tor	471	7	1.0	355	2	09MR79	09mr79 carabus por
399	1.0	355	2	085GU1	085GU1 carabus tor	472	7	1.0	355	2	09MR80	09mr80 carabus por
400	7	355	2	085GU2	085GU2 carabus cha	473	7	1.0	355	2	09MR81	09mr81 carabus por
401	1.0	355	2	085GU3	085GU3 carabus tor	474	7	1.0	355	2	09T2Z7	09t2z7 carabus bla
402	7	355	2	085GU4	085GU4 carabus pra	475	7	1.0	355	2	09T391	09t391 carabus bla
403	1.0	355	2	085HAX6	08hax6 carabus tit	476	7	1.0	355	2	09T392	09t392 carabus bla
404	7	355	2	08HDX2	08hdx2 carabus asc	477	7	1.0	355	2	09T393	09t393 carabus bla
405	1.0	355	2	08HDX3	08hdx3 carabus mas	478	7	1.0	355	2	09T3V1	09t3v1 carabus bla
406	7	355	2	08HDX4	08hdx4 carabus mas	479	7	1.0	355	2	09T3V2	09t3v2 carabus bla
407	1.0	355	2	08HDX5	08hdx5 carabus inf	480	7	1.0	355	2	09T3V3	09t3v3 carabus bla
408	7	355	2	08HDX6	08hdx6 carabus inf	481	7	1.0	355	2	09T3V4	09t3v4 carabus bla
409	1.0	355	2	08HDX8	08hdx8 carabus min	482	7	1.0	355	2	09T3V5	09t3v5 carabus bla
410	7	355	2	08HDX25	08hdx25 carabus tit	483	7	1.0	355	2	09T3Z7	09t3z7 carabus bla
411	1.0	355	2	08B9L8	08b9l8 carabus hum	484	7	1.0	355	2	09T4D6	09t4d6 carabus del
412	7	355	2	08B9L9	08b9l9 carabus hum	485	7	1.0	355	2	09T4K2	09t4k2 carabus bla
413	1.0	355	2	08B9M0	08b9m0 carabus hum	486	7	1.0	355	2	09T4R4	09t4r4 carabus bla
414	7	355	2	08B9M6	08b9m6 carabus ruf	487	7	1.0	355	2	09T4R5	09t4r5 carabus bla
415	1.0	355	2	08B9R7	08b9r7 carabus bal	488	7	1.0	355	2	09T4R8	09t4r8 carabus bem
416	7	355	2	08B9R8	08b9r8 carabus str	489	7	1.0	355	2	09T4V4	09t4v4 carabus bla
417	1.0	355	2	08B9R9	08b9r9 carabus lat	490	7	1.0	355	2	09TDX8	09tdx8 carabus cia
418	7	355	2	08B9S0	08b9s0 carabus aen	491	7	1.0	355	2	09TDX9	09tdx9 carabus mao
419	1.0	355	2	08B9S1	08b9s1 carabus aen	492	7	1.0	355	2	09TDY0	09tdy0 carabus cle
420	7	355	2	08B9S2	08b9s2 carabus sac	493	7	1.0	355	2	09TDY1	09tdy1 carabus crie
421	1.0	355	2	08B9S3	08b9s3 carabus lin	494	7	1.0	355	2	09TDY2	09tdy2 carabus arr
422	7	355	2	08B9S4	08b9s4 carabus kad	495	7	1.0	355	2	09TDY3	09tdy3 carabus lao
423	1.0	355	2	08B9S5	08b9s5 carabus str	496	7	1.0	355	2	09TDY4	09tdy4 carabus lao
424	7	355	2	08B9S6	08b9s6 carabus str	497	7	1.0	355	2	09TDY5	09tdy5 carabus cya
425	1.0	355	2	08B9K4	08b9k4 carabus con	498	7	1.0	355	2	09TDY6	09tdy6 carabus tou
426	7	355	2	08B9K5	08b9k5 carabus con	499	7	1.0	355	2	09TDY7	09tdy7 carabus lux
427	1.0	355	2	08B9K6	08b9k6 carabus gly	500	7	1.0	355	2	09TDY8	09tdy8 carabus ton
428	7	355	2	08B9K7	08b9k7 carabus gly	501	7	1.0	355	2	09TDY9	09tdy9 carabus ton
429	1.0	355	2	08B9K8	08b9k8 carabus sma	502	7	1.0	355	2	09TE01	09te01 carabus tru
430	7	355	2	08B9K9	08b9k9 carabus sma	503	7	1.0	355	2	09TE02	09te02 carabus can
431	1.0	355	2	08B9L0	08b9l0 carabus ale	504	7	1.0	355	2	09TE03	09te03 carabus can
432	7	355	2	08B9L2	08b9l2 carabus hae	505	7	1.0	355	2	09TE04	09te04 carabus can
433	1.0	355	2	08B9L3	08b9l3 carabus pot	506	7	1.0	355	2	09TE05	09te05 carabus can
434	7	355	2	08B9L4	08b9l4 carabus pot	507	7	1.0	355	2	09TE08	09te08 carabus sei
435	1.0	355	2	08B9L5	08b9l5 carabus ari	508	7	1.0	355	2	09TE09	09te09 carabus sei
436	7	355	2	08B9L6	08b9l6 carabus ari	509	7	1.0	355	2	09TE10	09te10 carabus sei
437	1.0	355	2	08B9L7	08b9l7 carabus exi	510	7	1.0	355	2	09TE11	09te11 carabus sei
438	7	355	2	08B9L8	08b9l8 carabus cra	511	7	1.0	355	2	09TE12	09te12 carabus sem
439	1.0	355	2	08B9L9	08b9l9 carabus cra	512	7	1.0	355	2	09TE13	09te13 carabus sem
440	7	355	2	08B9M0	08b9m0 carabus uen	513	7	1.0	355	2	09TE14	09te14 carabus sem
441	1.0	355	2	08B9M1	08b9m1 carabus vir	514	7	1.0	355	2	09TE15	09te15 carabus kor
442	7	355	2	08B9M2	08b9m2 carabus bra	515	7	1.0	355	2	09TE22	09te22 carabus bla
443	1.0	355	2	08B9M3	08b9m3 carabus ign	516	7	1.0	355	2	09TE23	09te23 carabus bla
444	7	355	2	08B9M4	08b9m4 carabus mir	517	7	1.0	355	2	09TE24	09te24 carabus bla
445	1.0	355	2	08B9M5	08b9m5 carabus oia	518	7	1.0	355	2	09TE25	09te25 carabus bla
446	7	355	2	08B9M6	08b9m6 carabus oia	519	7	1.0	355	2	09TE26	09te26 carabus bla
447	1.0	355	2	08B9M7	08b9m7 carabus oia	520	7	1.0	355	2	09TE27	09te27 carabus bla
448	7	355	2	08B9M8	08b9m8 carabus oia	521	7	1.0	355	2	09TE27	09te27 carabus bla
449	1.0	355	2	08B9M9	08b9m9 carabus vir	522	7	1.0	355	2	09TE83	09te83 carabus bla
450	7	355	2	08B9M2	08b9m2 carabus sma	523	7	1.0	355	2	09TE84	09te84 carabus bla
451	1.0	355	2	08B9N3	08b9n3 carabus nan	524	7	1.0	355	2	09TE85	09te85 carabus bla
452	7	355	2	08B9N3	08b9n3 carabus con	525	7	1.0	355	2	09TE86	09te86 carabus bla
453	1.0	355	2	08B9N3	08b9n3 carabus con	526	7	1.0	355	2	09TE87	09te87 carabus bla
454	7	355	2	08B9N3	08b9n3 carabus con	527	7	1.0	355	2	09TE88	09te88 carabus bla
455	1.0	355	2	08B9N3	08b9n3 carabus con	528	7	1.0	355	2	09TE89	09te89 carabus bla
456	7	355	2	08B9N3	08b9n3 carabus con	529	7	1.0	355	2	09TE90	09te90 carabus bla
457	1.0	355	2	08B9N3	08b9n3 carabus con	530	7	1.0	355	2	09TE91	09te91 carabus bla
458	7	355	2	08B9N3	08b9n3 carabus con	531	7	1.0	355	2	09TE93	09te93 carabus bla
459	1.0	355	2	08B9N3	08b9n3 carabus con	532	7	1.0	355	2	09TE94	09te94 carabus bla
460	7	355	2	08B9N3	08b9n3 carabus con	533	7	1.0	355	2	09TE95	09te95 carabus bla
461	1.0	355	2	08B9N3	08b9n3 carabus con	534	7	1.0	355	2	09TE96	09te96 carabus bla
462	7	355	2	08B9N3	08b9n3 carabus con	535	7	1.0	355	2	09TE97	09te97 carabus bla
463	1.0	355	2	08B9N3	08b9n3 carabus con	536	7	1.0	355	2	09TE98	09te98 carabus bla
464	7	355	2	08B9N3	08b9n3 carabus con	537	7	1.0	355	2	09TE99	09te99 carabus bla
465	1.0	355	2	08B9N3	08b9n3 carabus con	538	7	1.0	355	2	09TEA0	09tea0 carabus bla
466	7	355	2	08B9N3	08b9n3 carabus con	539	7	1.0	355	2	09TEA1	09tea1 carabus bla
467	1.0	355	2	08B9N3	08b9n3 carabus con	540	7	1.0	355	2	09TEA2	09tea2 carabus bla
468	7	355	2	08B9N3	08b9n3 carabus con	541	7	1.0	355	2	09TEA3	09tea3 carabus bla
469	1.0	355	2	08B9N3	08b9n3 carabus con	542	7	1.0	355	2	09TEA4	09tea4 carabus bla
											09TEA5	09tea5 carabus bla

543	7	1.0	355	2	Q9TEA6	Q9TEA6 carabus bla
544	7	1.0	355	2	Q9TEA7	Q9TEA7 carabus bla
545	7	1.0	355	2	Q9TEA8	Q9TEA8 carabus bla
546	7	1.0	355	2	Q9TEA9	Q9TEA9 carabus bla
547	7	1.0	355	2	Q9TEB0	Q9TEB0 carabus bla
548	7	1.0	355	2	Q9TEB1	Q9TEB1 carabus bla
549	7	1.0	355	2	Q9TEB2	Q9TEB2 carabus bla
550	7	1.0	355	2	Q9TEB3	Q9TEB3 carabus bla
551	7	1.0	357	2	Q9TEB4	Q9TEB4 carabus bla
552	7	1.0	357	2	Q9TEB5	Q9TEB5 carabus bla
553	7	1.0	359	1	MANR_PSEBU	MANR_PSEBU carabus bla
554	7	1.0	359	1	MANR_PSEBU	MANR_PSEBU carabus bla
555	7	1.0	359	2	Q9TEB6	Q9TEB6 carabus bla
556	7	1.0	359	2	Q9TEB7	Q9TEB7 carabus bla
557	7	1.0	359	2	Q9TEB8	Q9TEB8 carabus bla
558	7	1.0	360	1	AROB_BUCAP	AROB_BUCAP carabus bla
559	7	1.0	363	2	Q9TEB9	Q9TEB9 carabus bla
560	7	1.0	363	2	Q9TEB0	Q9TEB0 carabus bla
561	7	1.0	367	2	Q9TEB1	Q9TEB1 carabus bla
562	7	1.0	367	2	Q9TEB2	Q9TEB2 carabus bla
563	7	1.0	368	2	Q9TEB3	Q9TEB3 carabus bla
564	7	1.0	372	2	Q9TEB4	Q9TEB4 carabus bla
565	7	1.0	373	2	Q9TEB5	Q9TEB5 carabus bla
566	7	1.0	373	2	Q9TEB6	Q9TEB6 carabus bla
567	7	1.0	374	1	TCT_ANASP	TCT_ANASP carabus bla
568	7	1.0	375	1	Q9TEB7	Q9TEB7 carabus bla
569	7	1.0	375	2	Q9TEB8	Q9TEB8 carabus bla
570	7	1.0	376	2	Q9TEB9	Q9TEB9 carabus bla
571	7	1.0	377	2	Q9TEB0	Q9TEB0 carabus bla
572	7	1.0	378	2	Q9TEB1	Q9TEB1 carabus bla
573	7	1.0	382	2	Q9TEB2	Q9TEB2 carabus bla
574	7	1.0	383	2	Q9TEB3	Q9TEB3 carabus bla
575	7	1.0	383	2	Q9TEB4	Q9TEB4 carabus bla
576	7	1.0	383	2	Q9TEB5	Q9TEB5 carabus bla
577	7	1.0	387	2	Q9TEB6	Q9TEB6 carabus bla
578	7	1.0	387	2	Q9TEB7	Q9TEB7 carabus bla
579	7	1.0	387	2	Q9TEB8	Q9TEB8 carabus bla
580	7	1.0	387	2	Q9TEB9	Q9TEB9 carabus bla
581	7	1.0	387	2	Q9TEB0	Q9TEB0 carabus bla
582	7	1.0	387	2	Q9TEB1	Q9TEB1 carabus bla
583	7	1.0	388	2	Q9TEB2	Q9TEB2 carabus bla
584	7	1.0	389	1	Q9TEB3	Q9TEB3 carabus bla
585	7	1.0	391	2	Q9TEB4	Q9TEB4 carabus bla
586	7	1.0	391	2	Q9TEB5	Q9TEB5 carabus bla
587	7	1.0	392	2	Q9TEB6	Q9TEB6 carabus bla
588	7	1.0	394	2	Q9TEB7	Q9TEB7 carabus bla
589	7	1.0	396	2	Q9TEB8	Q9TEB8 carabus bla
590	7	1.0	397	2	Q9TEB9	Q9TEB9 carabus bla
591	7	1.0	398	2	Q9TEB0	Q9TEB0 carabus bla
592	7	1.0	399	2	Q9TEB1	Q9TEB1 carabus bla
593	7	1.0	407	2	Q9TEB2	Q9TEB2 carabus bla
594	7	1.0	408	2	Q9TEB3	Q9TEB3 carabus bla
595	7	1.0	408	2	Q9TEB4	Q9TEB4 carabus bla
596	7	1.0	410	2	Q9TEB5	Q9TEB5 carabus bla
597	7	1.0	410	2	Q9TEB6	Q9TEB6 carabus bla
598	7	1.0	410	2	Q9TEB7	Q9TEB7 carabus bla
599	7	1.0	410	2	Q9TEB8	Q9TEB8 carabus bla
600	7	1.0	413	2	Q9TEB9	Q9TEB9 carabus bla
601	7	1.0	413	2	Q9TEB0	Q9TEB0 carabus bla
602	7	1.0	414	2	Q9TEB1	Q9TEB1 carabus bla
603	7	1.0	416	2	Q9TEB2	Q9TEB2 carabus bla
604	7	1.0	420	1	Q9TEB3	Q9TEB3 carabus bla
605	7	1.0	421	2	Q9TEB4	Q9TEB4 carabus bla
606	7	1.0	426	2	Q9TEB5	Q9TEB5 carabus bla
607	7	1.0	429	2	Q9TEB6	Q9TEB6 carabus bla
608	7	1.0	432	2	Q9TEB7	Q9TEB7 carabus bla
609	7	1.0	436	2	Q9TEB8	Q9TEB8 carabus bla
610	7	1.0	437	2	Q9TEB9	Q9TEB9 carabus bla
611	7	1.0	437	2	Q9TEB0	Q9TEB0 carabus bla
612	7	1.0	439	2	Q9TEB1	Q9TEB1 carabus bla
613	7	1.0	441	2	Q9TEB2	Q9TEB2 carabus bla
614	7	1.0	442	2	Q9TEB3	Q9TEB3 carabus bla
615	7	1.0	445	2	Q9TEB4	Q9TEB4 carabus bla

669	1.0	507	2	Q9SE93	Q9SE93	parodia maa	762	7	1.0	544	2	Q8TFN9	Q8TFN9	emericella
690	1.0	507	2	Q9SE96	Q9SE96	matucana in	763	7	1.0	545	2	Q8TLM0	Q8TLM0	symbiobacte
691	1.0	507	2	Q9SE97	Q9SE97	rauhocereus	764	7	1.0	549	2	Q9DM53	Q9DM53	rat cytoMeg
692	1.0	507	2	Q9SEAO	Q9SEAO	trichocereus	765	7	1.0	553	2	Q97810	Q97810	streptococc
693	1.0	507	2	Q9SEEA	Q9SEEA	uebelmannia	766	7	1.0	553	2	Q8DOR3	Q8DOR3	streptococc
694	1.0	507	2	Q9SEEA2	Q9SEEA2	coleocephal	767	7	1.0	556	1	NU2M_PODAN	NU2M_PODAN	pl5578 podopora a
695	1.0	507	2	Q9SEEA4	Q9SEEA4	browningia	768	7	1.0	556	2	Q6DEK7	Q6DEK7	brachydania
696	1.0	507	2	Q9SEEC4	Q9SEEC4	copiapa la	769	7	1.0	560	2	Q49141	Q49141	arabidopsis
697	1.0	507	2	Q9SEEC5	Q9SEEC5	copiapa br	770	7	1.0	560	2	Q50057	Q50057	arabidopsis
698	1.0	507	2	Q9SEEC6	Q9SEEC6	copiapa so	771	7	1.0	561	2	Q9KY69	Q9KY69	streptomyc
699	1.0	507	2	Q9SEED8	Q9SEED8	pereskiopei	772	7	1.0	561	2	Q9RX81	Q9RX81	deinococcus
700	1.0	507	2	Q7HF87	Q7HF87	parodia mag	773	7	1.0	563	2	Q74JC6	Q74JC6	lactobacill
701	1.0	507	2	Q7HF88	Q7HF88	oreocereus	774	7	1.0	568	2	Q88W64	Q88W64	lactobacill
702	1.0	507	2	Q7HF89	Q7HF89	samaipaticce	775	7	1.0	576	2	Q6YID6	Q6YID6	panaeus mon
703	1.0	507	2	Q7HF89	Q7HF89	micranthoce	776	7	1.0	579	2	Q65X75	Q65X75	oryza sativ
704	1.0	507	2	Q7HF89	Q7HF89	cereus alac	777	7	1.0	580	2	Q92QP6	Q92QP6	arabidopsis
705	1.0	508	2	Q9SEB2	Q9SEB2	pleiffera m	778	7	1.0	581	1	YD15_SCHPO	YD15_SCHPO	schizosacch
706	1.0	508	2	Q9SEB2	Q9SEB2	pleiffera m	779	7	1.0	581	2	Q91KH1	Q91KH1	mesembryant
707	1.0	508	2	Q9SEB2	Q9SEB2	pleiffera m	780	7	1.0	581	2	Q8D7C1	Q8D7C1	vibrio vuln
708	1.0	509	2	Q9SEB3	Q9SEB3	staphylococ	781	7	1.0	582	2	Q23492	Q23492	arabidopsis
709	1.0	509	2	Q9SEB3	Q9SEB3	leptamiliu c	782	7	1.0	584	2	Q9SQZ0	Q9SQZ0	arabidopsis
710	1.0	509	2	Q9SEB5	Q9SEB5	rhopalais f	783	7	1.0	584	2	Q67RH6	Q67RH6	symbiobacte
711	1.0	509	2	Q9SEB6	Q9SEB6	haciara sal	784	7	1.0	585	2	Q17491	Q17491	caenorhabdi
712	1.0	509	2	Q9SEB9	Q9SEB9	parodia oct	785	7	1.0	585	2	Q8SZY4	Q8SZY4	caenorhabdi
713	1.0	509	2	Q9SEB9	Q9SEB9	parodia mic	786	7	1.0	600	2	Q93GX8	Q93GX8	strepomyce
714	1.0	509	2	Q9SEB9	Q9SEB9	selenicereu	787	7	1.0	600	2	Q6A2T2	Q6A2T2	xenopus lae
715	1.0	509	2	Q9SEB9	Q9SEB9	hylocereus	788	7	1.0	602	2	Q65DM0	Q65DM0	bacillus li
716	1.0	509	2	Q9SEB9	Q9SEB9	pachycereus	789	7	1.0	607	2	Q6DFJ5	Q6DFJ5	xenopus lae
717	1.0	509	2	Q9SEB9	Q9SEB9	echinocereus	790	7	1.0	608	2	Q9GMB0	Q9GMB0	sus scrofa
718	1.0	509	2	Q9SEB9	Q9SEB9	pleiffera m	791	7	1.0	611	2	Q7MEC8	Q7MEC8	vibrio vuln
719	1.0	509	2	Q9SEB9	Q9SEB9	pleiffera i	792	7	1.0	612	2	Q804W7	Q804W7	fugu rubrip
720	1.0	509	2	Q9SEB5	Q9SEB5	corryocactu	793	7	1.0	614	1	SPAS_MOUSE	SPAS_MOUSE	mus musculu
721	1.0	509	2	Q9SEB6	Q9SEB6	corryocactu	794	7	1.0	615	2	Q6GNK4	Q6GNK4	mus musculu
722	1.0	509	2	Q9SEB7	Q9SEB7	eulychmia i	795	7	1.0	616	1	SPAS_HUMAN	SPAS_HUMAN	homo sapien
723	1.0	509	2	Q9SEB8	Q9SEB8	autrocactu	796	7	1.0	617	1	THRB_RAT	THRB_RAT	ratius norv
724	1.0	509	2	Q9SEB9	Q9SEB9	neoraimondi	797	7	1.0	617	2	Q97UG5	Q97UG5	sulfolobus
725	1.0	509	2	Q9SEB9	Q9SEB9	caecellanos	798	7	1.0	618	1	CTR3_MOUSE	CTR3_MOUSE	mus musculu
726	1.0	509	2	Q9SEB9	Q9SEB9	leptocereus	799	7	1.0	618	1	THRB_MOUSE	THRB_MOUSE	mus musculu
727	1.0	509	2	Q9SEB9	Q9SEB9	armatocereus	800	7	1.0	620	2	Q38940	Q38940	arabidopsis
728	1.0	509	2	Q9SEB9	Q9SEB9	acanthocere	801	7	1.0	622	2	THRB_HUMAN	THRB_HUMAN	homo sapien
729	1.0	509	2	Q9SEB9	Q9SEB9	calymnanchi	802	7	1.0	622	2	Q7Z7F3	Q7Z7F3	homo sapien
730	1.0	509	2	Q9SEB9	Q9SEB9	aztekium ri	803	7	1.0	624	2	Q94CP4	Q94CP4	arabidopsis
731	1.0	509	2	Q9SEB9	Q9SEB9	astrophytum	804	7	1.0	625	1	THRB_BOVIN	THRB_BOVIN	bos taurus
732	1.0	509	2	Q9SEB9	Q9SEB9	echinocactu	805	7	1.0	629	1	THIC_PSSSM	THIC_PSSSM	pseudomonas
733	1.0	509	2	Q9SEB9	Q9SEB9	firella pha	806	7	1.0	633	2	Q90Z56	Q90Z56	scophthalmu
734	1.0	509	2	Q9SEB9	Q9SEB9	firella gra	807	7	1.0	648	2	Q9NKD7	Q9NKD7	drosophila
735	1.0	509	2	Q9SEB9	Q9SEB9	blotsfeldia	808	7	1.0	651	2	Q7NGA4	Q7NGA4	gloeobacter
736	1.0	509	2	Q9SEB9	Q9SEB9	blotsfeldia	809	7	1.0	658	2	Q65466	Q65466	arabidopsis
737	1.0	509	2	Q9SEB9	Q9SEB9	opuntia qui	810	7	1.0	663	2	Q8U2H8	Q8U2H8	pyrococcus
738	1.0	509	2	Q9SEB9	Q9SEB9	autrococyllin	811	7	1.0	674	2	Q9C559	Q9C559	arabidopsis
739	1.0	509	2	Q9SEB9	Q9SEB9	pereskia st	812	7	1.0	678	2	Q9A4E2	Q9A4E2	caulobacter
740	1.0	509	2	Q9SEB9	Q9SEB9	pereskia gu	813	7	1.0	680	2	Q8GX18	Q8GX18	arabidopsis
741	1.0	509	2	Q9SEB9	Q9SEB9	talium pan	814	7	1.0	682	2	Q6DKG5	Q6DKG5	homo sapien
742	1.0	510	1	MARK_GABR	Q9SEB9	grahania br	815	7	1.0	682	2	Q8EWR4	Q8EWR4	mycoplasma
743	1.0	510	1	Q7SEH0	Q7SEH0	neurospora	816	7	1.0	684	2	Q80709	Q80709	arabidopsis
744	1.0	517	2	Q67SM0	Q67SM0	symbiobacte	817	7	1.0	700	2	Q8ECU0	Q8ECU0	shewanella
745	1.0	521	1	GM12_METAC	GM12_METAC	mechanosarc	818	7	1.0	703	2	Q8R917	Q8R917	thermoanaer
746	1.0	521	1	GPMI_METMA	GPMI_METMA	mechanosarc	819	7	1.0	705	2	Q7RSJ9	Q7RSJ9	giardia lam
747	1.0	525	2	Q7SXH8	Q7SXH8	brachydania	820	7	1.0	707	1	BMP1_XENLA	BMP1_XENLA	xenopus lae
748	1.0	525	2	Q6BJ17	Q6BJ17	debarowyce	821	7	1.0	708	2	Q87ZJ9	Q87ZJ9	lactococcus
749	1.0	526	2	Q6AVS5	Q6AVS5	homo sapien	822	7	1.0	713	2	Q6ZAN6	Q6ZAN6	burkholderi
750	1.0	527	2	Q8P606	Q8P606	xanthomonas	823	7	1.0	720	2	Q63NR2	Q63NR2	burkholderi
751	1.0	529	2	Q17403	Q17403	caenorhabdi	824	7	1.0	732	2	Q65QI8	Q65QI8	mannheimia
752	1.0	529	2	Q7ND04	Q7ND04	gloeobacter	825	7	1.0	735	2	Q57381	Q57381	xenopus lae
753	1.0	530	2	Q94900	Q94900	homo sapien	826	7	1.0	735	2	Q66K13	Q66K13	xenopus lae
754	1.0	532	2	Q9YDB4	Q9YDB4	aeropyrum p	827	7	1.0	746	2	Q6M7J3	Q6M7J3	corynebacte
755	1.0	533	2	Q9B147	Q9B147	caenorhabdi	828	7	1.0	746	2	Q9Y7R4	Q9Y7R4	strepococc
756	1.0	535	2	Q9JP77	Q9JP77	thermomonas	829	7	1.0	749	2	Q9Y7G8	Q9Y7G8	oncorhynch
757	1.0	535	2	Q6MR14	Q6MR14	bdellovibri	830	7	1.0	754	2	Q49144	Q49144	arabidopsis
758	1.0	541	2	Q7P546	Q7P546	fusobacteri	831	7	1.0	754	2	Q7G196	Q7G196	arabidopsis
759	1.0	541	2	Q8RFL3	Q8RFL3	fusobacteri	832	7	1.0	765	2	Q8XY74	Q8XY74	ratisonia s
760	1.0	541	2	Q7WPA4	Q7WPA4	botriocella	833	7	1.0	778	2	Q6CP63	Q6CP63	kluveromyc
761	1.0	542	1	MODU_DROME	MODU_DROME	drosophila	834	7	1.0	783	1	YX11_PSEAE	YX11_PSEAE	pseudomonas

835	7	1.0	783	2	Q7R5Y0	Q75Y0 giardia lam	908	7	1.0	1450	2	Q6BCK1	Q6bck1 tetrathymena
836	7	1.0	783	2	Q6BL63	Q6b113 giardia lam	909	7	1.0	1506	2	Q6NS59	Q6ns59 mus musculus
837	7	1.0	783	2	Q6DW63	Q6dw76 glycine max	910	7	1.0	1522	1	DNA2_YEAST	P8859 saccaromyce
838	7	1.0	783	2	Q9E126	Q9e126 cercopithec	911	7	1.0	1527	2	Q6F1I8	Q6f1i8 candida gla
839	7	1.0	786	2	Q6DM74	Q6dw74 locus japon	912	7	1.0	1544	2	Q86ZB3	Q86zb3 botrytis ci
840	7	1.0	787	2	Q9V1E8	Q9vie8 drosophila	913	7	1.0	1569	2	Q9FHD0	Q9fhd0 arabidopsis
841	7	1.0	790	1	CADI_HUMAN	Q1b34 homo sapien	914	7	1.0	1608	2	Q9SVAS	Q9svas arabidopsis
842	7	1.0	790	2	Q8N522	Q8n522 homo sapien	915	7	1.0	1631	2	Q8D237	Q8d237 drosophila
843	7	1.0	791	2	Q49137	Q49137 arabidopsis	916	7	1.0	1640	2	Q86Z91	Q86z91 gibberella
844	7	1.0	791	2	Q49139	Q49139 arabidopsis	917	7	1.0	1660	2	Q94729	Q94729 oryza sativ
845	7	1.0	791	2	Q50073	Q50073 arabidopsis	918	7	1.0	1660	2	Q7XFK3	Q7xfk3 oryza sativ
846	7	1.0	793	2	Q7QUH8	Q7qub8 giardia lam	919	7	1.0	1666	2	Q8LP68	Q8lp68 chlamydomon
847	7	1.0	799	2	Q7SAU1	Q7sau1 aethya goss	920	7	1.0	1755	2	Q7RV31	Q7rv31 neurospora
848	7	1.0	799	2	Q8NSU9	Q8nsu9 corynebacte	921	7	1.0	1768	2	Q9N8K7	Q9n8k7 trypanosoma
849	7	1.0	803	2	Q6FV15	Q6fv15 candida gla	922	7	1.0	1822	1	SC72_SCHPO	Q9p7v5 schizosacch
850	7	1.0	805	2	Q95RK7	Q95rk7 drosophila	923	7	1.0	1826	2	Q7RXK8	Q7rxk8 neurospora
851	7	1.0	805	2	Q636U8	Q636u8 bacillus ce	924	7	1.0	1831	2	Q86T77	Q86t77 homo sapien
852	7	1.0	805	2	Q733A2	Q733a2 bacillus ce	925	7	1.0	1863	2	Q81VX2	Q81vx2 homo sapien
853	7	1.0	805	2	Q81WV6	Q81wv6 bacillus an	926	7	1.0	1865	2	Q7Z401	Q7z401 homo sapien
854	7	1.0	805	2	Q6HF81	Q6hf81 bacillus th	927	7	1.0	1877	2	Q9XKW1	Q9xkw1 plasmodium
855	7	1.0	806	2	Q81A60	Q81a60 bacillus ce	928	7	1.0	1879	2	Q7PDP1	Q7pdp1 plasmodium
856	7	1.0	808	2	Q9S7D1	Q9s7d1 arabidopsis	929	7	1.0	1903	2	Q9U0N7	Q9u0n7 plasmodium
857	7	1.0	826	2	Q8BPV4	Q8bvf4 methanobarc	930	7	1.0	1952	2	Q95SN5	Q95sn5 drosophila
858	7	1.0	826	2	Q8TQX6	Q8tqx6 methanobarc	931	7	1.0	1961	2	Q6W689	Q6w689 ratus norv
859	7	1.0	826	2	Q9T041	Q9t041 arabidopsis	932	7	1.0	1966	2	Q81QV6	Q81qv6 drosophila
860	7	1.0	841	1	TRK1_SCHPO	P47946 schizosacch	933	7	1.0	1966	2	Q9NMX6	Q9nmx6 drosophila
861	7	1.0	842	1	Q9LSB8	Q9lsb8 arabidopsis	934	7	1.0	1968	2	Q8XOC5	Q8xoc5 neurospora
862	7	1.0	859	1	ALR1_YEAST	Q08269 saccaromyce	935	7	1.0	1985	2	Q8T9N4	Q8t9n4 drosophila
863	7	1.0	864	2	Q68VX4	Q68vx4 arabidopsis	936	7	1.0	1985	2	Q7KUN8	Q7kun8 drosophila
864	7	1.0	867	2	Q211B6	Q211b6 caenorhabdi	937	7	1.0	1985	2	Q9VSK5	Q9vsk5 drosophila
865	7	1.0	869	2	Q81G55	Q81g55 caenorhabdi	938	7	1.0	1988	2	Q86BH2	Q86bh2 drosophila
866	7	1.0	873	2	Q9S0Z4	Q9s0z4 escherichia	939	7	1.0	2381	2	Q7R4R8	Q7r4r8 giardia lam
867	7	1.0	917	2	Q9V4B8	Q9v4b8 drosophila	940	7	1.0	2393	2	Q81461	Q81461 plasmodium
868	7	1.0	921	2	Q9VJ29	Q9vj29 drosophila	941	7	1.0	2549	2	Q7PPV7	Q7ppv7 anopheles g
869	7	1.0	921	2	Q9BDU0	Q9bdu0 dendrothyrax	942	7	1.0	2605	2	Q50B58	Q50b58 myxococcus
870	7	1.0	922	2	Q6BTU4	Q6btj4 debaryomyce	943	7	1.0	2906	2	Q9WUH9	Q9wuh9 ratus norv
871	7	1.0	950	2	Q8RZX0	Q8rxz0 oryza sativ	944	7	1.0	2907	1	FBN2_MOUSE	Q61555 mus musculu
872	7	1.0	955	2	Q726R1	Q726r1 desulfovibr	945	7	1.0	2911	1	FBN2_HUMAN	P35556 homo sapien
873	7	1.0	961	2	Q8SVH3	Q8svh3 encephalito	946	7	1.0	3306	2	Q9FT44	Q9ft44 arabidopsis
874	7	1.0	970	2	Q7XFK3	Q7xfk3 oryza sativ	947	7	1.0	3446	2	Q86AC8	Q86ac8 dictyosteli
875	7	1.0	970	2	Q9AYF2	Q9ayf2 oryza sativ	948	7	1.0	3523	2	Q7QCP4	Q7qcp4 anopheles g
876	7	1.0	977	2	Q91925	Q91925 xenopus lae	949	7	1.0	3564	1	CSM1_MOUSE	Q92313 mus musculu
877	7	1.0	980	2	Q22088	Q22088 caenorhabdi	950	7	1.0	3666	2	Q6UDX0	Q6udx0 plasmodium
878	7	1.0	982	2	Q6CWM6	Q6cwm6 kluyveromyce	951	7	1.0	3972	2	Q9S0R8	Q9s0r8 streptomyce
879	7	1.0	991	2	Q8TDH1	Q8tdh1 homo sapien	952	7	1.0	3996	2	Q7KTP2	Q7ktp2 drosophila
880	7	1.0	995	1	YPD1_CAEEL	P48053 caenorhabdi	953	7	1.0	4547	2	Q9W3J3	Q9w3j3 drosophila
881	7	1.0	1007	2	Q8C1Z8	Q8c1z8 xenopus lae	954	7	1.0	4569	2	Q7PS35	Q7ps35 anopheles g
882	7	1.0	1013	2	Q6MFF7	Q6mff7 parachlamyd	955	7	1.0	4899	2	Q9VR91	Q9vr91 drosophila
883	7	1.0	1022	1	TLD_BRARE	Q85460 brachydanio	956	7	1.0	23015	2	Q81Q18	Q81q18 drosophila
884	7	1.0	1031	2	Q8GSK2	Q8gsk2 bifidobacte	957	6	0.8	27	1	ANF_ANGJA	P18144 anguilla ja
885	7	1.0	1046	2	Q6C1R8	Q6c1r8 yarrowia li	958	6	0.8	27	1	Q8FZ50	Q8fz50 brucea su
886	7	1.0	1047	2	Q9PKM9	Q9pkw9 arabidopsis	959	6	0.8	33	2	Q8B9R2	Q8b9r2 emilliana h
887	7	1.0	1048	2	Q9NA71	Q9na71 caenorhabdi	960	6	0.8	33	2	Q8B9R3	Q8b9r3 emilliana h
888	7	1.0	1074	2	Q831Z5	Q831z5 enterococcu	961	6	0.8	33	2	Q8B9R4	Q8b9r4 emilliana h
889	7	1.0	1079	2	Q6MLZ8	Q6mlz8 bdellovibri	962	6	0.8	33	2	Q8B9R5	Q8b9r5 emilliana h
890	7	1.0	1081	2	Q8BZL9	Q8bz19 mus musculu	963	6	0.8	33	2	Q8B9R6	Q8b9r6 emilliana h
891	7	1.0	1100	2	Q86UDH1	Q86udh1 homo sapien	964	6	0.8	33	2	Q8B9R7	Q8b9r7 emilliana h
892	7	1.0	1111	2	Q8S5Z2	Q8s5z2 mycobacteri	965	6	0.8	33	2	Q8B9R8	Q8b9r8 emilliana h
893	7	1.0	1120	2	Q8P8S7	Q8p8s7 corynebacte	966	6	0.8	33	2	Q8B9R9	Q8b9r9 emilliana h
894	7	1.0	1135	2	Q7Q1J7	Q7q1j7 anopheles g	967	6	0.8	35	2	Q9KSL5	Q9ksl5 vibrio chol
895	7	1.0	1136	2	Q81UD8	Q81ud8 plasmodium	968	6	0.8	36	2	Q96W36	Q96w36 ophiostoma
896	7	1.0	1158	2	Q7Q2S3	Q7q2s3 anopheles g	969	6	0.8	36	2	Q72CQ3	Q72cq3 desulfovibr
897	7	1.0	1201	2	Q71RU0	Q71ru0 nitrobacter	970	6	0.8	37	2	Q9DRR2	Q9dr2 human immun
898	7	1.0	1231	2	Q6CAC2	Q6cac2 yarrowia li	971	6	0.8	38	2	Q7VM96	Q7vm96 haemophilus
899	7	1.0	1234	2	Q7SF30	Q7sf30 neurospora	972	6	0.8	39	2	Q29360	Q29360 sus scrofa
900	7	1.0	1240	2	DLT_DROME	Q8f626 drosophila	973	6	0.8	39	2	Q6IEB9	Q6ieb9 macaca mula
901	7	1.0	1243	2	Q55954	Q55954 mus musculu	974	6	0.8	40	2	Q9RAD0	Q9rad0 thermus agu
902	7	1.0	1300	2	Q8XOV5	Q8xov5 neurospora	975	6	0.8	40	2	Q73510	Q73510 bacillus ce
903	7	1.0	1327	2	Q6C4J5	Q6c4j5 yarrowia li	976	6	0.8	40	2	Q9KLT1	Q9klt1 vibrio chol
904	7	1.0	1340	2	Q9GYW4	Q9gyw4 anopheles g	977	6	0.8	40	2	Q8UM87	Q8um87 human immun
905	7	1.0	1346	2	Q9ZG12	Q9zgi2 streptomyce	978	6	0.8	41	2	Q90SM4	Q90sm4 human immun
906	7	1.0	1355	2	Q7Q7S9	Q7q7s9 anopheles g	979	6	0.8	41	2	Q90SM5	Q90sm5 human immun
907	7	1.0	1355	2	Q7Q7S9	Q7q7s9 anopheles g	980	6	0.8	41	2	Q90SM5	Q90sm5 human immun

981	6	0.8	41	2	Q90SM6	Q96n6 human immun	1054	6	0.8	56	2	Q97AA0	Q97a7 thermoplas
982	6	0.8	41	2	Q78Z26	Q78226 human immun	1055	6	0.8	56	2	Q81P47	Q81p47 bacillus an
983	6	0.8	41	2	Q9G37	Q9G37 human immun	1056	6	0.8	56	2	Q9CB5	Q9CB5 mycobacteri
984	6	0.8	42	2	Q85WV3	Q85WV3 pinus korai	1057	6	0.8	57	2	Q38990	Q38990 arabidopsis
985	6	0.8	42	2	Q67PK6	Q67PK6 symbiobacte	1058	6	0.8	57	2	Q38991	Q38991 arabidopsis
986	6	0.8	43	2	Q704X0	Q704X0 bos taurus	1059	6	0.8	57	2	Q38992	Q38992 arabidopsis
987	6	0.8	44	2	Q8F2Y9	Q8F2Y9 leptospira	1060	6	0.8	57	2	Q8D859	Q8D859 vibrio vuln
988	6	0.8	44	2	Q8F9N3	Q8F9N3 leptospira	1061	6	0.8	59	2	Q81Z30	Q81z30 bacillus an
989	6	0.8	45	2	Q80HK8	Q80HK8 hepatitis c	1062	6	0.8	59	2	Q9HYB3	Q9HYB3 pseudomonas
990	6	0.8	45	2	Q80I53	Q80I53 hepatitis c	1063	6	0.8	60	2	Q6ZGX7	Q6ZGX7 oryza sativ
991	6	0.8	45	2	Q80I54	Q80I54 hepatitis c	1064	6	0.8	60	2	Q6Z963	Q6Z963 rattus norv
992	6	0.8	45	2	Q80I55	Q80I55 hepatitis c	1065	6	0.8	60	2	Q6SPV9	Q6SPV9 human immun
993	6	0.8	45	2	Q80I56	Q80I56 hepatitis c	1066	6	0.8	61	2	Q6Z4L9	Q6Z4L9 oryza sativ
994	6	0.8	45	2	Q80I57	Q80I57 hepatitis c	1067	6	0.8	61	2	Q45045	Q45045 borellia bu
995	6	0.8	45	2	Q80I58	Q80I58 hepatitis c	1068	6	0.8	61	2	Q75777	Q75777 human immun
996	6	0.8	45	2	Q80I59	Q80I59 hepatitis c	1069	6	0.8	62	1	CX51_CONIM	Q9k6z5 conus imper
997	6	0.8	45	2	Q80I60	Q80I60 hepatitis c	1070	6	0.8	63	2	Q6BKM4	Q6BK44 debaryomyce
998	6	0.8	45	2	Q80I61	Q80I61 hepatitis c	1071	6	0.8	63	2	Q19260	Q19260 pongo pygma
999	6	0.8	45	2	Q80I62	Q80I62 hepatitis c	1072	6	0.8	63	2	Q841B5	Q841B5 metohermus
1000	6	0.8	45	2	Q9G3F1	Q9G3F1 human immun	1073	6	0.8	63	2	Q8K6X6	Q8K6X6 streptococ
1001	6	0.8	47	2	Q71IY3	Q71IY3 lactobacill	1074	6	0.8	63	2	Q6OK44	Q6OK44 classisal s
1002	6	0.8	48	2	Q9P1I5	Q9P1I5 homo sapien	1075	6	0.8	63	2	Q6OK45	Q6OK45 classisal s
1003	6	0.8	48	2	Q9B8D3	Q9B8D3 candida alb	1076	6	0.8	63	2	Q6OK46	Q6OK46 classisal s
1004	6	0.8	48	2	Q9K201	Q9K201 chlamydia p	1077	6	0.8	63	2	Q6OK47	Q6OK47 classisal s
1005	6	0.8	49	2	P74885	P74885 salmonella	1078	6	0.8	63	2	Q6QLN6	Q6QLN6 classisal s
1006	6	0.8	49	2	Q9F800	Q9F800 erwina amy	1079	6	0.8	63	2	Q6QW4	Q6QW4 classisal s
1007	6	0.8	50	2	Q18986	Q18986 canis faml	1080	6	0.8	63	2	Q7BE63	Q7BE63 classisal s
1008	6	0.8	50	2	Q72YPI	Q72YPI bacillus ce	1081	6	0.8	63	2	Q7BE64	Q7BE64 classisal s
1009	6	0.8	51	2	Q9G3E5	Q9G3E5 human immun	1082	6	0.8	63	2	Q7BE65	Q7BE65 classisal s
1010	6	0.8	51	2	Q9G3E7	Q9G3E7 human immun	1083	6	0.8	63	2	Q7BE66	Q7BE66 classisal s
1011	6	0.8	51	2	Q9G3E9	Q9G3E9 human immun	1084	6	0.8	63	2	Q7BE67	Q7BE67 classisal s
1012	6	0.8	51	2	Q9G3F3	Q9G3F3 human immun	1085	6	0.8	63	2	Q7BE68	Q7BE68 classisal s
1013	6	0.8	51	2	Q9G3F5	Q9G3F5 human immun	1086	6	0.8	63	2	Q7BE69	Q7BE69 classisal s
1014	6	0.8	51	2	Q9G3F7	Q9G3F7 human immun	1087	6	0.8	63	2	Q7BE73	Q7BE73 classisal s
1015	6	0.8	51	2	Q9G3G1	Q9G3G1 human immun	1088	6	0.8	63	2	Q7BE74	Q7BE74 classisal s
1016	6	0.8	51	2	Q9G3G3	Q9G3G3 human immun	1089	6	0.8	63	2	Q7BE75	Q7BE75 classisal s
1017	6	0.8	51	2	Q9G3G5	Q9G3G5 human immun	1090	6	0.8	63	2	Q7BE76	Q7BE76 classisal s
1018	6	0.8	52	2	Q76YQ6	Q76YQ6 bacterioph	1091	6	0.8	63	2	Q7BE77	Q7BE77 classisal s
1019	6	0.8	52	2	Q77369	Q77369 human immun	1092	6	0.8	63	2	Q7BE78	Q7BE78 classisal s
1020	6	0.8	53	2	Q9PGC6	Q9PGC6 xyella fas	1093	6	0.8	63	2	Q7BE79	Q7BE79 classisal s
1021	6	0.8	54	2	Q6JLK6	Q6JLK6 penicillium	1094	6	0.8	64	2	Q7TE80	Q7TE80 classisal s
1022	6	0.8	54	2	Q6JLK9	Q6JLK9 penicillium	1095	6	0.8	64	2	Q9V2B1	Q9V2B1 pyrococcus
1023	6	0.8	54	2	Q6JLL1	Q6JLL1 penicillium	1096	6	0.8	64	2	Q75UP1	Q75UP1 patinopecte
1024	6	0.8	54	2	Q6JLL2	Q6JLL2 penicillium	1097	6	0.8	64	2	Q9SV4	Q9SV4 arabidopsis
1025	6	0.8	54	2	Q6JLL3	Q6JLL3 penicillium	1098	6	0.8	64	2	Q9S27	Q9S27 human immun
1026	6	0.8	54	2	Q6JLL5	Q6JLL5 penicillium	1099	6	0.8	64	2	P88426	P88426 human immun
1027	6	0.8	54	2	Q6JLL6	Q6JLL6 penicillium	1100	6	0.8	65	2	Q7PCU9	Q7PCU9 plasmodium
1028	6	0.8	54	2	Q6JLL7	Q6JLL7 penicillium	1101	6	0.8	65	2	Q8NW16	Q8NW16 strephyllococ
1029	6	0.8	54	2	Q6JLL9	Q6JLL9 penicillium	1102	6	0.8	66	2	Q98GK0	Q98GK0 rhizobium l
1030	6	0.8	54	2	Q6JLM1	Q6JLM1 penicillium	1103	6	0.8	66	2	Q87Q04	Q87Q04 vibrio para
1031	6	0.8	54	2	Q6JLM2	Q6JLM2 penicillium	1104	6	0.8	66	2	Q8DNS2	Q8DNS2 streptococ
1032	6	0.8	54	2	Q6JLM3	Q6JLM3 penicillium	1105	6	0.8	66	2	Q91QU4	Q91QU4 human herpe
1033	6	0.8	54	2	Q6JLM4	Q6JLM4 penicillium	1106	6	0.8	66	2	Q91QU6	Q91QU6 human herpe
1034	6	0.8	54	2	Q6JLM5	Q6JLM5 penicillium	1107	6	0.8	66	2	Q91QZ4	Q91QZ4 cercopithec
1035	6	0.8	54	2	Q6JLM6	Q6JLM6 penicillium	1108	6	0.8	67	2	Q01676	Q01676 pneumocyeti
1036	6	0.8	54	2	Q6JLM7	Q6JLM7 penicillium	1109	6	0.8	67	2	Q9U8X3	Q9U8X3 tachyleus
1037	6	0.8	54	2	Q6JLM8	Q6JLM8 penicillium	1110	6	0.8	67	2	Q63N90	Q63N90 burkholderi
1038	6	0.8	54	2	Q6JLM9	Q6JLM9 penicillium	1111	6	0.8	67	2	Q8YXN0	Q8YXN0 anabaena sp
1039	6	0.8	54	2	Q6JLNL	Q6JLNL penicillium	1112	6	0.8	68	2	Q8U094	Q8U094 strephyllococ
1040	6	0.8	54	2	Q6JLNL	Q6JLNL penicillium	1113	6	0.8	68	2	Q92UC5	Q92UC5 rhizobium m
1041	6	0.8	54	2	Q6JLNL	Q6JLNL penicillium	1114	6	0.8	68	2	Q7MTX3	Q7MTX3 vibrio vuln
1042	6	0.8	54	2	Q9XCE2	Q9XCE2 micromonsp	1115	6	0.8	68	2	Q91Q51	Q91Q51 pongine her
1043	6	0.8	54	2	Q8NNU5	Q8NNU5 staphylococ	1116	6	0.8	68	2	Q38492	Q38492 human immun
1044	6	0.8	54	2	Q97P43	Q97P43 streptococ	1117	6	0.8	69	2	Q8UBR2	Q8UBR2 agrobacteri
1045	6	0.8	54	2	Q7UTY8	Q7UTY8 rhodospirell	1118	6	0.8	70	1	RL31_ECOLI	RL31_ECOLI escherichia
1046	6	0.8	54	2	Q8FYT6	Q8FYT6 brucella su	1119	6	0.8	70	2	Q7MTV4	Q7MTV4 porphyromon
1047	6	0.8	54	2	Q9JTC3	Q9JTC3 neisseria m	1120	6	0.8	70	2	Q7VAV4	Q7VAV4 prochlorococ
1048	6	0.8	54	2	Q6G5Y7	Q6G5Y7 staphylococ	1121	6	0.8	70	2	Q813J7	Q813J7 bacillus ce
1049	6	0.8	55	1	FEBR_CLOAC	P00198 clostridium	1122	6	0.8	70	2	Q9PBR4	Q9PBR4 xyella fas
1050	6	0.8	55	2	P76955	P76955 escherichia	1123	6	0.8	70	2	Q83PD4	Q83PD4 shigella fl
1051	6	0.8	55	2	Q6TPA6	Q6TPA6 aeromonas h	1124	6	0.8	71	2	Q91Q53	Q91Q53 pongine her
1052	6	0.8	55	2	Q8V9P1	Q8V9P1 sulfolobus	1125	6	0.8	71	2	Q13969	Q13969 homo sapien
1053	6	0.8	55	2	Q6SPW5	Q6SPW5 human immun	1126	6	0.8	71	2	Q38272	Q38272 lactococcus

1127	6	0.8	71	2	Q77JUS	Q77J15 bacterioph	1200	6	0.8	81	2	Q10811	Q10811 human immu
1128	6	0.8	71	2	Q77JMS	Q77Jm5 bacterioph	1201	6	0.8	81	2	Q18933	Q18933 human immu
1129	6	0.8	71	2	Q9XJEB	Q9XJEB lactococcus	1202	6	0.8	81	2	Q04271	Q04271 human immu
1130	6	0.8	71	2	Q75161	Q75161 oryza sativ	1203	6	0.8	81	2	Q90M39	Q90M39 human immu
1131	6	0.8	71	2	Q6FCL0	Q6FCL0 acinetobact	1204	6	0.8	81	2	Q90VH8	Q90VH8 human immu
1132	6	0.8	71	2	Q6ZEJ3	Q6ZEJ3 synecocyst	1205	6	0.8	81	2	Q6JN14	Q6JN14 human immu
1133	6	0.8	71	2	Q7MYC6	Q7MYC6 photorhabdu	1206	6	0.8	81	2	Q6JN11	Q6JN11 human immu
1134	6	0.8	71	2	Q83N19	Q83N19 tropheryma	1207	6	0.8	81	2	Q6JN14	Q6JN14 human immu
1135	6	0.8	71	2	Q9CB16	Q9CB16 lactococcus	1208	6	0.8	81	2	Q6JN14	Q6JN14 human immu
1136	6	0.8	71	2	Q79955	Q79955 human immu	1209	6	0.8	81	2	Q6Q461	Q6Q461 human immu
1137	6	0.8	71	2	Q79957	Q79957 human immu	1210	6	0.8	81	2	Q78324	Q78324 human immu
1138	6	0.8	71	2	Q79959	Q79959 human immu	1211	6	0.8	81	2	Q79289	Q79289 human immu
1139	6	0.8	71	2	Q79965	Q79965 human immu	1212	6	0.8	81	2	Q7SKG5	Q7SKG5 human immu
1140	6	0.8	71	2	Q79967	Q79967 human immu	1213	6	0.8	81	2	Q91G74	Q91G74 human immu
1141	6	0.8	71	2	Q79969	Q79969 human immu	1214	6	0.8	82	1	VPU HV1BN	
1142	6	0.8	71	2	Q79970	Q79970 human immu	1215	6	0.8	82	2	Q8SC64	Q8SC64 stx2 conver
1143	6	0.8	71	2	Q79971	Q79971 human immu	1216	6	0.8	82	2	Q7Y202	Q7Y202 stx2 conver
1144	6	0.8	71	2	Q79974	Q79974 human immu	1217	6	0.8	82	2	Q7Y363	Q7Y363 stx1 conver
1145	6	0.8	71	2	Q79976	Q79976 human immu	1218	6	0.8	82	2	Q8F7V5	Q8F7V5 leptospira
1146	6	0.8	71	2	Q79979	Q79979 human immu	1219	6	0.8	82	2	Q6M9U3	Q6M9U3 parachlamyd
1147	6	0.8	71	2	Q79982	Q79982 human immu	1220	6	0.8	82	2	Q9D2H1	Q9D2H1 m musc muscu
1148	6	0.8	72	2	Q9P1H3	Q9P1H3 homo sapien	1221	6	0.8	82	2	Q9Q313	Q9Q313 hepatitis c
1149	6	0.8	72	2	Q26687	Q26687 trypanosoma	1222	6	0.8	82	2	Q90M11	Q90M11 human immu
1150	6	0.8	72	2	Q93229	Q93229 mycoplasma	1223	6	0.8	83	2	Q8NW72	Q8NW72 corynebacte
1151	6	0.8	72	2	Q64P11	Q64P11 bacteroides	1224	6	0.8	83	2	Q90VF3	Q90VF3 human immu
1152	6	0.8	72	2	Q8K7S9	Q8K7S9 streptococc	1225	6	0.8	84	2	Q8R7W3	Q8R7W3 thermoanaer
1153	6	0.8	72	2	Q7N1J8	Q7N1J8 gloeobacter	1226	6	0.8	85	1	RS17 MYCGE	
1154	6	0.8	72	2	Q83214	Q83214 enterococcu	1227	6	0.8	85	2	Q9G1P8	Q9G1P8 mesenteric
1155	6	0.8	72	2	Q87X19	Q87X19 pseudomonas	1228	6	0.8	85	2	Q65168	Q65168 mesenteric
1156	6	0.8	72	2	P90297	P90297 human immu	1229	6	0.8	85	2	Q8RUB9	Q8RUB9 chlamydia p
1157	6	0.8	72	2	Q78261	Q78261 human immu	1230	6	0.8	85	2	Q6SK56	Q6SK56 arthrobacte
1158	6	0.8	72	2	Q79534	Q79534 human immu	1231	6	0.8	85	2	Q8E9J9	Q8E9J9 shewanella
1159	6	0.8	72	2	Q79551	Q79551 human immu	1232	6	0.8	86	1	D1N1 ECOLI	Q47150 escherichia
1160	6	0.8	72	2	Q79561	Q79561 human immu	1233	6	0.8	86	2	Q8T30	Q8T30 methanosarc
1161	6	0.8	73	2	Q8RXW8	Q8RXW8 arabidopsis	1234	6	0.8	86	2	Q89530	Q89530 bradyrhizob
1162	6	0.8	73	2	Q69U82	Q69U82 oryza sativ	1235	6	0.8	86	2	Q8X7Q6	Q8X7Q6 escherichia
1163	6	0.8	73	2	Q97HT9	Q97HT9 clostridium	1236	6	0.8	86	2	Q9W166	Q9W166 hepatitis c
1164	6	0.8	73	2	Q8F557	Q8F557 leptospira	1237	6	0.8	87	2	Q8W1B7	Q8W1B7 oryza sativ
1165	6	0.8	73	2	Q9HY60	Q9HY60 pseudomonas	1238	6	0.8	87	2	Q9LX24	Q9LX24 arabidopsis
1166	6	0.8	74	2	Q8TKU9	Q8TKU9 methanosarc	1239	6	0.8	87	2	Q69M08	Q69M08 oryza sativ
1167	6	0.8	74	2	Q8FMB5	Q8FMB5 brucella su	1240	6	0.8	87	2	Q05325	Q05325 pseudomonas
1168	6	0.8	74	2	P88432	P88432 human immu	1241	6	0.8	87	2	Q63325	Q63325 brucellideteri
1169	6	0.8	75	1	YOR4 SMYEA	YOR4 SMYEA	1242	6	0.8	88	2	Q9H316	Q9H316 homo sapien
1170	6	0.8	75	2	Q8PYR9	Q8PYR9 methanosarc	1243	6	0.8	88	2	Q49249	Q49249 alstroemeria
1171	6	0.8	75	2	Q9P1C9	Q9P1C9 homo sapien	1244	6	0.8	88	2	Q93444	Q93444 chlamydia p
1172	6	0.8	75	2	Q7PGQ2	Q7PGQ2 anopheles g	1245	6	0.8	88	2	Q8Y1U0	Q8Y1U0 anabacna sp
1173	6	0.8	75	2	Q691W9	Q691W9 oryza sativ	1246	6	0.8	88	2	Q97F86	Q97F86 clostridium
1174	6	0.8	75	2	Q8U5R3	Q8U5R3 agrobacteri	1247	6	0.8	88	2	Q7TU28	Q7TU28 prochloroco
1175	6	0.8	75	2	Q835D8	Q835D8 enterococcu	1248	6	0.8	88	2	Q9PHB0	Q9PHB0 xylella fas
1176	6	0.8	75	2	Q87C72	Q87C72 xylella fas	1249	6	0.8	88	2	Q70007	Q70007 human immu
1177	6	0.8	75	2	Q9PB10	Q9PB10 xylella fas	1250	6	0.8	88	2	Q8PW30	Q8PW30 methanosarc
1178	6	0.8	75	2	Q41279	Q41279 strawberry	1251	6	0.8	89	2	Q9UEB8	Q9UEB8 homo sapien
1179	6	0.8	76	2	Q84XF0	Q84XF0 oryza sativ	1252	6	0.8	89	2	Q9ZAF0	Q9ZAF0 thermus the
1180	6	0.8	76	2	Q09529	Q09529 human immu	1253	6	0.8	89	2	Q73824	Q73824 mycobacteri
1181	6	0.8	77	1	YCXB CYAPA	YCXB CYAPA	1254	6	0.8	89	2	Q41547	Q41547 human immu
1182	6	0.8	77	2	Q6ZD12	Q6ZD12 cyanophora	1255	6	0.8	89	2	Q90VH2	Q90VH2 human immu
1183	6	0.8	77	2	Q9LDK3	Q9LDK3 oryza sativ	1256	6	0.8	90	2	Q8WY10	Q8WY10 pelliculum nu
1184	6	0.8	77	2	Q8YU14	Q8YU14 anabacna sp	1257	6	0.8	90	2	Q42020	Q42020 arabidopsis
1185	6	0.8	78	1	YVFB VACCC	YVFB VACCC	1258	6	0.8	90	2	Q6M010	Q6M010 mycoplasma
1186	6	0.8	78	2	Q96HMO	Q96HMO homo sapien	1259	6	0.8	90	2	Q89ZD8	Q89ZD8 bacteroides
1187	6	0.8	78	2	Q6YL42	Q6YL42 homo sapien	1260	6	0.8	90	2	Q8V200	Q8V200 millantia h
1188	6	0.8	78	2	Q7THW1	Q7THW1 comox viru	1261	6	0.8	90	2	Q41533	Q41533 human immu
1189	6	0.8	79	1	Y476 ARCTU	Y476 ARCTU	1262	6	0.8	90	2	Q41538	Q41538 human immu
1190	6	0.8	79	2	Q8C3F5	Q8C3F5 mus musculu	1263	6	0.8	90	2	Q41557	Q41557 human immu
1191	6	0.8	80	1	NUSM CERCA	NUSM CERCA	1264	6	0.8	90	2	Q41561	Q41561 human immu
1192	6	0.8	80	2	Q8U4J1	Q8U4J1 pyrococcus	1265	6	0.8	90	2	Q41594	Q41594 human immu
1193	6	0.8	80	2	Q8K1W5	Q8K1W5 proteus vul	1266	6	0.8	90	2	Q41645	Q41645 human immu
1194	6	0.8	80	2	Q7U3T4	Q7U3T4 synecococc	1267	6	0.8	90	2	P88528	P88528 human immu
1195	6	0.8	80	2	Q7UVG1	Q7UVG1 rhodopirell	1268	6	0.8	90	2	Q69993	Q69993 human immu
1196	6	0.8	80	2	Q8BDL2	Q8BDL2 streptococc	1269	6	0.8	90	2	Q74750	Q74750 human immu
1197	6	0.8	80	2	Q991V0	Q991V0 uncultured	1270	6	0.8	90	2	Q91QN4	Q91QN4 human immu
1198	6	0.8	80	2	Q7ZP14	Q7ZP14 human immu	1271	6	0.8	90	2	Q91QN6	Q91QN6 human immu
1199	6	0.8	81	2	Q7ULV1	Q7ULV1 rhodopirell	1272	6	0.8	90	2	Q91QN7	Q91QN7 human immu

1273	6	0.8	90	2	Q91Q8	Q91gn8 human immun	1346	6	0.8	102	2	Q87G3	Q87g3 vibrio para
1274	6	0.8	91	2	Q82E7	Q82e7 salmonella	1347	6	0.8	102	2	Q89E2	Q89e2 bradyrhicob
1275	6	0.8	91	2	Q82PV4	Q82pv4 salmonella	1348	6	0.8	102	2	Q9K8L0	Q9k8l0 bacillus ha
1276	6	0.8	91	2	Q9JVM4	Q9jvm4 neisseria m	1349	6	0.8	103	2	Q972J7	Q972j7 sulfolobus
1277	6	0.8	91	2	Q70004	Q70004 human immun	1350	6	0.8	103	2	Q95M89	Q95m89 equus caball
1278	6	0.8	91	2	Q70009	Q70009 human immun	1351	6	0.8	103	2	Q74G06	Q74g06 geobacter s
1279	6	0.8	91	2	Q72787	Q72787 human immun	1352	6	0.8	103	2	Q7UCU8	Q7uc8 rhodospirell
1280	6	0.8	92	1	YLPK_BACSU	P32730 bacillus su	1353	6	0.8	103	2	Q87706	Q87706 vibrio para
1281	6	0.8	92	2	Q8HQ5	Q8hq5 ornithodoro	1354	6	0.8	103	2	Q6D9M5	Q6d9m5 erwinia car
1282	6	0.8	92	2	Q93KE9	Q93ke9 chlamydia p	1355	6	0.8	103	2	Q9D5D6	Q9d5d6 mus musculu
1283	6	0.8	92	2	Q65J10	Q65j10 bacillus li	1356	6	0.8	104	2	Q8SQY2	Q8sqy2 enccephalito
1284	6	0.8	92	2	Q8V129	Q8v129 emilliania h	1357	6	0.8	104	2	Q8SX12	Q8sx12 drosophila
1285	6	0.8	93	2	Q8SF10	Q8sf10 adiantum ca	1358	6	0.8	104	2	Q6IK98	Q6ik98 drosophila
1286	6	0.8	93	2	Q8LML6	Q8lml6 oryza sativ	1359	6	0.8	104	2	Q7R8C5	Q7r8c5 plasmodium
1287	6	0.8	93	2	Q42278	Q42278 arabidopsis	1360	6	0.8	104	2	Q38556	Q38556 bacteriopho
1288	6	0.8	93	2	Q629K2	Q629k2 haemophilus	1361	6	0.8	104	2	Q6V8N3	Q6v8n3 malus domes
1289	6	0.8	93	2	Q41565	Q41565 human immun	1362	6	0.8	104	2	Q45117	Q45117 bacteroides
1290	6	0.8	94	2	Q61L90	Q61l90 drosophila	1363	6	0.8	104	2	Q73139	Q73139 wolbachia p
1291	6	0.8	94	2	Q7QWNI	Q7qwn1 giardia lam	1364	6	0.8	104	2	Q7P0H7	Q7p0h7 chromobacte
1292	6	0.8	94	2	Q9BDR2	Q9bdr2 bos taurus	1365	6	0.8	104	2	Q88594	Q88594 mus musculu
1293	6	0.8	94	2	Q94MT3	Q94mt3 bacteriopho	1366	6	0.8	105	2	Q27553	Q27553 methanobact
1294	6	0.8	94	2	Q49475	Q49475 mycoplasma	1367	6	0.8	105	2	Q97C63	Q97c63 thermoplasm
1295	6	0.8	94	2	Q9ZBM8	Q9zbm8 mycobacteri	1368	6	0.8	105	2	Q23899	Q23899 dictyostel
1296	6	0.8	94	2	Q8V126	Q8v126 emilliania h	1369	6	0.8	105	2	Q8S005	Q8s005 oryza sativ
1297	6	0.8	94	2	Q8V128	Q8v128 emilliania h	1370	6	0.8	105	2	Q6ZLD9	Q6zld9 oryza sativ
1298	6	0.8	94	2	Q8V202	Q8v202 emilliania h	1371	6	0.8	105	2	Q91HNI	Q91hni arabidopsis
1299	6	0.8	94	2	Q8V203	Q8v203 emilliania h	1372	6	0.8	105	2	Q7N4V8	Q7n4v8 photorhabdu
1300	6	0.8	94	2	Q8V204	Q8v204 emilliania h	1373	6	0.8	105	2	Q7NT32	Q7nt32 chromobacte
1301	6	0.8	94	2	Q41599	Q41599 human immun	1374	6	0.8	105	2	Q8BP51	Q8bp51 mus musculu
1302	6	0.8	94	2	Q70001	Q70001 human immun	1375	6	0.8	106	1	RMP4_SUSO	RMP4j1 sulfolobus
1303	6	0.8	95	2	Q914U5	Q914u5 pseudomonas	1376	6	0.8	106	1	Q74K55	Q74k55 lactobacill
1304	6	0.8	95	2	Q80XZ8	Q80xz8 mus musculu	1377	6	0.8	107	1	RL21_CHLTR	RL21 chlamydia t
1305	6	0.8	95	2	Q61EC0	Q61ec0 ictalurus p	1378	6	0.8	107	2	Q61GL6	Q61gl6 drosophila
1306	6	0.8	96	2	Q7PEK0	Q7pek0 anopheles g	1379	6	0.8	107	2	Q8E7H9	Q8e7h9 streptococ
1307	6	0.8	96	2	Q7QSG2	Q7qsg2 giardia lam	1380	6	0.8	107	2	Q9C8P1	Q9c8p1 mycobacteri
1308	6	0.8	96	2	Q9MPY9	Q9mpy9 anopheles c	1381	6	0.8	107	2	Q6AKO7	Q6akg7 desulfotale
1309	6	0.8	96	2	Q9C7L8	Q9c7l8 arabidopsis	1382	6	0.8	107	2	Q8BM14	Q8bm14 mus musculu
1310	6	0.8	96	2	Q7NWI1	Q7wnj1 chromobacte	1383	6	0.8	108	1	PT05_STYPL	PT05 styela plic
1311	6	0.8	96	2	Q7UGN6	Q7ugn6 rhodospirell	1384	6	0.8	108	2	Q8K3Z8	Q8k3z8 arabidopsis
1312	6	0.8	97	2	Q7R1M5	Q7r1m5 giardia lam	1385	6	0.8	108	2	Q6K4F7	Q6k4f7 oryza sativ
1313	6	0.8	97	2	Q7YVG4	Q7yvg4 trypanosoma	1386	6	0.8	108	2	Q7NMK6	Q7nmk6 gloeobacter
1314	6	0.8	98	2	Q884H1	Q884h1 pseudomonas	1387	6	0.8	108	2	Q10826	Q10826 human immun
1315	6	0.8	98	2	Q800E3	Q80e3 methanosarc	1388	6	0.8	108	2	Q9QNF8	Q9qnf8 human immun
1316	6	0.8	98	2	Q6R2Z3	Q6r2z3 endoxyla sp	1389	6	0.8	108	2	Q9QNF8	Q9qnf8 human immun
1317	6	0.8	98	2	Q25731	Q25731 plasmodium	1390	6	0.8	108	2	TCMI_STRGA	TCMI streptomyce
1318	6	0.8	98	2	Q9NFM0	Q9nfh0 plasmodium	1391	6	0.8	109	1	Q9M272	Q9m272 arabidopsis
1319	6	0.8	98	2	Q6SE60	Q6se60 lactobacill	1392	6	0.8	109	2	Q92LFS	Q92lfs rhizobium m
1320	6	0.8	98	2	Q52096	Q52096 pseudomonas	1393	6	0.8	109	2	Q92LFS	Q92lfs rhizobium m
1321	6	0.8	98	2	Q6S509	Q6s509 mycobacteri	1394	6	0.8	110	1	M280_ARATH	M280 arabidopsis
1322	6	0.8	98	2	Q7TUT9	Q7tut9 prochloroco	1395	6	0.8	110	2	Q46207	Q46207 clostridium
1323	6	0.8	98	2	Q9KMT4	Q9kmt4 vibrio chol	1396	6	0.8	110	2	Q92SA8	Q92sa8 rhizobium m
1324	6	0.8	98	2	Q65PM7	Q65pm7 lactobacill	1397	6	0.8	110	2	Q9F5L4	Q9f5l4 bradyrhizob
1325	6	0.8	98	2	Q6DSN1	Q6dsn1 erwinia car	1398	6	0.8	110	2	Q8CDY6	Q8cdy6 mus musculu
1326	6	0.8	99	1	YQJ2_CABEU	P34625 caenorhabdi	1399	6	0.8	110	2	Q69141	Q69141 human herpe
1327	6	0.8	99	2	Q91S64	Q91s64 arabidopsis	1400	6	0.8	111	2	Q8T056	Q8t056 methanosarc
1328	6	0.8	99	2	Q82VDB	Q82vdb nitrosomona	1401	6	0.8	111	2	Q6ITH6	Q6ith6 drosophila
1329	6	0.8	99	2	Q89H95	Q89h95 bradyrhizob	1402	6	0.8	111	2	Q6DN49	Q6dn49 streptomyce
1330	6	0.8	99	2	Q924W3	Q924w3 ractus norv	1403	6	0.8	111	2	Q725M5	Q725m5 deulfovibr
1331	6	0.8	99	2	P88433	P88433 human immun	1404	6	0.8	111	2	Q8FLI7	Q8fli7 corynebacte
1332	6	0.8	99	2	P88433	P88433 human immun	1405	6	0.8	111	2	Q9JHB8	Q9jhb8 spodoptera
1333	6	0.8	100	2	Q50101	Q50101 pyrococcus	1406	6	0.8	112	1	PT17_STYPL	PT17 styela plic
1334	6	0.8	100	2	Q6VYV4	Q6vyv4 oryza sativ	1407	6	0.8	112	2	Q9GLK5	Q9glk5 felis silve
1335	6	0.8	100	2	Q7MS23	Q7me23 wolfinella s	1408	6	0.8	112	2	PT2474	PT2474 streptococ
1336	6	0.8	101	2	Q979B6	Q979b6 thermoplasm	1409	6	0.8	112	2	Q62J69	Q62j69 burkholderi
1337	6	0.8	101	2	Q94JPF2	Q94jpf2 neisseria m	1410	6	0.8	112	2	Q63SW1	Q63sw1 burkholderi
1338	6	0.8	101	2	Q91Z64	Q91z64 sigmodon hi	1411	6	0.8	112	2	Q684B5	Q684b5 sulfolobus
1339	6	0.8	101	2	Q88TY4	Q88ty4 mus musculu	1412	6	0.8	112	2	Q9PSU2	Q9psu2 xenopus lae
1340	6	0.8	101	2	Q8K3D7	Q8k3d7 mus musculu	1413	6	0.8	113	2	Q8LSR1	Q8lsr1 pecunia hyb
1341	6	0.8	102	2	Q14278	Q14278 homo sapien	1414	6	0.8	113	2	Q84V28	Q84v28 crypthecodi
1342	6	0.8	102	2	Q7R3J1	Q7r3j1 giardia lam	1415	6	0.8	113	2	Q49970	Q49970 mycobacteri
1343	6	0.8	102	2	Q67N07	Q67n07 oryza sativ	1416	6	0.8	113	2	Q925X2	Q925x2 frankia sp.
1344	6	0.8	102	2	Q925K2	Q925k2 mycobacteri	1417	6	0.8	113	2	Q64GA6	Q64ga6 cylindrope
1345	6	0.8	102	2	Q65RK9	Q65r9 mannheimia	1418	6	0.8	113	2	Q87DR0	Q87d0 xyella fas



1419	6	0.8	113	2	Q6FJZ5	Q6FJZ5 escherichia
1420	6	0.8	114	2	Q6GUR2	Q6GUR2 axonopus co
1421	6	0.8	114	2	Q6MNV6	Q6MNV6 bdellovibrio
1422	6	0.8	114	2	Q6ND11	Q6ND11 bradyrhizob
1423	6	0.8	114	2	Q6QKX9	Q6QKX9 human immun
1424	6	0.8	115	1	Q6E9K9	Q6E9K9 mus musculu
1425	6	0.8	115	2	Q6YD49	Q6YD49 aeropyrum p
1426	6	0.8	115	2	Q6BTD1	Q6BTD1 homo sapien
1427	6	0.8	115	2	Q6LTV8	Q6LTV8 lactococcus
1428	6	0.8	115	2	Q6B132	Q6B132 bacteriopho
1429	6	0.8	115	2	Q6D410	Q6D410 vibrio vuln
1430	6	0.8	115	2	Q6PB12	Q6PB12 brachydario
1431	6	0.8	115	2	Q6T2S7	Q6T2S7 human immun
1432	6	0.8	116	1	RL22_GLOV1	RL22_GLOV1
1433	6	0.8	116	2	Q6HLU4	Q6HLU4 thermoplas
1434	6	0.8	116	2	Q6B8B3	Q6B8B3 ixodes paci
1435	6	0.8	116	2	Q6B8C4	Q6B8C4 ixodes paci
1436	6	0.8	116	2	Q6B8E6	Q6B8E6 ixodes paci
1437	6	0.8	116	2	Q6HA82	Q6HA82 salmone
1438	6	0.8	116	2	Q6XIA6	Q6XIA6 arabidopsis
1439	6	0.8	116	2	Q67R66	Q67R66 symbiobacte
1440	6	0.8	116	2	Q67M11	Q67M11 vibrio vuln
1441	6	0.8	116	2	Q67922	Q67922 human immun
1442	6	0.8	116	2	Q60Z68	Q60Z68 human immun
1443	6	0.8	116	2	Q6Q453	Q6Q453 human immun
1444	6	0.8	117	1	RL22_STAM	RL22_STAM
1445	6	0.8	117	1	RL22_STAM	RL22_STAM
1446	6	0.8	117	1	RL22_STAM	RL22_STAM
1447	6	0.8	117	1	RL22_STAM	RL22_STAM
1448	6	0.8	117	1	Q6YAT7	Q6YAT7 aeropyrum p
1449	6	0.8	117	2	Q6S013	Q6S013 neoplasma
1450	6	0.8	117	2	Q6QON3	Q6QON3 anopheles g
1451	6	0.8	117	2	Q6QK15	Q6QK15 anopheles g
1452	6	0.8	117	2	Q6RPA0	Q6RPA0 plasmodium
1453	6	0.8	117	2	Q6G776	Q6G776 staphylococ
1454	6	0.8	117	2	Q6GE18	Q6GE18 staphylococ
1455	6	0.8	118	2	Q64226	Q64226 drosophila
1456	6	0.8	118	2	Q61G72	Q61G72 drosophila
1457	6	0.8	118	2	Q61G72	Q61G72 anopheles g
1458	6	0.8	118	2	Q65UD4	Q65UD4 oryza sativ
1459	6	0.8	118	2	Q6ZAR7	Q6ZAR7 oryza sativ
1460	6	0.8	118	2	Q6BTW1	Q6BTW1 yerania pe
1461	6	0.8	118	2	Q64040	Q64040 chlamydia t
1462	6	0.8	118	2	Q6ZMY2	Q6ZMY2 leptospira
1463	6	0.8	118	2	Q6F809	Q6F809 leptospira
1464	6	0.8	119	2	Q6MG24	Q6MG24 calithrix
1465	6	0.8	119	2	Q6WG25	Q6WG25 calithrix
1466	6	0.8	119	2	Q64577	Q64577 chlamydia t
1467	6	0.8	119	2	Q63469	Q63469 mycobacteri
1468	6	0.8	119	2	Q67Z50	Q67Z50 mycobacteri
1469	6	0.8	119	2	Q63755	Q63755 rattus norv
1470	6	0.8	120	2	Q65715	Q65715 saccharomyc
1471	6	0.8	120	2	Q64LT1	Q64LT1 lactobacill
1472	6	0.8	120	2	Q6C3D7	Q6C3D7 mus musculu
1473	6	0.8	120	2	Q6BDJ8	Q6BDJ8 xenopus tro
1474	6	0.8	121	2	Q6BNA7	Q6BNA7 debaryomyc
1475	6	0.8	121	2	Q67XCS	Q67XCS caenorhabdi
1476	6	0.8	121	2	Q667A3	Q667A3 trypanosoma
1477	6	0.8	121	2	Q6V633	Q6V633 prochloroco
1478	6	0.8	121	2	Q61450	Q61450 saalveinlus
1479	6	0.8	121	2	Q67978	Q67978 human immun
1480	6	0.8	122	1	RL14_MYCGE	RL14_MYCGE
1481	6	0.8	122	1	RL14_MYCN	RL14_MYCN
1482	6	0.8	122	1	Q6MP21	Q6MP21 mycoplasma
1483	6	0.8	122	2	Q6PTG5	Q6PTG5 anopheles f
1484	6	0.8	122	2	Q66093	Q66093 taenia hyda
1485	6	0.8	123	1	NEF_HV1B1	NEF_HV1B1
1486	6	0.8	123	1	NEF_HV1H2	NEF_HV1H2
1487	6	0.8	123	2	Q6S824	Q6S824 pyrococcus
1488	6	0.8	123	2	Q6S954	Q6S954 bullifolobus
1489	6	0.8	123	2	Q6TGT1	Q6TGT1 taenia soli
1490	6	0.8	123	2	Q67794	Q67794 enterococcu
1491	6	0.8	123	2	Q63DY7	Q63DY7 bacillus ce

1492	5	0.8	123	2	Q7VWU2	Q7VWU2 bordetella
1493	6	0.8	123	2	Q7W3Z5	Q7W3Z5 bordetella
1494	6	0.8	123	2	Q7WFC7	Q7WFC7 bordetella
1495	6	0.8	123	2	Q81T77	Q81T77 bacillus an
1496	6	0.8	123	2	Q8B103	Q8B103 bradyrhizob
1497	6	0.8	123	2	Q6D7P8	Q6D7P8 erwinia car
1498	6	0.8	123	2	Q6HUG2	Q6HUG2 bacillus th
1499	6	0.8	124	1	VNS1_IATKR	P08276 influenza a
1500	6	0.8	124	2	Q8ZY11	Q8ZY11 pyrobaculum
ALIGNMENTS						
RESULT 1						
Q6UXH9	PRELIMINARY;	PRT;	720 AA.			
ID Q6UXH9						
AC Q6UXH9;						
DT 05-JUL-2004 (TREMBlrel. 27, Created)						
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)						
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)						
DE EIGC699.						
CN ORNames=UNQ699;						
OS Homo sapiens (Human).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
OX NCBI_TaxId=9606;						
RN [1]						
RP SEQUENCE FROM N.A.						
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;						
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,						
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,						
RA Batson D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,						
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,						
RA Lewis L., Lao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,						
RA Seshagiri S., Simmons L., Singh V., Smith V., Stinson J., Vagts A.,						
RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,						
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,						
RA Godowski P.;						
RT "The secreted protein discovery initiative (SPDI), a large-scale						
RT effort to identify novel human secreted and transmembrane proteins: a						
RT bioinformatics assessment."						
RL Genome Res. 13:2265-2270(2003).						
CC -1- SIMILARITY: Belongs to peptidase family S1.						
CC -1- SIMILARITY: Contains 1 EGF-like domain.						
DR EMBL; AY358346; AAQ8712.1; -.						
DR HSSP; P00734; IBB0.						
DR GO; GO:0005509; F:calcium ion binding; IEA.						
DR GO; GO:0004263; F:chymotrypsin activity; IEA.						
DR GO; GO:0008233; F:peptidase activity; IEA.						
DR GO; GO:0004295; F:trypsin activity; IEA.						
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.						
DR InterPro; IPR000859; CUB.						
DR InterPro; IPR000742; EGF_2.						
DR InterPro; IPR001881; EGF_Ca.						
DR InterPro; IPR006209; EGF_1like.						
DR InterPro; IPR006210; IEGF.						
DR InterPro; IPR001254; peptidase_S1.						
DR InterPro; IPR001314; peptidase_S1A.						
DR InterPro; IPR009003; Pept_Ser_Cys.						
DR InterPro; IPR000436; Sushi_SCR_CCP.						
DR Pfam; PF00431; CUB; 1.						
DR Pfam; PF00008; EGF; 1.						
DR Pfam; PF00084; Sushi; 1.						
DR PRINTS; PR00722; CHYMOTRYPSIN.						
DR SMART; SM00032; CCP; 2.						
DR SMART; SM00042; CUB; 1.						
DR SMART; SM00181; EGF; 2.						
DR SMART; SM00179; EGF_CA; 1.						
DR SMART; SM00020; TRYD_SPC; 1.						
DR PROSITE; PS01180; CUB; 1.						
DR PROSITE; PS00022; EGF_1; 1.						
DR PROSITE; PS01166; EGF_2; 1.						

DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSH1; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW EGF-like domain; Hydroxylase; Protease; Serine protease.  
 SQ SEQUENCE 720 AA; 80198 MW; DC9898C7241289D3 CRC64;

Query Match 100.0%; Score 720; DB 2; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGCMTQGLTFLDILLISLPREYTYINACPGAENIMCRCECEYDOIECVCPGRRE 60  
 DB 1 MELGCMTQGLTFLDILLISLPREYTYINACPGAENIMCRCECEYDOIECVCPGRRE 60  
 QY 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGGLTDFYVKGFYCAECRAGW 120  
 DB 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGGLTDFYVKGFYCAECRAGW 120  
 QY 121 YGDCMRCGOVLRAPKQGLLESYPLNAHCWTTHAKGPFYQLRFVWLSLEFDYMCQYD 180  
 DB 121 YGDCMRCGOVLRAPKQGLLESYPLNAHCWTTHAKGPFYQLRFVWLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSISSSLHVLPHSDGSKNPFDFHAIYEETACS 240  
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSISSSLHVLPHSDGSKNPFDFHAIYEETACS 240  
 QY 241 SSPCFHDTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGPGPVNGYKITGPGGLI 300  
 DB 241 SSPCFHDTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGPGPVNGYKITGPGGLI 300  
 QY 301 NGRNAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKOPICICAKCREPKISDLVRRVYL 360  
 DB 301 NGRNAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKOPICICAKCREPKISDLVRRVYL 360  
 QY 361 PMQVSRRTPLHQLYSAFSAFKOKLSAAPTCKPALPFGDLPMGYOHLHTOLOYECSIPYR 420  
 DB 361 PMQVSRRTPLHQLYSAFSAFKOKLSAAPTCKPALPFGDLPMGYOHLHTOLOYECSIPYR 420  
 QY 421 RLGSSRRCTCLRTGKMGSRAPSCIPICGKIENITAKTQGLRMPWOAALYRRISGVHDSL 480  
 DB 421 RLGSSRRCTCLRTGKMGSRAPSCIPICGKIENITAKTQGLRMPWOAALYRRISGVHDSL 480  
 QY 481 HKGANFLVCSGALVNERTVVAACHCTYDIDGKTYMKTADLKVYLGFRRDDREKTIQS 540  
 DB 481 HKGANFLVCSGALVNERTVVAACHCTYDIDGKTYMKTADLKVYLGFRRDDREKTIQS 540  
 QY 541 LOISAIILHPNYDPIILLADIAILKLDKARISTRVOPICLAASRDLSTSPQESHITVAG 600  
 DB 541 LOISAIILHPNYDPIILLADIAILKLDKARISTRVOPICLAASRDLSTSPQESHITVAG 600  
 QY 601 WNVLDVNSPGFKNDTLRSQVSVVDSLLCEQHDHGI PVSVTDNMFCAWEPAPSADI 660  
 DB 601 WNVLDVNSPGFKNDTLRSQVSVVDSLLCEQHDHGI PVSVTDNMFCAWEPAPSADI 660  
 QY 661 CTAETGCGIAAVSPFGASPEPRMHLMLGLVNSYDXTCSHRLESTATKYLPEFQMIERNMK 720  
 DB 661 CTAETGCGIAAVSPFGASPEPRMHLMLGLVNSYDXTCSHRLESTATKYLPEFQMIERNMK 720

RESULT 2  
 Q6N062 PRELIMINARY; PRT; 720 AA.

AC Q6N062; 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Hypothetical protein DKFZp686N24154;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NC NCB1\_Taxid=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Colon endothel;  
 RG The German cDNA Consortium;  
 RA Kocher K., Beyer A., Mewes H.W., Weil B., Amid C., Oeanger A.,  
 RA Fobo G., Han M., Mleemann S.,  
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 DR EMBL; BX640676; CAE45808.1; -.  
 DR HSBP; P00734; IBB0.  
 DR GO; GO:0005509; F:calcium ion binding; IEA.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteinolysis and peptidolysis; IEA.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sush1\_SCF\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sush1; 1.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00179; EGF\_CA; 1.  
 DR SMART; SM00020; TRYD\_SPC; 1.  
 DR PROSITE; PS01180; CUB; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50923; SUSH1; 2.  
 DR PROSITE; PS50923; SUSH1; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
 KW EGF-like domain; Hydroxylase; Hypothetical protein; Protease;  
 KW Serine protease.  
 SQ SEQUENCE 720 AA; 80196 MW; E98A9F948EE777D CRC64;

Query Match 78.2%; Score 563; DB 2; Length 720;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELGCMTQGLTFLDILLISLPREYTYINACPGAENIMCRCECEYDOIECVCPGRRE 60  
 DB 1 MELGCMTQGLTFLDILLISLPREYTYINACPGAENIMCRCECEYDOIECVCPGRRE 60  
 QY 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGGLTDFYVKGFYCAECRAGW 120  
 DB 61 VVGYYTIPCCRNENECDSCLIHPGCTIFENCKSCRNCSWGGLTDFYVKGFYCAECRAGW 120  
 QY 121 YGDCMRCGOVLRAPKQGLLESYPLNAHCWTTHAKGPFYQLRFVWLSLEFDYMCQYD 180  
 DB 121 YGDCMRCGOVLRAPKQGLLESYPLNAHCWTTHAKGPFYQLRFVWLSLEFDYMCQYD 180  
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSISSSLHVLPHSDGSKNPFDFHAIYEETACS 240  
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSISSSLHVLPHSDGSKNPFDFHAIYEETACS 240  
 QY 241 SSPCFHDTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGPGPVNGYKITGPGGLI 300  
 DB 241 SSPCFHDTCVLDKAGSYKACLAGYTGRCENLLEBRNCSDPGPGPVNGYKITGPGGLI 300  
 QY 301 NGRNAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKOPICICAKCREPKISDLVRRVYL 360  
 DB 301 NGRNAKIGTVVSFFCNSYVLSGNEKRTCOQNGESGKOPICICAKCREPKISDLVRRVYL 360  
 QY 361 PMQVSRRTPLHQLYSAFSAFKOKLSAAPTCKPALPFGDLPMGYOHLHTOLOYECSIPYR 420  
 DB 361 PMQVSRRTPLHQLYSAFSAFKOKLSAAPTCKPALPFGDLPMGYOHLHTOLOYECSIPYR 420

Db 361 PMOVQSETEPLHOLYSAAFSKOKQASAPTKKRALPFQGLDPMGVGHULTOLOECISPFYR 420  
Qy 421 RLGSRRRTCLRTGMSGRAPSCIPICGKIENITAPKTQGLRMPQOAIYRRTSGVHDSGL 480  
Db 421 RLGSRRRTCLRTGMSGRAPSCIPICGKIENITAPKTQGLRMPQOAIYRRTSGVHDSGL 480  
Qy 481 HKGAMFLVCGSALNERTVVAACVTDLGKVTMIKTADLKVYLGGKYRDDDRDEKTIQS 540  
Db 481 HKGAMFLVCGSALNERTVVAACVTDLGKVTMIKTADLKVYLGGKYRDDDRDEKTIQS 540  
Qy 541 LQTSAILLHPYVDIILLDADIAIKLIDKARISTRVOPICLAASRDSTSPQESHITVAG 600  
Db 541 LRSAILLHPYVDIILLDADIAIKLIDKARISTRVOPICLAASRDSTSPQESHITVAG 600  
Qy 601 MNVLADVRSRPGKNDTLRSQVSVVDSLLCEQHEHGGIPVSVTDNMFCAWEPAPSDI 660  
Db 601 MNVLADVRSRPGKNDTLRSQVSVVDSLLCEQHEHGGIPVSVTDNMFCAWEPAPSDI 660  
Qy 661 CTAE 664  
Db 661 CTAE 664  
RESULT 3  
ID 096JW2 PRELIMINARY; PRT; 737 AA.  
AC 096JW2;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Hypothetical protein FLJ14935.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX PubMed=14702039; DOI=10.1038/ng1285;  
RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
RA Sekine M., Odayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,  
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,  
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Kanda K., Yokoi T., Puruya T., Kikkawa E., Omura Y.,  
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
RA Nishimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,  
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Houchi T., Kusano J.,  
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,  
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
RA Mueselino K., Yuki H., Oshima A., Sasaki N., Aocetuka S.,  
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,  
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
RA Yamagaki M., Watanabe K., Taniguchi A., Itakura S., Fukuyama T.,  
RA Fujimori Y., Komiyama M., Taehiro H., Tanigami A., Fujizawa T.,  
RA Oho T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,  
RA Kawabata A., Hikiji T., Kobatake K., Inagaki H., Ikema Y., Okamoto S.,  
RA Ohtsuri R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
RA Togeishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maehuo Y., Yamashita R.,  
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;  
RT "Complete sequencing and characterization of 21,243 full-length human  
RT cDNAs";  
RL Nat. Genet. 36:40-45(2004).  
CC -1- SIMILARITY: Belongs to peptidase family S1.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
DR EMBL; AK027841; BAB55404.1; -.

DR HSP, P00736, 1GPZ.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR006209; EGF\_1like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR009003; Pept. Ser. Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR SMART; SM00032; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00020; Tryp. SPC; 1.  
DR PROSITE; PS00180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS50923; SUSI; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 61.9%; Score 446; DB 2; Length 737;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 LEBRNCSDPGPVPNGYKITYGREGLINGRHAKIGTVSPFCNNSTYVSGNEKRTCOONGE 334  
Db 292 LEBRNCSDPGPVPNGYKITYGREGLINGRHAKIGTVSPFCNNSTYVSGNEKRTCOONGE 351  
Qy 335 WSGKOPICIRACBPKISDLVRRVLPMOVSRBTPHOLYSAAFSKOKQASAPTKKRAL 394  
Db 352 WSGKOPICIRACBPKISDLVRRVLPMOVSRBTPHOLYSAAFSKOKQASAPTKKRAL 411  
Qy 395 PFGDLPMGVGHULTOLOECISPFYRLSGSRRTCLRTGMSGRAPSCIPICGKIENITA 454  
Db 412 PFGDLPMGVGHULTOLOECISPFYRLSGSRRTCLRTGMSGRAPSCIPICGKIENITA 471  
Qy 455 PFGDLPMGVGHULTOLOECISPFYRLSGSRRTCLRTGMSGRAPSCIPICGKIENITA 514  
Db 472 PFGDLPMGVGHULTOLOECISPFYRLSGSRRTCLRTGMSGRAPSCIPICGKIENITA 531  
Qy 515 IKTADLKVYLGGKYRDDDRDEKTIQSIOISAILLHPYVDIILLDADIAIKLIDKARIST 574  
Db 532 IKTADLKVYLGGKYRDDDRDEKTIQSIOISAILLHPYVDIILLDADIAIKLIDKARIST 591  
Qy 575 RVOPICLAASRDSTSPQESHITVAGMNVADVRSRPGKNDTLRSQVSVVDSLLCEQH 634  
Db 592 RVOPICLAASRDSTSPQESHITVAGMNVADVRSRPGKNDTLRSQVSVVDSLLCEQH 651  
Qy 635 EDHGIPVSVTDNMFCAWEPAPSDICTAETGGIAAVSPGRASPERRMHLMGVMSYD 694  
Db 652 EDHGIPVSVTDNMFCAWEPAPSDICTAETGGIAAVSPGRASPERRMHLMGVMSYD 711  
Qy 695 KTCSHRLSTAFYTLVLPKDWIERNMK 720  
Db 712 KTCSHRLSTAFYTLVLPKDWIERNMK 737  
RESULT 4  
ID 071RE9 PRELIMINARY; PRT; 417 AA.  
AC 071RE9;  
DT 05-JUL-2004 (TREMblrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE FP38.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCB1\_TaxID=9606;  
 RX (1)  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,  
 RA Wan D.F., Gu J.R.;  
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 DR EMBL; AF370388; AAQ15224.1; -.  
 DR HSSP; P00734; 1BD0.  
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR01254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR PRINTS; PR00722; CHYMOTRYPSIN.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50923; SUSHI; 1.  
 DR PROSITE; PS50240; TRYP\_SIN\_DOM; 1.  
 KW Hydroxylase; Protease; Serine protease.  
 SQ SEQUENCE 417 AA; 46703 MW; 2546A52A3697C1C4 CRC64;

Query Match 53.6%; Score 386; DB 2; Length 417;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 MSGKOPITKACREPKISDVARRVLPMOVSRRETLHQLVSAFSGKQKLSAPTKKPAL 394  
 DB 32 MSGKOPITKACREPKISDVARRVLPMOVSRRETLHQLVSAFSGKQKLSAPTKKPAL 91  
 QY 395 PFGDLPWGYOHLHTOLQYECISPFYRRLGSSRRCTLRGKMSGRAPSCIPICGKIENTA 454  
 DB 92 PFGDLPWGYOHLHTOLQYECISPFYRRLGSSRRCTLRGKMSGRAPSCIPICGKIENTA 151  
 QY 455 PRTQGLRMPWQAIYRRTSGVHDSLHKGMFLVCSGALVNERIVVAACHCTDIDGKTM 514  
 DB 152 PRTQGLRMPWQAIYRRTSGVHDSLHKGMFLVCSGALVNERIVVAACHCTDIDGKTM 211  
 QY 515 IKTADLKVLGKFEYDDDDREKTIQSLQISATILHPNDPILLDADIALIKLIDKARIST 574  
 DB 212 IKTADLKVLGKFEYDDDDREKTIQSLQISATILHPNDPILLDADIALIKLIDKARIST 271  
 QY 575 RVQPICLAASRDLSFQESHITTVAGMNVLDVRSFGKNDTLRSGVSVVDSLLCEBQH 634  
 DB 272 RVQPICLAASRDLSFQESHITTVAGMNVLDVRSFGKNDTLRSGVSVVDSLLCEBQH 331  
 QY 635 EDHGIPVSVTDNMFCAWEPFAPSICIAETGCIAAVSFPGASPEPRWHLGLVSWSYD 694  
 DB 332 EDHGIPVSVTDNMFCAWEPFAPSICIAETGCIAAVSFPGASPEPRWHLGLVSWSYD 391  
 QY 695 KTCSHRLSTAFKTVLPFKDMIERNNK 720  
 DB 392 KTCSHRLSTAFKTVLPFKDMIERNNK 417

## RESULT 5

QY432 PRELIMINARY; PRT; 181 AA.  
 AC QY432;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Hypothetical protein DKFZps56H2123 (Fragment).  
 GN Name=DKFZps56H2123;  
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 RN NCB1\_TaxID=9606;  
 RX (1)  
 RP SEQUENCE FROM N.A.  
 RA Ansoerge W., Winkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AL050214; CAB43317.1; -.  
 DR PIR; T08805; T08805.  
 DR HSSP; P00736; 1MD7.  
 DR MEROPS; S01.998; -.  
 DR GO; GO:0008233; F:peptidase activity; IEA.  
 DR GO; GO:0004295; F:trypsin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR01254; Peptidase\_S1.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR SMART; SM00020; TRYP\_SPC; 1.  
 DR PROSITE; PS50240; TRYP\_SIN\_DOM; 1.  
 KW Hydroxylase; Hypothetical protein; Protease; Serine protease.  
 FT NON TER 1  
 SQ SEQUENCE 181 AA; 19962 MW; ABC793BBE682D439 CRC64;

Query Match 24.7%; Score 178; DB 2; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 2,5e-181;  
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 543 ISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITTVAGM 602  
 DB 4 ISATILHPNDPILLDADIALIKLIDKARISTRVQPICLAASRDLSFQESHITTVAGM 63  
 QY 603 VLADVRSPFGKNDTLRSGVSVVDSLLCEBQEDHGIPVSVTDNMFCAWEPFAPSICT 662  
 DB 64 VLADVRSPFGKNDTLRSGVSVVDSLLCEBQEDHGIPVSVTDNMFCAWEPFAPSICT 123  
 QY 663 AETGCIAAVSFPGASPEPRWHLGLVSWSYDTCSSRLSTAFKTVLPFKDMIERNNK 720  
 DB 124 AETGCIAAVSFPGASPEPRWHLGLVSWSYDTCSSRLSTAFKTVLPFKDMIERNNK 181

## RESULT 6

Q8BU25 PRELIMINARY; PRT; 720 AA.  
 AC Q8BU25;  
 DT 01-MAR-2003 (TReMBLrel. 23, Created)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:R430002G05 product:hypothetical EGF-like domain, CUB domain, Sushi domain / SCR repeat / CCP module and DE Serine proteases, trypsin family domain containing protein, full insert sequence.  
 GN Name=R430002G05R1k;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCB1\_TaxID=10090;  
 RX (1)  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN=NOD; TISSUE=Thymus;  
 RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=ND; TISSUE=Thymus;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ND; TISSUE=Thymus;  
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes."  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ND; TISSUE=Thymus;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Alzawa K., Nagaoaka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitamura T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ND; TISSUE=Thymus;  
 RA Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Horii F., Imclanti K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kuribara C., Maruyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC -1- SIMILARITY: Contains 1 EGF-like domain.  
 CC EMBL; AK088017; BAC40098.1; -.  
 DR HSP; P00736; IGPZ.  
 DR MGD; MGI:2445082; E430002G05R1K.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.  
 DR InterPro; IPR006209; EGF\_1like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_S1A.  
 DR InterPro; IPR009003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
 DR Pfam; PF00431; CUB; 1.  
 DR Pfam; PF00008; EGF; 1.  
 DR Pfam; PF00084; Sushi; 1.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR PRINTS; PRO0722; CHYMOTRYPSIN.  
 DR SMART; SM00032; CCP; 2.  
 DR SMART; SM00042; CUB; 1.  
 DR SMART; SM00181; EGF; 2.  
 DR SMART; SM00020; Tryp\_Spc; 1.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 1.  
 DR PROSITE; PS50026; EGF\_3; 1.  
 DR PROSITE; PS50923; SUSHI; 2.

DR PROSITE; PS50240; TRYPsin\_DOM; 1.  
 KW EGF-like domain; Hydroxylase; Hypothetical protein; Protease;  
 KW Serine protease.  
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;  
 Query Match 8.5%; Score 61; DB 2; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-55;  
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 74 NECDSCILHPCGCTIFENCKSCRNMGCTDDFYVKGFCACBGRAGWYGGDCRCQVLR 133  
 DB 74 NECDSCILHPCGCTIFENCKSCRNMGCTDDFYVKGFCACBGRAGWYGGDCRCQVLR 133  
 QY 134 A 134  
 DB 134 A 134  
 RESULT 7  
 Q8K2B8 PRELIMINARY; PRT; 720 AA.  
 AC Q8K2B8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Regeneration associated muscle protease.  
 GN Name=E430002G05R1K;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,  
 RA Krzyzanski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
 RA Strauberg R.;  
 RN Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
 RA Strauberg R.;  
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to peptidase family S1.  
 CC EMBL; BC031841; AA31841.1; -.  
 DR EMBL; BC031841; AA31841.1; -.  
 DR HSP; P00736; IGPZ.  
 DR MGD; MGI:2445082; E430002G05R1K.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR000859; CUB.  
 DR InterPro; IPR000742; EGF\_2.

DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 1.  
DR Pfam; PF00089; Trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS50923; SUSHI; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 720 AA; 80377 MW; 7172B7F1E69FD0E CRC64;

Query Match 5.7%; Score 41; DB 2; Length 720;  
Best Local Similarity 100.0%; Pred. No. 4,2e-34;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 FLOLLILSLPREYVINEACGAFAMNIMCECCYDIEC 53  
Db 13 FLOLLILSLPREYVINEACGAFAMNIMCECCYDIEC 53

## RESULT 8

O6DIV5 PRELIMINARY; PRT; 722 AA.

ID O6DIV5;  
AC O6DIV5;  
DT 25-OCT-2004 (TREMBLrel. 28, Created)  
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
DE MG89196 protein.  
GN Name=MG89196;  
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8364;

RN (1)  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefel C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carinci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.V., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Rialesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN SEQUENCE FROM N.A.  
RP TISSUE=whole body;  
RC Klein S., Gerhard D.S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Contains 1 EGF-like domain.  
EMBL; BC075430; AAH75430.1; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000859; CUB.  
DR InterPro; IPR000742; EGF\_2.  
DR InterPro; IPR001881; EGF\_Ca.  
DR InterPro; IPR006209; EGF\_like.  
DR InterPro; IPR006210; IEGF.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR009003; Pept\_Ser\_Cys.  
DR InterPro; IPR000436; Sushi\_SCR\_CCP.  
DR Pfam; PF00431; CUB; 1.  
DR Pfam; PF00008; EGF; 1.  
DR Pfam; PF00084; Sushi; 2.  
DR Pfam; PF00089; Trypsin; 1.  
DR SMART; SM00042; CCP; 2.  
DR SMART; SM00042; CUB; 1.  
DR SMART; SM00181; EGF; 2.  
DR SMART; SM00179; EGF\_Ca; 1.  
DR SMART; SM00020; TRYP\_SPC; 1.  
DR PROSITE; PS01180; CUB; 1.  
DR PROSITE; PS00022; EGF\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50026; EGF\_3; 1.  
DR PROSITE; PS50923; SUSHI; 2.  
DR PROSITE; PS50240; TRYPSIN\_DOM; 1.  
KW EGF-like domain; Hydrolase; Protease; Serine protease.  
SQ SEQUENCE 722 AA; 80366 MW; F173563206D1AE82 CRC64;

Query Match 3.3%; Score 24; DB 2; Length 722;  
Best Local Similarity 100.0%; Pred. No. 6.7e-16;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 62 VGTYTPCCRNENECDSCLIHFGC 85  
Db 64 VGTYTPCCRNENECDSCLIHFGC 87

## RESULT 9

O91WZ0 PRELIMINARY; PRT; 222 AA.

ID O91WZ0  
AC O91WZ0;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Bone morphogenetic protein 1 (Fragment).  
GN Name=Bmp-1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;

RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Mistar; TISSUE=E18 whole embryo;  
RA Kataoka H., Enomoto K.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB073100; BAB69961.1; -.  
DR HSSP; Q9UCV4; INZI.  
DR GO; GO:0008533; F:actinin activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR Pfam; PF01400; Actactin; 1.  
DR Pfam; PF00431; CUB; 2.  
DR PROSITE; PS01180; CUB; 2.  
FT NON\_TER 1  
FT NON\_TER 222  
SQ SEQUENCE 222 AA; 25426 MW; F6A9052DA98B57A CRC64;

Query Match 1.2%; Score 9; DB 2; Length 222;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 179 YDYVEVRDG 187  
|||||

Db 80 YDYEVRDGS 88

RESULT 10

Y836\_AQUAE STANDARD; PRT; 232 AA.

ID 067008;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Hypothetical protein AQ\_836.

GN OrderedLocustNames=AQ\_836;

OS Aquifex aeolicus.

OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.

OX NCBI\_TaxID=63363;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RX Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., Ausley M., Huber R., Feldman R.A., Short J.M., Olsen G.J., Swanson M.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";

RL Nature 352:353-358(1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC -----

DR EMBL; AE000709; AAC06970.1; -

DR PIR; E70372; E70372.

KW Complete proteome; Hypothetical protein; Transmembrane.

FT TRANSMEM 4 24 Potential.

FT TRANSMEM 42 62 Potential.

FT TRANSMEM 100 120 Potential.

FT TRANSMEM 145 165 Potential.

FT TRANSMEM 171 191 Potential.

FT TRANSMEM 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

SQ SEQUENCE

Query Match 1.2%; Score 9; DB 1; Length 232;

Best Local Similarity 100.0%; Pred. No. 2.7;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96

Db 23 FENCKSCRN 31

RESULT 11

086553 PRELIMINARY; PRT; 276 AA.

AC 086553;

DT 01-NOV-1998 (TEMBLrel. 08, Created)

DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)

DE Putative dehydrogenase.

GN ORFNames=SCIP2.16c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomycetes.

OX NCBI\_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RX MEDLINE=2196410; PubMed=12000953; DOI=10.1038/417141a;

RT Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleeer H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Frazer A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L.D., Oliver K., O'Neill S., Rabinowitz E., Rajendram M.A., Rutherford K.M., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J., Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

RL Nature 417:141-147(2002).

CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.

CC (SDR) family.

DR EMBL; AL939128; CA920507.1; -

DR PIR; T29125; T29125.

DR HSSP; P08074; 1CYD.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH\_short.

DR InterPro; IPR002347; Adh\_short\_C2.

DR Pfam; PF00106; adh\_short; 1.

DR PRINTS; PR00081; GDRDH.

DR PRINTS; PR00080; SDRFAMILY.

DR PROSITE; PS00061; ADH\_SHORT; 1.

KW Complete proteome; Oxidoreductase.

SQ SEQUENCE 276 AA; 29010 MW; 30F0038B70D63C7C CRC64;

QY 670 AVSFGGRAS 678

Db 225 AVSFGGRAS 233

RESULT 12

06PUN5 PRELIMINARY; PRT; 593 AA.

AC 06PUN5;

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

DE TIL2 protein (Fragment).

GN Name=TIL2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Mcwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heitlen E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

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RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013871; AAH13871.1; -.
DR HSSP; P07584; IAST.
DR GO; GO:0008533; F:actin activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_zn_BS.
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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-) (SUIMP).
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=94215496; PubMed=8162855;
RA Hwang S.P.L., Partin J.S., Lennarz W.J.;
RT "Characterization of a homolog of human bone morphogenetic protein 1
in the embryo of the sea urchin, Strongylocentrotus purpuratus.";
RL Development 120:559-568(1994).
CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
hatched blastula.
CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.
CC -1- SIMILARITY: Belongs to the peptidase M12A family.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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CC EMBL; L23838; AAA30081.1; -.
CC HSSP; P35555; IEMN.
CC MEROPS; M12.005; -.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.

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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006025; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
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RESULT 14
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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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RP SEQUENCE FROM N.A.
RX MEDLINE=20267865; PubMed=10806368; DOI=10.1016/S0378-1119(00)00114-1;
RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosier R.N.,
RT "Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
tissues.";
RL Gene 248:233-243(2000).

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## OM protein - protein search, using sw model

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(without alignments)  
1249.938 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1500 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	16	2.2	46	4 US-10-067-422-17	Sequence 17, Appl1
3	12	1.7	12	4 US-10-067-422-16	Sequence 16, Appl1
4	9	1.2	101	3 US-09-374-135-4	Sequence 4, Appl1
5	9	1.2	110	4 US-09-341-461-28	Sequence 28, Appl1
6	9	1.2	113	4 US-09-438-046-20	Sequence 20, Appl1
7	9	1.2	730	3 US-08-872-757-2	Sequence 2, Appl1
8	9	1.2	730	3 US-09-850-048A-2	Sequence 2, Appl1
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137	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl	210	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl
138	6	0.8	20	1	US-08-205-938A-13	Sequence 13, Appl	211	6	0.8	86	1	US-08-456-201-19	Sequence 19, Appl
139	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	212	6	0.8	86	2	US-08-330-161-17	Sequence 17, Appl
140	6	0.8	25	3	US-09-660-587-28	Sequence 28, Appl	213	6	0.8	86	2	US-08-456-241-19	Sequence 19, Appl
141	6	0.8	25	4	US-09-261-358A-28	Sequence 28, Appl	214	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl
142	6	0.8	25	4	US-09-201-458-20	Sequence 20, Appl	215	6	0.8	86	3	US-08-419-878B-17	Sequence 17, Appl
143	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	216	6	0.8	86	3	US-09-134-001C-3359	Sequence 3359, Ap
144	6	0.8	31	4	US-08-437-943D-14	Sequence 14, Appl	217	6	0.8	86	3	US-09-173-480-17	Sequence 17, Appl
145	6	0.8	35	2	US-08-145-708A-15	Sequence 15, Appl	218	6	0.8	86	4	US-09-252-991A-29383	Sequence 29383, A
146	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	219	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl
147	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	220	6	0.8	87	4	US-09-252-991A-28740	Sequence 28740, A
148	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	221	6	0.8	90	4	US-09-252-991A-24674	Sequence 24674, A
149	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	222	6	0.8	91	4	US-09-107-433-4244	Sequence 4244, Ap
150	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	223	6	0.8	93	4	US-09-252-991A-17535	Sequence 17535, A
151	6	0.8	37	4	US-09-252-404A-39	Sequence 39, Appl	224	6	0.8	93	4	US-09-270-767-39947	Sequence 39947, A
152	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	225	6	0.8	93	4	US-09-270-767-55164	Sequence 55164, A
153	6	0.8	37	4	US-09-821-861-16	Sequence 16, Appl	226	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl
154	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	227	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appl1
155	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	228	6	0.8	94	4	US-08-470-998-8	Sequence 8, Appl
156	6	0.8	40	4	US-08-331-454-19	Sequence 19, Appl	229	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
157	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	230	6	0.8	94	4	US-09-270-767-33056	Sequence 33056, A
158	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	231	6	0.8	94	4	US-09-270-767-35703	Sequence 35703, A
159	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	232	6	0.8	95	4	US-09-270-767-46409	Sequence 46409, A
160	6	0.8	40	4	US-09-270-767-40577	Sequence 40577, A	233	6	0.8	95	4	US-09-248-796A-25418	Sequence 25418, A
161	6	0.8	40	4	US-09-270-767-55793	Sequence 55793, A	234	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
162	6	0.8	41	4	US-08-424-550B-467	Sequence 467, App	235	6	0.8	99	4	US-09-270-767-32461	Sequence 32461, A
163	6	0.8	41	4	US-08-168-091A-41	Sequence 41, Appl	236	6	0.8	99	4	US-09-270-767-47668	Sequence 47668, A
164	6	0.8	42	1	US-09-066-330-3	Sequence 3, Appl1	237	6	0.8	100	4	US-09-270-767-50920	Sequence 50920, A
165	6	0.8	43	1	US-07-998-003A-73	Sequence 73, Appl	238	6	0.8	100	4	US-09-471-276-832	Sequence 832, App
166	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	239	6	0.8	100	4	US-09-390-134B-42	Sequence 42, Appl
167	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	240	6	0.8	101	4	US-09-270-767-58844	Sequence 58844, A
168	6	0.8	43	1	US-08-268-161A-73	Sequence 73, Appl	241	6	0.8	102	4	US-09-199-637A-271	Sequence 271, App
169	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	242	6	0.8	103	3	US-09-252-991A-32642	Sequence 32642, A
170	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appl1	243	6	0.8	103	4	US-09-543-681A-8232	Sequence 8232, Ap
171	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	244	6	0.8	103	4	US-09-621-876-4109	Sequence 4109, Ap
172	6	0.8	43	3	PCT-US93-12588-73	Sequence 73, Appl	245	6	0.8	103	4	US-09-513-999C-3560	Sequence 5560, Ap
173	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	246	6	0.8	103	4	US-09-513-999C-3560	Sequence 5560, Ap

247	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl	320	6	0.8	151	3	US-08-679-493A-74	Sequence 74, Appl
248	6	0.8	106	4	US-09-248-796A-14519	Sequence 1519, A	321	6	0.8	152	4	US-09-885-723-11	Sequence 11, Appl
249	6	0.8	107	4	US-09-732-210-230	Sequence 230, App	322	6	0.8	153	4	US-09-288-143-123	Sequence 123, App
250	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, 'Ap	323	6	0.8	153	4	US-09-252-991A-22634	Sequence 2634, A
251	6	0.8	107	4	US-09-710-279-1586	Sequence 1586, Ap	324	6	0.8	153	4	US-09-134-000C-5186	Sequence 5186, Ap
252	6	0.8	108	4	US-09-489-039A-9393	Sequence 9392, Ap	325	6	0.8	154	3	US-09-387-418A-80	Sequence 8, Appl
253	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A	326	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
254	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap	327	6	0.8	156	3	US-09-224-110-20	Sequence 20, Appl
255	6	0.8	109	4	US-09-270-767-60583	Sequence 60583, A	328	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
256	6	0.8	110	3	US-09-376-330-24	Sequence 24, Appl	329	6	0.8	156	4	US-09-988-991A-20	Sequence 20, Appl
257	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A	330	6	0.8	156	5	PCT-US95-07289-20	Sequence 20, Appl
258	6	0.8	111	4	US-09-294-298A-12	Sequence 12, Appl	331	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
259	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap	332	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appl
260	6	0.8	112	4	US-09-270-767-44754	Sequence 34754, A	333	6	0.8	157	3	US-08-981-392-68	Sequence 66, Appl
261	6	0.8	112	4	US-09-270-767-49971	Sequence 49971, A	334	6	0.8	157	4	US-09-071-035-446	Sequence 46, Appl
262	6	0.8	112	4	US-09-902-540-5940	Sequence 9940, Ap	335	6	0.8	157	4	US-09-908-322-68	Sequence 66, Appl
263	6	0.8	113	4	US-09-438-046-23	Sequence 23, Appl	336	6	0.8	159	3	US-08-796-792-2	Sequence 2, Appl
264	6	0.8	115	4	US-09-270-767-47912	Sequence 47912, A	337	6	0.8	159	4	US-09-491-795-2	Sequence 2, Appl
265	6	0.8	115	4	US-09-902-540-10750	Sequence 10750, A	338	6	0.8	162	1	US-08-266-451B-29	Sequence 29, Appl
266	6	0.8	120	4	US-09-583-110-5022	Sequence 5022, Ap	339	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
267	6	0.8	121	1	US-08-307-499-7	Sequence 7, Appl	340	6	0.8	162	4	US-09-540-236-2636	Sequence 2636, Ap
268	6	0.8	121	3	US-09-299-268-7	Sequence 63, App	341	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
269	6	0.8	121	4	US-10-101-654A-683	Sequence 683, App	342	6	0.8	167	4	US-09-270-767-41274	Sequence 41274, A
270	6	0.8	122	4	US-09-732-210-598	Sequence 598, App	343	6	0.8	167	4	US-09-270-767-56490	Sequence 56490, A
271	6	0.8	122	4	US-09-732-210-600	Sequence 600, App	344	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
272	6	0.8	122	4	US-10-101-464A-712	Sequence 712, App	345	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap
273	6	0.8	122	4	US-09-424-840B-14	Sequence 14, Appl	346	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap
274	6	0.8	122	4	US-09-107-433-3697	Sequence 3697, Ap	347	6	0.8	175	4	US-09-902-540-11425	Sequence 11425, A
275	6	0.8	123	3	US-09-124-900-10	Sequence 10, Appl	348	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A
276	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap	349	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A
277	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App	350	6	0.8	176	4	US-09-489-039A-12706	Sequence 12706, A
278	6	0.8	124	4	US-09-270-767-61747	Sequence 61747, A	351	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl
279	6	0.8	125	4	US-09-543-681A-7177	Sequence 7177, Ap	352	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl
280	6	0.8	126	4	US-09-902-540-12158	Sequence 12158, A	353	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap
281	6	0.8	127	3	US-09-134-001C-2936	Sequence 2936, Ap	354	6	0.8	177	4	US-09-650-324A-20	Sequence 20, Appl
282	6	0.8	127	3	US-09-134-001C-2937	Sequence 2937, Ap	355	6	0.8	177	4	US-09-583-110-3692	Sequence 3692, Ap
283	6	0.8	127	3	US-09-809-739-10	Sequence 10, Appl	356	6	0.8	178	4	US-09-270-767-31704	Sequence 31704, A
284	6	0.8	128	3	US-09-134-001C-2881	Sequence 2881, Ap	357	6	0.8	178	4	US-09-270-767-46921	Sequence 46921, A
285	6	0.8	128	4	US-09-134-000C-3953	Sequence 3953, Ap	358	6	0.8	179	3	US-09-612-126-11	Sequence 11, Appl
286	6	0.8	128	4	US-09-513-999C-8084	Sequence 8084, Ap	359	6	0.8	179	4	US-09-248-796A-21646	Sequence 21646, A
287	6	0.8	129	4	US-09-513-999C-5740	Sequence 5740, Ap	360	6	0.8	180	4	US-09-543-681A-7669	Sequence 7669, Ap
288	6	0.8	130	4	US-09-902-540-11601	Sequence 11601, A	361	6	0.8	180	4	US-09-270-767-37167	Sequence 37167, A
289	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A	362	6	0.8	180	4	US-09-270-767-52384	Sequence 52384, A
290	6	0.8	132	4	US-09-311-021-162	Sequence 162, App	363	6	0.8	180	4	US-09-878-281A-15	Sequence 15, Appl
291	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A	364	6	0.8	180	4	US-09-878-281A-16	Sequence 16, Appl
292	6	0.8	134	3	US-09-134-001C-3817	Sequence 3817, Ap	365	6	0.8	180	4	US-09-878-281A-18	Sequence 18, Appl
293	6	0.8	134	4	US-09-252-991A-24635	Sequence 24635, A	366	6	0.8	180	4	US-09-878-281A-20	Sequence 20, Appl
294	6	0.8	134	4	US-09-513-999C-8169	Sequence 8169, Ap	367	6	0.8	180	4	US-09-878-281A-22	Sequence 22, Appl
295	6	0.8	136	4	US-09-252-991A-24692	Sequence 24692, A	368	6	0.8	180	4	US-09-878-281A-24	Sequence 24, Appl
296	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appl	369	6	0.8	180	4	US-09-878-281A-26	Sequence 26, Appl
297	6	0.8	138	3	US-09-375-419-1	Sequence 1, Appl	370	6	0.8	180	4	US-09-878-281A-28	Sequence 28, Appl
298	6	0.8	139	3	US-08-444-818-174	Sequence 174, App	371	6	0.8	180	4	US-09-502-540-10368	Sequence 10368, A
299	6	0.8	139	4	US-09-270-767-44805	Sequence 44805, A	372	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A
300	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A	373	6	0.8	181	4	US-09-134-000C-4633	Sequence 4633, Ap
301	6	0.8	140	4	US-09-270-767-11800	Sequence 11800, A	374	6	0.8	181	4	US-09-640-211A-1033	Sequence 1033, Ap
302	6	0.8	141	3	US-08-906-769-135	Sequence 135, App	375	6	0.8	183	4	US-09-621-976-4025	Sequence 4025, Ap
303	6	0.8	141	3	US-08-906-616-135	Sequence 135, App	376	6	0.8	183	4	US-09-976-451-2	Sequence 2, Appl
304	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App	377	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appl
305	6	0.8	141	3	US-09-012-431-135	Sequence 135, App	378	6	0.8	184	3	US-08-969-317-7	Sequence 2, Appl
306	6	0.8	141	3	US-09-012-692-135	Sequence 135, App	379	6	0.8	184	4	US-09-270-767-44233	Sequence 44233, A
307	6	0.8	141	3	US-08-906-613-135	Sequence 135, App	380	6	0.8	184	4	US-09-107-433-4306	Sequence 4306, Ap
308	6	0.8	141	4	US-09-270-767-60471	Sequence 60471, A	381	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl
309	6	0.8	143	4	US-09-538-092-237	Sequence 237, App	382	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl
310	6	0.8	144	3	US-09-199-637A-17	Sequence 17, Appl	383	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl
311	6	0.8	144	3	US-09-134-001C-4218	Sequence 4218, Ap	384	6	0.8	185	3	US-09-106-582-11	Sequence 11, Appl
312	6	0.8	145	4	US-09-252-991A-21532	Sequence 21532, A	385	6	0.8	185	4	US-09-159-469-11	Sequence 11, Appl
313	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A	386	6	0.8	185	4	US-09-693-542-11	Sequence 11, Appl
314	6	0.8	146	4	US-09-270-767-39779	Sequence 39779, A	387	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appl
315	6	0.8	146	4	US-09-270-767-54966	Sequence 54966, A	388	6	0.8	187	4	US-08-635-886C-207	Sequence 207, App
316	6	0.8	146	4	US-09-248-796A-26332	Sequence 26332, A	389	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App
317	6	0.8	149	2	US-08-039-364-18	Sequence 18, Appl	390	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App
318	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl	391	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App
319	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A	392	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App

393	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	466	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
394	6	0.8	187	4	US-09-248-796A-14589	Sequence 14589, A	467	6	0.8	209	4	US-09-438-185A-949	Sequence 949, App
395	6	0.8	187	4	US-09-248-796A-16267	Sequence 16267, A	468	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
396	6	0.8	188	4	US-09-248-796A-18153	Sequence 18153, A	469	6	0.8	210	3	US-09-489-774E-33	Sequence 33, Appl
397	6	0.8	188	4	US-10-101-464A-540	Sequence 540, App	470	6	0.8	210	4	US-09-252-991A-27171	Sequence 27171, A
398	6	0.8	189	4	US-09-270-767-46721	Sequence 46721, A	471	6	0.8	211	4	US-09-252-991A-28553	Sequence 28553, A
399	6	0.8	191	2	US-08-290-665A-187	Sequence 187, App	472	6	0.8	211	4	US-09-949-016-9913	Sequence 9913, App
400	6	0.8	191	2	US-08-290-665A-189	Sequence 189, App	473	6	0.8	212	3	US-08-861-774E-22	Sequence 22, Appl
401	6	0.8	191	2	US-08-290-665A-190	Sequence 190, App	474	6	0.8	212	3	US-08-861-774E-34	Sequence 34, Appl
402	6	0.8	191	2	PCT-US95-10398-187	Sequence 187, App	475	6	0.8	212	4	US-09-538-092-500	Sequence 500, App
403	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	476	6	0.8	213	3	US-08-861-774E-60	Sequence 60, Appl
404	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	477	6	0.8	213	3	US-08-861-774E-64	Sequence 64, Appl
405	6	0.8	192	4	US-09-198-452A-276	Sequence 276, App	478	6	0.8	213	3	US-08-861-774E-72	Sequence 72, Appl
406	6	0.8	192	4	US-09-248-796A-22528	Sequence 22528, A	479	6	0.8	213	4	US-09-902-540-13705	Sequence 13705, A
407	6	0.8	192	4	US-09-438-185A-266	Sequence 266, App	480	6	0.8	214	3	US-08-861-774E-30	Sequence 30, Appl
408	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	481	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
409	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appli	482	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
410	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appli	483	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
411	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appli	484	6	0.8	214	3	US-08-861-774E-56	Sequence 56, Appl
412	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	485	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
413	6	0.8	193	4	US-08-974-690C-210	Sequence 210, App	486	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
414	6	0.8	194	3	US-09-516-914-9	Sequence 9, Appli	487	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
415	6	0.8	194	4	US-09-489-039A-8286	Sequence 8286, App	488	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appli
416	6	0.8	194	4	US-09-248-796A-16995	Sequence 16995, A	489	6	0.8	214	5	PCT-US96-09127-2	Sequence 2, Appli
417	6	0.8	196	3	US-08-981-392-35	Sequence 35, Appl	490	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
418	6	0.8	196	4	US-09-908-322-35	Sequence 35, Appl	491	6	0.8	215	2	US-08-748-725-47	Sequence 20, Appl
419	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	492	6	0.8	215	3	US-08-861-774E-40	Sequence 40, Appl
420	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	493	6	0.8	215	4	US-09-270-767-15086	Sequence 4086, A
421	6	0.8	200	4	US-09-101-272G-73	Sequence 73, Appl	494	6	0.8	216	3	US-08-861-774E-58	Sequence 58, Appl
422	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	495	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
423	6	0.8	200	4	US-09-489-039A-1526	Sequence 1526, App	496	6	0.8	218	3	US-08-861-774E-46	Sequence 46, Appl
424	6	0.8	201	3	US-08-679-493A-190	Sequence 190, App	497	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
425	6	0.8	202	4	US-09-252-991A-26505	Sequence 26505, A	498	6	0.8	218	4	US-09-134-000C-3858	Sequence 3858, App
426	6	0.8	202	4	US-09-252-991A-27017	Sequence 27017, A	499	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
427	6	0.8	203	2	US-08-284-391B-31	Sequence 31, Appl	500	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
428	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	501	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
429	6	0.8	203	4	US-09-543-681A-4329	Sequence 4329, App	502	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
430	6	0.8	203	4	US-08-394-388A-31	Sequence 31, Appl	503	6	0.8	219	4	US-09-270-767-33084	Sequence 33084, A
431	6	0.8	203	4	US-10-101-464A-537	Sequence 537, App	504	6	0.8	219	4	US-09-270-767-48301	Sequence 48301, A
432	6	0.8	203	4	US-10-101-464A-658	Sequence 658, App	505	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App
433	6	0.8	204	4	US-09-252-991A-29225	Sequence 29225, A	506	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appli
434	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, App	507	6	0.8	222	4	US-09-252-991A-24147	Sequence 24147, A
435	6	0.8	205	3	US-09-134-001C-4766	Sequence 4766, App	508	6	0.8	223	4	US-09-198-452A-683	Sequence 19065, A
436	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	509	6	0.8	224	4	US-09-198-452A-683	Sequence 683, App
437	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, App	510	6	0.8	229	3	US-08-630-915A-221	Sequence 221, App
438	6	0.8	206	3	US-08-679-493A-75	Sequence 75, Appl	511	6	0.8	229	4	US-09-879-957-221	Sequence 221, App
439	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, App	512	6	0.8	229	4	US-09-438-185A-648	Sequence 648, App
440	6	0.8	206	4	US-09-270-767-35977	Sequence 35977, A	513	6	0.8	230	3	US-09-516-143A-6	Sequence 6, Appli
441	6	0.8	206	4	US-09-270-767-51194	Sequence 51194, A	514	6	0.8	230	4	US-09-984-205-6	Sequence 6, Appli
442	6	0.8	207	1	US-09-198-452A-1020	Sequence 1020, App	515	6	0.8	231	4	US-09-543-681A-6357	Sequence 6357, App
443	6	0.8	208	1	US-07-935-309-2	Sequence 2, Appli	516	6	0.8	231	3	US-09-069-023-16	Sequence 36, Appl
444	6	0.8	208	1	US-08-884-682-1	Sequence 1, Appli	517	6	0.8	233	4	US-09-270-767-16462	Sequence 36462, A
445	6	0.8	208	2	US-08-039-364-2	Sequence 2, Appli	518	6	0.8	233	4	US-09-270-767-11679	Sequence 51679, A
446	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	519	6	0.8	234	3	US-08-861-774E-52	Sequence 52, Appl
447	6	0.8	208	2	US-09-096-082-1	Sequence 1, Appli	520	6	0.8	235	1	US-08-287-959-8	Sequence 8, Appl
448	6	0.8	208	2	US-08-718-904-5	Sequence 5, Appli	521	6	0.8	235	4	US-09-107-532A-6979	Sequence 6979, App
449	6	0.8	208	3	US-08-718-904-7	Sequence 7, Appli	522	6	0.8	235	4	US-09-583-110-1199	Sequence 1199, App
450	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	523	6	0.8	235	4	US-09-107-433-1326	Sequence 4326, App
451	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appli	524	6	0.8	236	4	US-09-134-000C-4896	Sequence 4896, App
452	6	0.8	208	3	US-09-158-710-2	Sequence 2, Appli	525	6	0.8	237	3	US-08-861-774E-68	Sequence 68, Appl
453	6	0.8	208	3	US-08-927-597-30	Sequence 30, Appl	526	6	0.8	238	4	US-09-252-991A-29406	Sequence 29406, A
454	6	0.8	208	3	US-09-518-950-2	Sequence 2, Appli	527	6	0.8	238	4	US-09-902-540-13083	Sequence 13083, A
455	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appli	528	6	0.8	239	3	US-09-004-731-44	Sequence 44, Appl
456	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appli	529	6	0.8	239	3	US-08-749-699-44	Sequence 44, Appl
457	6	0.8	208	4	US-09-252-991A-22641	Sequence 22641, A	530	6	0.8	239	3	US-08-679-493A-76	Sequence 76, Appl
458	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl	531	6	0.8	239	4	US-09-004-729-44	Sequence 44, Appl
459	6	0.8	208	4	US-09-949-016-6149	Sequence 16149, App	532	6	0.8	239	4	US-09-328-352-7328	Sequence 7328, App
460	6	0.8	209	3	US-08-975-762-71	Sequence 71, Appl	533	6	0.8	240	4	US-09-328-352-7253	Sequence 7253, App
461	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl	534	6	0.8	242	3	US-09-004-731-41	Sequence 41, Appl
462	6	0.8	209	3	US-09-106-582-71	Sequence 71, Appl	535	6	0.8	242	3	US-09-032-215-47	Sequence 47, Appl
463	6	0.8	209	3	US-09-311-311C-20	Sequence 20, Appl	536	6	0.8	242	3	US-08-749-699-41	Sequence 41, Appl
464	6	0.8	209	4	US-09-252-991A-29571	Sequence 29571, A	537	6	0.8	242	4	US-09-004-729-41	Sequence 41, Appl
465	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl	538	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A

539	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap	612	6	0.8	281	4	US-09-270-767-43839	Sequence 43839, A
540	6	0.8	242	4	US-09-583-110-3522	Sequence 3522, Ap	613	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A
541	6	0.8	243	4	US-09-543-681A-7356	Sequence 7356, Ap	614	6	0.8	284	4	US-08-976-063E-2	Sequence 2, Appl1
542	6	0.8	244	4	US-09-461-325-463	Sequence 463, App	615	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appl1
543	6	0.8	244	4	US-09-252-991A-29762	Sequence 29762, A	616	6	0.8	285	3	US-09-344-441-3	Sequence 3, Appl1
544	6	0.8	244	4	US-10-012-542-463	Sequence 463, App	617	6	0.8	285	4	US-09-248-796A-16474	Sequence 16474, A
545	6	0.8	244	4	US-10-115-123-463	Sequence 463, App	618	6	0.8	285	4	US-09-248-796A-20009	Sequence 20009, A
546	6	0.8	245	4	US-08-956-171E-5222	Sequence 5222, Ap	619	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl1
547	6	0.8	245	4	US-08-781-986A-5222	Sequence 5222, Ap	620	6	0.8	288	4	US-09-489-039A-8919	Sequence 8919, Ap
548	6	0.8	245	4	US-09-640-211A-833	Sequence 833, App	621	6	0.8	288	4	US-09-248-796A-16494	Sequence 16494, A
549	6	0.8	248	1	US-08-266-451B-2	Sequence 2, Appl1	622	6	0.8	289	4	US-09-071-035-72	Sequence 72, Appl1
550	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appl1	623	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A
551	6	0.8	248	2	US-08-944-483-71	Sequence 71, Appl1	624	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appl1
552	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	625	6	0.8	292	3	US-09-344-441-1	Sequence 1, Appl1
553	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl1	626	6	0.8	292	4	US-09-328-352-6642	Sequence 6642, Ap
554	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appl1	627	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap
555	6	0.8	250	3	US-09-538-092-355	Sequence 355, App	628	6	0.8	295	4	US-09-114-000C-3737	Sequence 3737, Ap
556	6	0.8	251	3	US-08-630-915A-8	Sequence 8, Appl1	629	6	0.8	295	6	5223394-9	Patent No. 5223394
557	6	0.8	251	4	US-09-270-767-44693	Sequence 44693, A	630	6	0.8	295	6	5223394-9	Patent No. 5223394
558	6	0.8	251	4	US-09-879-957-8	Sequence 8, Appl1	631	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A
559	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl1	632	6	0.8	296	4	US-09-949-016-9495	Sequence 9495, Ap
560	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appl1	633	6	0.8	297	4	US-09-543-681A-7800	Sequence 7800, Ap
561	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl1	634	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A
562	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl1	635	6	0.8	298	4	US-09-270-767-41439	Sequence 41439, A
563	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl1	636	6	0.8	299	4	US-09-270-767-41683	Sequence 41683, A
564	6	0.8	253	3	US-09-106-582-52	Sequence 8, Appl1	637	6	0.8	300	1	US-08-148-910-1	Sequence 1, Appl1
565	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appl1	638	6	0.8	300	4	US-09-252-991A-20115	Sequence 20115, A
566	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl1	639	6	0.8	300	4	US-09-252-991A-25396	Sequence 25396, A
567	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	640	6	0.8	301	4	US-09-124-000C-6014	Sequence 6014, Ap
568	6	0.8	253	4	US-09-654-600A-8	Sequence 8, Appl1	641	6	0.8	301	4	US-09-252-991A-21331	Sequence 21331, A
569	6	0.8	254	2	US-08-693-542-52	Sequence 52, Appl1	642	6	0.8	302	4	US-09-328-352-5508	Sequence 5508, Ap
570	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl1	643	6	0.8	302	4	US-09-540-236-2119	Sequence 2119, Ap
571	6	0.8	254	4	US-09-270-767-46094	Sequence 46094, A	644	6	0.8	302	4	US-09-107-532A-5585	Sequence 5585, Ap
572	6	0.8	254	4	US-09-248-796A-19272	Sequence 19272, A	645	6	0.8	303	4	US-09-949-016-10112	Sequence 10112, A
573	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appl1	646	6	0.8	303	4	US-09-902-540-11322	Sequence 11322, A
574	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl1	647	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap
575	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	648	6	0.8	304	4	US-09-902-540-15483	Sequence 15483, A
576	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl1	649	6	0.8	304	4	US-08-560-098A-45	Sequence 45, Appl1
577	6	0.8	257	3	US-08-467-265-16	Sequence 16, Appl1	650	6	0.8	305	4	US-09-252-991A-27054	Sequence 27054, A
578	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl1	651	6	0.8	306	4	US-09-328-352-5398	Sequence 5398, Ap
579	6	0.8	257	4	US-09-375-907-5	Sequence 5, Appl1	652	6	0.8	306	4	US-09-602-787A-572	Sequence 572, App
580	6	0.8	257	4	US-09-828-447-14	Sequence 14, Appl1	653	6	0.8	306	4	US-09-393-634-53	Sequence 634, Appl1
581	6	0.8	258	3	US-09-248-796A-24697	Sequence 24697, A	654	6	0.8	307	4	US-09-107-532A-6023	Sequence 6023, Ap
582	6	0.8	258	3	US-09-227-357-198	Sequence 198, App	655	6	0.8	308	4	US-08-849-480A-6	Sequence 6, Appl1
583	6	0.8	258	4	US-09-252-991A-32929	Sequence 32929, A	656	6	0.8	308	4	US-08-477-460B-6	Sequence 6, Appl1
584	6	0.8	261	4	US-09-270-767-45003	Sequence 45003, A	657	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appl1
585	6	0.8	262	4	US-09-270-767-45003	Sequence 45003, A	658	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appl1
586	6	0.8	263	4	US-09-270-767-42374	Sequence 42374, A	659	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appl1
587	6	0.8	263	4	US-09-270-767-47591	Sequence 47591, A	660	6	0.8	310	3	US-09-409-006A-6	Sequence 6, Appl1
588	6	0.8	264	2	US-08-484-905-120	Sequence 120, App	661	6	0.8	310	3	US-08-484-681-6	Sequence 6, Appl1
589	6	0.8	264	3	US-08-481-985B-120	Sequence 120, App	662	6	0.8	310	4	US-09-766-995-6	Sequence 6, Appl1
590	6	0.8	264	3	US-08-370-476-120	Sequence 120, App	663	6	0.8	310	4	US-09-543-681A-5602	Sequence 5602, Ap
591	6	0.8	270	4	US-09-949-016-11038	Sequence 11038, A	664	6	0.8	310	4	US-09-543-681A-13013	Sequence 13013, A
592	6	0.8	272	4	US-09-252-991A-27911	Sequence 27911, A	665	6	0.8	311	4	US-09-071-035-70	Sequence 70, Appl1
593	6	0.8	274	4	US-09-270-767-40695	Sequence 40695, A	666	6	0.8	311	4	US-09-351-150A-11	Sequence 11, Appl1
594	6	0.8	274	4	US-09-270-767-55911	Sequence 55911, A	667	6	0.8	312	4	US-09-539-360B-96	Sequence 96, Appl1
595	6	0.8	276	3	US-08-953-326-18	Sequence 18, Appl1	668	6	0.8	312	4	US-09-148-545-233	Sequence 233, App
596	6	0.8	276	4	US-09-553-662-18	Sequence 18, Appl1	669	6	0.8	313	4	US-09-248-796A-17016	Sequence 17016, A
597	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl1	670	6	0.8	313	4	US-09-270-767-42766	Sequence 42766, A
598	6	0.8	276	4	US-09-880-503-5	Sequence 5, Appl1	671	6	0.8	315	4	US-09-603-208A-212	Sequence 212, App
599	6	0.8	277	4	US-09-252-991A-17567	Sequence 17567, A	672	6	0.8	315	4	US-09-583-110-5279	Sequence 5279, Ap
600	6	0.8	278	4	US-09-252-991A-28712	Sequence 28712, A	673	6	0.8	317	4	US-09-270-767-42650	Sequence 42650, A
601	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	674	6	0.8	318	4	US-09-252-991A-25243	Sequence 25243, A
602	6	0.8	278	4	US-09-902-540-11962	Sequence 11962, A	675	6	0.8	318	6	US-09-710-279-976	Sequence 976, App
603	6	0.8	280	4	US-09-107-532A-6088	Sequence 6088, Ap	676	6	0.8	318	6	5223394-11	Patent No. 5223394
604	6	0.8	280	4	US-09-270-767-40154	Sequence 40154, A	677	6	0.8	320	3	US-09-134-001C-3552	Sequence 3552, Ap
605	6	0.8	280	4	US-09-270-767-55370	Sequence 55370, A	678	6	0.8	320	3	US-09-134-001C-3823	Sequence 3823, Ap
606	6	0.8	280	4	US-10-101-464A-511	Sequence 511, App	679	6	0.8	320	3	US-09-489-039A-10349	Sequence 10349, A
607	6	0.8	281	3	US-09-660-587-9	Sequence 9, Appl1	680	6	0.8	320	4		
608	6	0.8	281	4	US-09-261-358A-9	Sequence 9, Appl1	681	6	0.8				
609	6	0.8	281	4	US-09-201-458-5	Sequence 5, Appl1	682	6	0.8				
610	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appl1	683	6	0.8				
611	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appl1	684	6	0.8				

685	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A	758	6	0.8	359	4	US-09-583-110-3909	Sequence 3909, Ap
686	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap	759	6	0.8	362	4	US-09-252-991A-18494	Sequence 18494, A
687	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A	760	6	0.8	363	4	US-09-107-433-3869	Sequence 3869, Ap
688	6	0.8	322	4	US-09-949-016-8007	Sequence 8007, Ap	761	6	0.8	364	4	US-09-252-991A-19037	Sequence 19037, A
689	6	0.8	322	4	US-09-270-767-61011	Sequence 61011, A	762	6	0.8	364	4	US-09-438-185A-815	Sequence 815, Ap
690	6	0.8	323	4	US-09-880-503-7	Sequence 7, Appli	763	6	0.8	365	1	US-08-093-741-83	Sequence 83, Appl
691	6	0.8	324	4	US-09-270-767-44986	Sequence 44986, A	764	6	0.8	365	1	US-08-720-012-83	Sequence 83, Appl
692	6	0.8	325	4	US-08-311-731A-249	Sequence 249, App	765	6	0.8	365	3	US-09-221-529-3	Sequence 3, Appli
693	6	0.8	325	4	US-09-248-796A-14929	Sequence 14929, A	766	6	0.8	365	3	US-08-977-816-3	Sequence 816, Appl
694	6	0.8	326	3	US-09-066-046-29	Sequence 29, Appl	767	6	0.8	366	4	US-09-252-991A-24466	Sequence 24466, A
695	6	0.8	326	3	US-09-066-047-15	Sequence 15, Appli	768	6	0.8	366	4	US-09-902-540-15482	Sequence 15482, A
696	6	0.8	326	3	US-09-411-977-3	Sequence 3, Appli	769	6	0.8	367	3	US-08-895-707-6	Sequence 6, Appli
697	6	0.8	326	3	US-09-543-681A-7709	Sequence 7709, Ap	770	6	0.8	367	4	US-09-252-991A-17240	Sequence 17240, A
698	6	0.8	327	4	US-10-057-951-3	Sequence 3, Appli	771	6	0.8	367	4	US-09-328-352-7662	Sequence 7662, Ap
699	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A	772	6	0.8	369	4	US-09-248-796A-14930	Sequence 14930, A
700	6	0.8	327	4	US-09-107-433-3331	Sequence 3331, Ap	773	6	0.8	370	4	US-09-902-540-9972	Sequence 9972, Ap
701	6	0.8	328	4	US-09-248-796A-20663	Sequence 20663, A	774	6	0.8	372	4	US-09-252-991A-28586	Sequence 28586, A
702	6	0.8	330	4	US-09-710-279-2476	Sequence 2476, Ap	775	6	0.8	372	4	US-09-973-963-4	Sequence 4, Appli
703	6	0.8	330	4	US-09-710-279-2734	Sequence 2734, Ap	776	6	0.8	372	4	US-09-949-016-6463	Sequence 6463, Ap
704	6	0.8	331	2	US-08-560-098A-46	Sequence 2734, Ap	777	6	0.8	373	4	US-09-404-296B-4	Sequence 4, Appli
705	6	0.8	332	3	US-09-134-001C-4323	Sequence 4323, Ap	778	6	0.8	374	2	US-08-820-170A-25	Sequence 25, Appl
706	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap	779	6	0.8	374	3	US-09-055-699-25	Sequence 25, Appl
707	6	0.8	334	3	US-09-218-363-11	Sequence 11, Appli	780	6	0.8	374	3	US-09-273-565-25	Sequence 25, Appl
708	6	0.8	336	1	US-07-904-073-2	Sequence 2, Appli	781	6	0.8	374	3	US-09-565-538-25	Sequence 25, Appl
709	6	0.8	336	1	US-07-904-071-2	Sequence 2, Appli	782	6	0.8	374	3	US-09-661-468-25	Sequence 25, Appl
710	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Appli	783	6	0.8	374	4	US-09-976-165-35	Sequence 25, Appl
711	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Appl	784	6	0.8	374	4	US-09-227-853A-2	Sequence 2, Appli
712	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A	785	6	0.8	374	4	US-09-540-236-2230	Sequence 2230, Ap
713	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A	786	6	0.8	374	5	PCT-US95-06385-2	Sequence 2, Appli
714	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap	787	6	0.8	375	3	US-08-872-979-3	Sequence 3, Appli
715	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap	788	6	0.8	375	4	US-09-328-352-6191	Sequence 6191, Ap
716	6	0.8	340	4	US-09-816-248-15	Sequence 15, Appl	789	6	0.8	375	4	US-09-489-039A-11560	Sequence 11560, A
717	6	0.8	341	4	US-09-543-681A-7713	Sequence 4713, Ap	790	6	0.8	377	4	US-09-679-279-3	Sequence 3, Appli
718	6	0.8	341	4	US-09-248-796A-17051	Sequence 17051, Ap	791	6	0.8	377	4	US-09-489-039A-12546	Sequence 12546, A
719	6	0.8	341	4	US-09-902-540-13921	Sequence 13921, A	792	6	0.8	378	3	US-09-553-498-10	Sequence 10, Appl
720	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A	793	6	0.8	378	4	US-09-618-869-10	Sequence 10, Appl
721	6	0.8	342	4	US-09-902-540-10704	Sequence 10704, A	794	6	0.8	378	4	US-09-673-385A-618	Sequence 618, App
722	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A	795	6	0.8	379	4	US-09-252-991A-17472	Sequence 17472, A
723	6	0.8	345	3	US-09-027-900-11	Sequence 11, Appl	796	6	0.8	381	4	US-09-673-395A-441	Sequence 441, App
724	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A	797	6	0.8	381	4	US-09-270-767-61883	Sequence 46183, A
725	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A	798	6	0.8	383	1	US-08-486-037B-2	Sequence 2, Appli
726	6	0.8	347	2	US-08-811-949-1	Sequence 1, Appli	799	6	0.8	383	2	US-08-558-269-6	Sequence 6, Appli
727	6	0.8	347	4	US-09-636-215-590	Sequence 590, App	800	6	0.8	383	2	US-09-410-882-6	Sequence 6, Appli
728	6	0.8	347	4	US-09-685-166A-590	Sequence 590, App	801	6	0.8	385	3	US-09-071-224-19	Sequence 19, Appl
729	6	0.8	347	4	US-09-679-426-590	Sequence 590, App	802	6	0.8	386	3	US-08-895-707-7	Sequence 7, Appli
730	6	0.8	347	4	US-09-759-143-590	Sequence 590, App	803	6	0.8	386	3	US-09-045-284A-2	Sequence 2, Appli
731	6	0.8	347	4	US-09-651-236-590	Sequence 590, App	804	6	0.8	386	3	US-09-190-911-1	Sequence 1, Appli
732	6	0.8	348	4	US-09-360-376-13	Sequence 13, Appl	805	6	0.8	386	4	US-09-786-240-11	Sequence 11, Appl
733	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap	806	6	0.8	386	4	US-09-489-039A-7410	Sequence 7410, Ap
734	6	0.8	351	1	US-08-324-483-2	Sequence 2, Appli	807	6	0.8	386	4	US-09-248-796A-15757	Sequence 15757, A
735	6	0.8	351	4	US-09-902-540-12944	Sequence 12944, A	808	6	0.8	389	2	US-08-811-949-67	Sequence 67, Appl
736	6	0.8	354	2	US-08-811-949-61	Sequence 61, Appl	809	6	0.8	389	3	US-09-071-224-47	Sequence 27, Appl
737	6	0.8	355	1	US-08-137-116-1	Sequence 1, Appli	810	6	0.8	389	4	US-09-107-532A-6185	Sequence 6185, Ap
738	6	0.8	355	1	US-08-217-618-1	Sequence 1, Appli	811	6	0.8	390	4	US-09-252-991A-26543	Sequence 26543, A
739	6	0.8	355	1	US-08-427-640-2	Sequence 2, Appli	812	6	0.8	391	4	US-09-543-681A-7025	Sequence 7029, Ap
740	6	0.8	355	1	US-08-427-640-6	Sequence 6, Appli	813	6	0.8	392	1	US-08-706-539-9	Sequence 9, Appli
741	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Appli	814	6	0.8	392	3	US-09-027-007-9	Sequence 7, Appli
742	6	0.8	355	1	US-08-217-616-1	Sequence 1, Appli	815	6	0.8	392	4	US-09-710-279-7794	Sequence 2874, Ap
743	6	0.8	355	2	US-08-811-949-45	Sequence 45, Appl	816	6	0.8	392	4	US-09-710-279-4874	Sequence 2874, Ap
744	6	0.8	355	2	US-08-811-949-47	Sequence 47, Appl	817	6	0.8	392	4	US-09-949-016-8786	Sequence 8786, Ap
745	6	0.8	355	2	US-08-811-949-53	Sequence 53, Appl	818	6	0.8	392	4	US-09-949-016-8787	Sequence 8787, Ap
746	6	0.8	355	2	US-08-811-949-59	Sequence 59, Appl	819	6	0.8	393	2	US-08-560-098A-44	Sequence 44, Appl
747	6	0.8	355	3	US-08-794-528-1	Sequence 1, Appli	820	6	0.8	393	3	US-08-967-024C-24	Sequence 24, Appl
748	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A	821	6	0.8	393	3	US-08-967-024C-25	Sequence 25, Appl
749	6	0.8	355	4	US-09-198-452A-871	Sequence 871, App	822	6	0.8	393	4	US-09-270-767-12793	Sequence 42793, A
750	6	0.8	355	4	US-09-902-540-11796	Sequence 11796, A	823	6	0.8	394	3	US-08-466-368-2	Sequence 2, Appli
751	6	0.8	355	6	5223256-1	Sequence 11796, A	824	6	0.8	394	4	US-09-144-914-4	Sequence 4, Appli
752	6	0.8	355	6	5223256-1	Patent No. 5223256	825	6	0.8	394	4	US-09-252-991A-18502	Sequence 18502, A
753	6	0.8	356	1	US-08-427-640-4	Sequence 4, Appli	826	6	0.8	394	4	US-08-328-500-2	Sequence 2, Appli
754	6	0.8	356	1	US-08-427-640-8	Sequence 8, Appli	827	6	0.8	394	6	5223418-2	Patent No. 5223418
755	6	0.8	356	4	US-09-252-991A-30030	Sequence 30030, A	828	6	0.8	394	6	US-08-485-859-2	Sequence 2, Appli
756	6	0.8	356	4	US-09-502-540-12881	Sequence 12881, A	829	6	0.8	395	1	US-08-485-859-2	Sequence 2, Appli
757	6	0.8	358	4	US-09-248-796A-19081	Sequence 19081, A	830	6	0.8	395	1	US-08-706-539-11	Sequence 11, Appl



831	6	0.8	395	1	US-08-522-166-2	Sequence 2, Appli	904	6	0.8	424	4	US-09-107-532A-5459	Sequence 5459, Ap
832	6	0.8	395	1	US-08-468-382A-2	Sequence 2, Appli	905	6	0.8	424	4	US-09-248-796A-18949	Sequence 18949, A
833	6	0.8	395	1	US-08-460-912-2	Sequence 2, Appli	906	6	0.8	424	4	US-10-027-450-45	Sequence 45, Appl
834	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appli	907	6	0.8	425	3	US-09-071-224-6	Sequence 6, Appli
835	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	908	6	0.8	425	3	US-09-134-001C-55619	Sequence 5619, Ap
836	6	0.8	397	1	US-08-647-928-6	Sequence 8, Appli	909	6	0.8	425	4	US-09-540-236-3466	Sequence 3466, Ap
837	6	0.8	397	4	US-09-469-039A-13498	Sequence 13498, A	910	6	0.8	426	4	US-09-252-991A-25192	Sequence 25192, A
838	6	0.8	397	4	US-09-949-016-10639	Sequence 10640, A	911	6	0.8	427	4	US-09-198-452A-31	Sequence 31, Appl
839	6	0.8	397	4	US-09-949-016-10639	Sequence 10640, A	912	6	0.8	427	4	US-09-328-352-5205	Sequence 5205, Ap
840	6	0.8	398	2	US-08-284-391B-29	Sequence 29, Appl	913	6	0.8	428	1	US-08-570-157-5	Sequence 5, Appli
841	6	0.8	398	3	US-09-218-950-29	Sequence 29, Appl	914	6	0.8	428	3	US-08-029-170-31	Sequence 31, Appl
842	6	0.8	398	4	US-08-394-388A-29	Sequence 29, Appl	915	6	0.8	428	3	US-08-403-797-2	Sequence 2, Appli
843	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	916	6	0.8	428	3	US-09-076-510-5	Sequence 5, Appli
844	6	0.8	399	4	US-09-270-767-41700	Sequence 45921, A	917	6	0.8	428	4	US-09-004-745-31	Sequence 31, Appl
845	6	0.8	399	4	US-09-710-279-2576	Sequence 2576, Ap	918	6	0.8	428	4	US-09-443-349-31	Sequence 31, Appl
846	6	0.8	400	3	US-09-134-001C-4785	Sequence 4785, Ap	919	6	0.8	428	4	US-09-949-016-10965	Sequence 10965, A
847	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	920	6	0.8	429	4	US-09-252-991A-28788	Sequence 28788, A
848	6	0.8	400	4	US-09-248-796A-15785	Sequence 15785, A	921	6	0.8	429	4	US-09-854-133-391	Sequence 391, App
849	6	0.8	401	4	US-09-489-847-202	Sequence 202, App	922	6	0.8	430	1	US-07-942-157A-3	Sequence 3, Appli
850	6	0.8	401	4	US-09-252-991A-17090	Sequence 17090, A	923	6	0.8	430	6	5219569-2	Patent No. 5219569
851	6	0.8	401	4	US-09-902-540-10491	Sequence 10491, A	924	6	0.8	430	6	5219569-2	Patent No. 5219569
852	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli	925	6	0.8	431	3	US-09-376-689-4	Sequence 4, Appli
853	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli	926	6	0.8	431	4	US-09-101-2726-1	Sequence 1, Appli
854	6	0.8	402	4	US-10-157-408-1	Sequence 1, Appli	927	6	0.8	431	4	US-09-540-236-3536	Sequence 3536, Ap
855	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli	928	6	0.8	431	4	US-09-270-767-45503	Sequence 45503, A
856	6	0.8	403	4	US-09-880-503-6	Sequence 6, Appli	929	6	0.8	431	4	US-09-248-796A-18354	Sequence 18354, A
857	6	0.8	405	3	US-09-144-914-5	Sequence 5, Appli	930	6	0.8	431	6	5188829-1	Patent No. 5188829
858	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A	931	6	0.8	431	6	5188829-1	Patent No. 5188829
859	6	0.8	405	4	US-09-134-000C-5465	Sequence 5465, Ap	932	6	0.8	432	2	US-08-560-098A-47	Sequence 47, Appl
860	6	0.8	408	4	US-09-252-991A-21303	Sequence 21303, A	933	6	0.8	432	3	US-08-477-460B-2	Sequence 2, Appli
861	6	0.8	408	4	US-09-198-452A-141	Sequence 141, App	934	6	0.8	432	3	US-08-379-516-2	Sequence 2, Appli
862	6	0.8	408	4	US-09-583-110-3016	Sequence 3016, Ap	935	6	0.8	432	3	US-09-329-916-2	Sequence 2, Appli
863	6	0.8	408	4	US-09-902-540-11436	Sequence 11436, A	936	6	0.8	432	3	US-08-485-3728-2	Sequence 2, Appli
864	6	0.8	409	4	US-09-710-279-2002	Sequence 2002, Ap	937	6	0.8	432	3	US-09-409-006A-2	Sequence 2, Appli
865	6	0.8	409	4	US-09-710-279-2306	Sequence 2306, Ap	938	6	0.8	432	4	US-08-484-681-2	Sequence 2, Appli
866	6	0.8	410	1	US-08-792-283A-9	Sequence 9, Appli	939	6	0.8	432	5	US-09-766-995-5	Sequence 2, Appli
867	6	0.8	410	3	US-09-105-908-9	Sequence 9, Appli	940	6	0.8	432	5	PCT-US93-07422-2	Sequence 2, Appli
868	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appl	941	6	0.8	433	2	US-08-867-149-1	Sequence 1, Appli
869	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli	942	6	0.8	433	2	US-08-808-374-1	Sequence 1, Appli
870	6	0.8	410	3	US-09-375-419-17	Sequence 17, Appli	943	6	0.8	433	3	US-09-100-409A-1	Sequence 1, Appli
871	6	0.8	410	4	US-09-252-991A-25812	Sequence 25812, A	944	6	0.8	433	3	US-09-364-230-14	Sequence 14, Appl
872	6	0.8	410	4	US-09-252-991A-31937	Sequence 31937, A	945	6	0.8	433	3	US-09-543-681A-7154	Sequence 7154, Ap
873	6	0.8	410	4	US-09-489-039A-10283	Sequence 10283, A	946	6	0.8	433	6	US-09-792-024-78	Sequence 2, Appli
874	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli	947	6	0.8	433	6	5171838-13	Patent No. 5171838
875	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appl	948	6	0.8	434	1	US-08-236-311-4	Sequence 4, Appli
876	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appl	949	6	0.8	434	1	US-08-457-918-4	Sequence 4, Appli
877	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appl	950	6	0.8	434	4	US-09-252-991A-23131	Sequence 23131, A
878	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli	951	6	0.8	434	4	US-09-543-681A-7154	Sequence 7154, Ap
879	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli	952	6	0.8	434	4	US-10-157-408-4	Sequence 4, Appli
880	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli	953	6	0.8	436	4	US-09-949-016-11448	Sequence 11448, A
881	6	0.8	412	4	US-09-880-503-1	Sequence 3, Appli	954	6	0.8	437	2	US-08-811-949-49	Sequence 49, Appl
882	6	0.8	412	4	US-09-902-540-13518	Sequence 13518, A	955	6	0.8	437	2	US-08-811-949-51	Sequence 51, Appl
883	6	0.8	413	4	US-09-949-016-10736	Sequence 10736, A	956	6	0.8	437	2	US-08-811-949-55	Sequence 55, Appl
884	6	0.8	413	4	US-09-949-016-10737	Sequence 10737, A	957	6	0.8	437	2	US-08-811-949-57	Sequence 57, Appl
885	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A	958	6	0.8	437	4	US-09-710-279-2960	Sequence 2960, Ap
886	6	0.8	415	1	US-08-110-386A-6	Sequence 6, Appli	959	6	0.8	438	4	US-09-252-991A-28398	Sequence 28398, A
887	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appl	960	6	0.8	438	4	US-09-489-039A-8464	Sequence 8464, Ap
888	6	0.8	415	3	US-08-482-746-6	Sequence 6, Appli	961	6	0.8	438	4	US-09-902-540-12277	Sequence 12277, A
889	6	0.8	415	4	US-09-180-109A-9	Sequence 9, Appli	962	6	0.8	439	2	US-08-959-638-9	Sequence 9, Appli
890	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appl	963	6	0.8	439	4	US-09-543-681A-7293	Sequence 7293, Ap
891	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli	964	6	0.8	440	4	US-09-489-039A-10782	Sequence 10782, A
892	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli	965	6	0.8	441	3	US-09-457-046B-54	Sequence 54, Appl
893	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli	966	6	0.8	441	3	US-09-237-937C-11	Sequence 11, Appl
894	6	0.8	415	4	US-09-799-978-46	Sequence 16, Appl	967	6	0.8	441	4	US-09-949-016-10792	Sequence 10792, A
895	6	0.8	418	4	US-09-591-279A-42	Sequence 42, Appl	968	6	0.8	441	4	US-09-866-570B-54	Sequence 54, Appl
896	6	0.8	419	4	US-09-270-767-41700	Sequence 41700, A	969	6	0.8	443	1	US-08-570-157-6	Sequence 6, Appli
897	6	0.8	419	4	US-09-902-540-13149	Sequence 13149, A	970	6	0.8	443	3	US-09-076-510-6	Sequence 6, Appli
898	6	0.8	420	4	US-09-252-991A-17500	Sequence 17500, A	971	6	0.8	443	4	US-09-004-319-6	Sequence 6, Appli
899	6	0.8	420	4	US-09-583-110-5061	Sequence 5061, Ap	972	6	0.8	444	1	US-07-937-609-14	Sequence 14, Appl
900	6	0.8	420	4	US-09-107-433-919	Sequence 3519, Ap	973	6	0.8	444	3	US-08-029-170-14	Sequence 14, Appl
901	6	0.8	422	4	US-09-489-847-357	Sequence 357, App	974	6	0.8	444	4	US-09-252-991A-28809	Sequence 28809, A
902	6	0.8	424	3	US-09-134-001C-5009	Sequence 5009, Ap	975	6	0.8	444	4	US-09-270-767-43807	Sequence 43807, A
903	6	0.8	424	4	US-09-173-300-45	Sequence 45, Appl	976	6	0.8	444	4	US-09-443-745-14	Sequence 14, Appl

977	6	0.8	445	4	US-09-710-279-2858	Sequence 2658, Ap	1050	6	0.8	492	4	US-09-248-796A-17174	Sequence 17174, A
978	6	0.8	451	4	US-09-328-352-7659	Sequence 7659, Ap	1051	6	0.8	493	4	US-09-543-681A-7006	Sequence 7006, Ap
979	6	0.8	451	4	US-09-134-000C-3849	Sequence 3849, Ap	1052	6	0.8	494	4	US-09-517-779-2	Sequence 2, Appli
980	6	0.8	454	4	US-09-134-001C-4438	Sequence 4438, A	1053	6	0.8	495	4	US-08-311-731A-3	Sequence 3, Appli
981	6	0.8	454	4	US-09-902-540-12501	Sequence 12501, A	1054	6	0.8	497	1	US-08-278-635B-5	Sequence 5, Appli
982	6	0.8	456	1	US-08-205-719-4	Sequence 4, Appli	1055	6	0.8	497	3	US-08-464-258B-5	Sequence 5, Appli
983	6	0.8	456	3	US-08-431-517F-6	Sequence 6, Appli	1056	6	0.8	497	3	US-08-471-961-5	Sequence 5, Appli
984	6	0.8	456	3	US-09-328-352-5446	Sequence 5446, Ap	1057	6	0.8	497	4	US-09-345-109C-5	Sequence 5, Appli
985	6	0.8	456	4	US-09-919-172-31	Sequence 31, Appli	1058	6	0.8	497	4	US-09-270-767-62287	Sequence 62287, A
986	6	0.8	457	4	US-08-328-500-9	Sequence 9, Appli	1059	6	0.8	497	4	US-09-949-016-6616	Sequence 6616, Ap
987	6	0.8	458	3	US-09-039-555B-15	Sequence 15, Appli	1060	6	0.8	497	6	5486473-4	Patent No. 5486473
988	6	0.8	458	3	US-08-466-368-4	Sequence 4, Appli	1061	6	0.8	497	6	5486473-4	Patent No. 5486473
989	6	0.8	458	3	US-09-517-605-3	Sequence 3, Appli	1062	6	0.8	499	4	US-09-949-016-67370	Sequence 7370, Ap
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992	6	0.8	458	4	US-09-612-402B-36	Sequence 36, Appli	1065	6	0.8	501	3	US-09-111-730-1	Sequence 1, Appli
993	6	0.8	458	4	US-10-092-138A-25	Sequence 25, Appli	1066	6	0.8	502	3	US-09-499-302A-7	Sequence 7, Appli
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998	6	0.8	459	4	US-09-252-991A-29528	Sequence 29528, A	1071	6	0.8	504	3	US-09-217-345-4	Sequence 4, Appli
999	6	0.8	459	4	US-09-710-279-2462	Sequence 2462, Ap	1072	6	0.8	504	4	US-08-487-596-4	Sequence 4, Appli
1000	6	0.8	460	4	US-09-543-681A-5773	Sequence 5773, Ap	1073	6	0.8	504	4	US-08-660-451A-4	Sequence 4, Appli
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1006	6	0.8	462	4	US-08-394-398A-5	Sequence 5, Appli	1079	6	0.8	511	4	US-09-949-016-6034	Sequence 6034, Ap
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1019	6	0.8	468	4	US-09-248-796A-17456	Sequence 17456, A	1092	6	0.8	523	4	US-09-767-878-2	Sequence 2, Appli
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1024	6	0.8	471	4	US-09-645-337A-4	Sequence 4, Appli	1097	6	0.8	526	2	US-07-609-510B-16	Sequence 16, Appli
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1195	6	0.8	597	4	US-09-252-991A-17139	Sequence 17139, A	1268	6	0.8	685	3	US-09-272-796-1	Sequence 1, Appli

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## ALIGNMENTS

RESULT 1  
 US-10-067-422-9  
 ; Sequence 9, Application US/10067422  
 ; Patent No. 6743613  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nt et al.  
 ; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and  
 ; FILE REFERENCE: PTO04P1  
 ; CURRENT APPLICATION NUMBER: US/10/067,422  
 ; PRIOR FILING DATE: 2002-02-07  
 ; PRIOR APPLICATION NUMBER: 09/685,899  
 ; PRIOR FILING DATE: 2000-10-11  
 ; PRIOR APPLICATION NUMBER: PCT/US00/09028  
 ; PRIOR FILING DATE: 2000-04-06  
 ; PRIOR APPLICATION NUMBER: 60/152,933  
 ; PRIOR FILING DATE: 1999-09-09  
 ; PRIOR APPLICATION NUMBER: 60/147,020  
 ; PRIOR FILING DATE: 1999-08-03  
 ; PRIOR APPLICATION NUMBER: 60/131,672  
 ; PRIOR FILING DATE: 1999-04-29  
 ; PRIOR APPLICATION NUMBER: 60/130,693  
 ; PRIOR FILING DATE: 1999-04-23  
 ; NUMBER OF SEQ ID NOS: 32  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 570  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-067-422-9  
 Query Match 49.3%; Score 355; DB 4; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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## RESULT 2

US-10-067-422-17  
; Sequence 17, Application US/10067422  
; Patent No. 6743613  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and  
; FILE REFERENCE: PTO04P1  
; CURRENT APPLICATION NUMBER: US/10/067,422  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/685,899  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09028  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/152,933  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: 60/147,020  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: 60/131,672  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 60/130,693  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 46  
; TYPE: PRT  
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US-10-067-422-17

Query Match 2.2%; Score 16; DB 4; Length 46;  
Best Local Similarity 100.0%; Pred. No. 2.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 275 LEERNCSDPGPGVNGY 290  
Db 31 LEERNCSDPGPGVNGI 46

## RESULT 3

US-10-067-422-16  
; Sequence 16, Application US/10067422  
; Patent No. 6743613  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: Bone Morphogenic Protein (BMP) Polynucleotides, Polypeptides, and  
; FILE REFERENCE: PTO04P1  
; CURRENT APPLICATION NUMBER: US/10/067,422  
; PRIOR FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: 09/685,899  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09028  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/152,933  
; PRIOR FILING DATE: 1999-09-09  
; PRIOR APPLICATION NUMBER: 60/147,020  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: 60/131,672  
; PRIOR FILING DATE: 1999-04-29  
; PRIOR APPLICATION NUMBER: 60/130,693  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-067-422-16

Query Match 1.7%; Score 12; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 7.4e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 260 CACLAGYTGQRC 271  
Db 1 CACLAGYTGQRC 12

## RESULT 4

US-09-374-135-4  
; Sequence 4, Application US/09374135  
; Patent No. 6277972  
; GENERAL INFORMATION:  
; APPLICANT: Afari, Daniel E.  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Leong, Kahan  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Saffran, Douglas C.  
; APPLICANT: Jakobovits, Aya  
; TITLE OF INVENTION: SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND  
; FILE REFERENCE: 1703-017.US1  
; CURRENT APPLICATION NUMBER: US/09/374,135  
; PRIOR FILING DATE: 1999-08-10  
; PRIOR APPLICATION NUMBER: 60/095,982  
; PRIOR FILING DATE: 1998-08-10  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.59;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 179 YDYVEVRDG 187  
Db 47 YDYVEVRDG 55

## RESULT 5

US-09-341-461-28  
; Sequence 28, Application US/09341461  
; Patent No. 6586389  
; GENERAL INFORMATION:  
; APPLICANT: Hammond, Timothy G.  
; APPLICANT: Verroust, Pierre J.  
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin  
; FILE REFERENCE: D6148  
; CURRENT APPLICATION NUMBER: US/09/341,461  
; PRIOR FILING DATE: 2000-07-20  
; PRIOR APPLICATION NUMBER: PCT/US99/01259  
; PRIOR FILING DATE: 1999-01-21  
; NUMBER OF SEQ ID NOS: 40  
; SEQ ID NO 28  
; LENGTH: 110  
; TYPE: PRT  
; ORGANISM: human  
; FEATURES:  
; OTHER INFORMATION: amino acid sequence of Bmp-1 Cub1 domain  
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;  
Best Local Similarity 100.0%; Pred. No. 0.64;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187  
Db 56 YDYVEVRDG 64

## RESULT 6

US-09-438-046-20  
Sequence 20, Application US/09438046  
Patent No. 6706687  
GENERAL INFORMATION:  
APPLICANT: ERIKSSON, ULF  
APPLICANT: AASE, Karin  
APPLICANT: LEE, Xuri  
APPLICANT: PONTN, Annica  
APPLICANT: UTELLA, Marko  
APPLICANT: ALITALO, Kari  
APPLICANT: OESTMAN, Arne  
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR D, DNA CODING  
TITLE OF INVENTION: THEREFOR, AND USES THEREOF  
FILE REFERENCE: Ulf Eriksson et al 1064-44833  
CURRENT APPLICATION NUMBER: US/09/438,046  
CURRENT FILING DATE: 1999-11-10  
EARLIER APPLICATION NUMBER: 60/107,852  
EARLIER FILING DATE: 1998-11-10  
EARLIER APPLICATION NUMBER: 60/113,997  
EARLIER FILING DATE: 1999-12-28  
EARLIER APPLICATION NUMBER: 60/150,604  
EARLIER FILING DATE: 1999-08-26  
EARLIER APPLICATION NUMBER: 60/157,108  
EARLIER FILING DATE: 1999-10-04  
EARLIER APPLICATION NUMBER: 60/157,756  
EARLIER FILING DATE: 1999-10-05  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 20  
LENGTH: 113  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-438-046-20

Query Match 1.2%; Score 9; DB 4; Length 113;  
Best Local Similarity 100.0%; Pred. No. 0.65;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187  
Db 56 YDYVEVRDG 64

## RESULT 7

US-08-872-757-2  
Sequence 2, Application US/08872757  
Patent No. 6258584  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Hojima, Yoshio  
APPLICANT: Li, Shi-Wu  
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND  
TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/872,757  
FILING DATE: 10-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/609,187  
FILING DATE: 01-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8389-028-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 730 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-872-757-2

Query Match 1.2%; Score 9; DB 3; Length 730;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

## RESULT 8

US-09-850-048A-2  
Sequence 2, Application US/09850048A  
Patent No. 6562613  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Hojima, Yoshio  
APPLICANT: Li, Shi-Wu

TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND  
TITLE OF INVENTION: PROCESSES, METHODS AND USES THEREOF  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/850,048A  
FILING DATE: 07-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/609,187  
FILING DATE: 1996-03-01  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8389-028-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 730 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-850-048A-2

Query Match 1.2%; Score 9; DB 4; Length 730;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

RESULT 9  
US-08-572-225-1  
Sequence 1, Application US/08572225  
Patent No. 5807981  
GENERAL INFORMATION:  
APPLICANT: Prockop, Darwin J.  
APPLICANT: Hojima, Yoshio  
APPLICANT: Li, Shi-Wu  
APPLICANT: Sieron, Alexander  
APPLICANT: Brenner, Mitch  
TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR  
TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/572,225  
FILING DATE: 13-DEC-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8389-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 788 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-572-225-1

Query Match 1.2%; Score 9; DB 1; Length 788;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 179 YDYVEVRDG 187

RESULT 10  
US-09-285-385C-19  
Sequence 19, Application US/09285385C  
Patent No. 6579702  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Daniel S.  
APPLICANT: Scott, Ian C.  
APPLICANT: Thomas, Christina L.  
TITLE OF INVENTION: MAMMALIAN TOLL-RECEPTOR-LIKE GENE AND PROTEIN  
FILE REFERENCE: 960296.9611  
CURRENT APPLICATION NUMBER: US/09/285,385C  
CURRENT FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: 60/111873  
PRIOR FILING DATE: 1998-12-11  
PRIOR APPLICATION NUMBER: 60/080550  
PRIOR FILING DATE: 1998-04-03  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 19  
LENGTH: 986  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-285-385C-19

Query Match 1.2%; Score 9; DB 4; Length 986;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

RESULT 11  
US-09-949-016-6690  
Sequence 6690, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CU001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6690  
LENGTH: 986  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6690

Query Match 1.2%; Score 9; DB 4; Length 986;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187  
Db 377 YDYVEVRDG 385

RESULT 12  
US-09-285-385C-2  
Sequence 2, Application US/09285385C  
Patent No. 6579702  
GENERAL INFORMATION:  
APPLICANT: Greenspan, Daniel S.



```

; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960236.96111
; CURRENT APPLICATION NUMBER: US/09/285.385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: human
; US-09-285-385C-2

Query Match          1.2%; Score 9; DB 4; Length 1015;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      179 YDYVEVRDG 187
Db      406 YDYVEVRDG 414

RESULT 13
US-09-188-930-342
; Sequence 342, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188.930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
; US-09-188-930-342

Query Match          1.1%; Score 8; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      265 GYTGORCE 272
Db      36 GYTGORCE 43

RESULT 14
US-09-312-283C-342
; Sequence 342, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; FILE REFERENCE: 11000.1011c2
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; CURRENT APPLICATION NUMBER: US/09/312.283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
; US-09-312-283C-342

Query Match          1.1%; Score 8; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      265 GYTGORCE 272
Db      36 GYTGORCE 43

RESULT 15
US-09-472-087-99
; Sequence 99, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVER, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PE1
; CURRENT APPLICATION NUMBER: US/09/472.087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 99
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-99

Query Match          1.1%; Score 8; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      208 QSIGSSLAH 215
Db      27 QSIGSSLAH 34
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- 9: /cgn2\_6/prodata/2/pubppaa/US09A\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/prodata/2/pubppaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
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- 22: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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27	720	100.0	720	10	US-09-997-428-231
562	720	100.0	720	14	US-10-174-587-170
626	720	100.0	720	14	US-10-063-742-38
741	720	100.0	720	17	US-10-972-317-38
742	556	77.2	567	14	US-10-004-551-2
743	518	71.9	720	14	US-10-004-551-4
744	518	71.9	720	14	US-10-098-871-26
745	446	61.9	737	16	US-10-408-765A-1796
746	375	52.1	649	15	US-10-274-639-17
747	375	52.1	649	15	US-10-333-574-17
748	355	49.3	570	13	US-10-067-422-9
749	277	38.5	455	11	US-09-833-245-1401

750	276	38.3	323	11	US-09-833-245-1402	Sequence 1402, Ap
751	16	2.2	46	13	US-10-067-422-17	Sequence 17, Appl
752	12	1.7	12	13	US-10-067-422-16	Sequence 16, Appl
753	9	1.2	101	9	US-09-887-593-4	Sequence 4, Appl1
754	9	1.2	113	9	US-09-852-309A-20	Sequence 20, Appl
755	9	1.2	113	13	US-10-086-623-20	Sequence 20, Appl
756	9	1.2	113	14	US-10-260-539-20	Sequence 20, Appl
757	9	1.2	113	14	US-10-131-600-20	Sequence 20, Appl
758	9	1.2	113	15	US-10-303-997B-20	Sequence 20, Appl
759	9	1.2	113	15	US-10-439-337A-20	Sequence 20, Appl
760	9	1.2	730	9	US-09-850-048A-2	Sequence 2, Appl1
761	9	1.2	823	15	US-10-016-248-98	Sequence 98, Appl
762	9	1.2	823	15	US-10-112-944-309	Sequence 309, Appl
763	9	1.2	970	15	US-10-016-248-42	Sequence 42, Appl
764	9	1.2	966	9	US-09-285-385C-19	Sequence 19, Appl
765	9	1.2	966	15	US-09-918-715-242	Sequence 242, Appl
766	9	1.2	966	15	US-10-366-345-23	Sequence 33, Appl
767	9	1.2	966	16	US-10-474-794-242	Sequence 242, Appl
768	9	1.2	966	16	US-10-723-860-1377	Sequence 1377, Ap
769	9	1.2	966	18	US-10-979-159-242	Sequence 242, Appl
770	9	1.2	992	15	US-10-016-248-40	Sequence 40, Appl
771	9	1.2	1015	9	US-09-285-385C-2	Sequence 2, Appl1
772	9	1.2	1015	15	US-10-016-248-97	Sequence 97, Appl
773	9	1.2	1015	16	US-10-719-993-644	Sequence 644, Appl
774	9	1.2	1579	16	US-10-437-963-196551	Sequence 196551, Appl
775	8	1.1	11	15	US-10-443-466A-8	Sequence 8, Appl1
776	8	1.1	11	15	US-10-656-769-71	Sequence 71, Appl
777	8	1.1	11	18	US-10-993-395-5	Sequence 5, Appl1
778	8	1.1	47	16	US-10-425-115-279870	Sequence 279870, Appl
779	8	1.1	50	16	US-10-485-683-11	Sequence 11, Appl
780	8	1.1	51	10	US-09-866-050A-342	Sequence 342, Appl
781	8	1.1	88	9	US-09-905-243-30	Sequence 30, Appl
782	8	1.1	95	14	US-10-194-975-92	Sequence 92, Appl
783	8	1.1	95	14	US-10-194-975-92	Sequence 92, Appl
784	8	1.1	95	15	US-10-308-817-38	Sequence 38, Appl
785	8	1.1	95	15	US-10-308-817-39	Sequence 39, Appl
786	8	1.1	95	15	US-10-453-698-38	Sequence 38, Appl
787	8	1.1	95	15	US-10-453-698-39	Sequence 39, Appl
788	8	1.1	95	16	US-10-379-392-105	Sequence 105, Appl
789	8	1.1	95	16	US-10-379-392-106	Sequence 106, Appl
790	8	1.1	96	14	US-10-153-382-34	Sequence 34, Appl
791	8	1.1	96	16	US-10-612-497-99	Sequence 99, Appl
792	8	1.1	96	16	US-10-776-649-99	Sequence 99, Appl
793	8	1.1	108	17	US-10-805-177-67	Sequence 67, Appl
794	8	1.1	108	17	US-10-805-177-71	Sequence 71, Appl
795	8	1.1	124	9	US-09-764-877-1346	Sequence 1346, Ap
796	8	1.1	124	15	US-10-242-515-1346	Sequence 1346, Ap
797	8	1.1	126	15	US-10-362-082-2	Sequence 2, Appl1
798	8	1.1	126	15	US-10-656-769-18	Sequence 18, Appl
799	8	1.1	127	16	US-10-478-056-35	Sequence 35, Appl
800	8	1.1	128	15	US-10-443-466A-2	Sequence 2, Appl1
801	8	1.1	128	15	US-10-443-466A-41	Sequence 41, Appl
802	8	1.1	128	15	US-10-443-466A-43	Sequence 43, Appl
803	8	1.1	128	15	US-10-443-466A-72	Sequence 72, Appl
804	8	1.1	128	15	US-10-443-466A-74	Sequence 74, Appl
805	8	1.1	128	15	US-10-443-466A-76	Sequence 76, Appl
806	8	1.1	128	15	US-10-443-466A-78	Sequence 78, Appl
807	8	1.1	128	18	US-10-993-395-2	Sequence 2, Appl1
808	8	1.1	128	18	US-10-993-395-13	Sequence 13, Appl
809	8	1.1	151	16	US-10-437-963-107837	Sequence 107837, Appl
810	8	1.1	152	15	US-09-866-050A-187	Sequence 187, Appl
811	8	1.1	152	15	US-10-099-322-57	Sequence 57, Appl
812	8	1.1	152	15	US-10-044-564-57	Sequence 57, Appl
813	8	1.1	155	14	US-10-153-382-35	Sequence 35, Appl
814	8	1.1	155	16	US-10-612-497-20	Sequence 20, Appl
815	8	1.1	155	16	US-10-612-497-112	Sequence 112, Appl
816	8	1.1	155	16	US-10-776-649-20	Sequence 20, Appl
817	8	1.1	155	16	US-10-776-649-112	Sequence 112, Appl
818	8	1.1	157	17	US-10-644-277-36	Sequence 36, Appl
819	8	1.1	223	14	US-10-656-769-40	Sequence 40, Appl
820	8	1.1	223	14	US-10-148-671-25	Sequence 25, Appl
821	8	1.1	302	15	US-10-369-493-6656	Sequence 6656, Ap
822	8	1.1	397	16	US-10-425-115-284880	Sequence 284880, Ap

823	8	1.1	411	16	US-10-437-963-111499	Sequence 111499, A	896	7	1.0	133	16	US-10-437-963-151149	Sequence 151149,
824	8	1.1	425	15	US-10-425-114-68970	Sequence 68970, A	897	7	1.0	134	15	US-10-424-599-274398	Sequence 274398,
825	8	1.1	481	15	US-10-425-114-72031	Sequence 72031, A	898	7	1.0	136	15	US-10-424-599-274378	Sequence 274378,
826	8	1.1	481	16	US-10-425-115-35201	Sequence 352301, A	899	7	1.0	139	16	US-10-425-115-337979	Sequence 337979,
827	8	1.1	596	15	US-10-282-122A-50055	Sequence 50055, A	900	7	1.0	141	16	US-10-767-701-52201	Sequence 52201, A
828	8	1.1	675	16	US-10-437-963-166405	Sequence 166405, A	901	7	1.0	142	15	US-10-424-599-274613	Sequence 274613,
829	8	1.1	807	14	US-10-132-350-44	Sequence 42, Appl	902	7	1.0	142	16	US-10-425-115-307867	Sequence 307867,
830	8	1.1	807	14	US-10-132-350-44	Sequence 44, Appl	903	7	1.0	143	16	US-10-425-115-295660	Sequence 295660,
831	8	1.1	863	16	US-10-425-115-352299	Sequence 352299, A	904	7	1.0	144	16	US-10-437-963-102869	Sequence 102869,
832	8	1.1	963	17	US-10-732-923-10766	Sequence 10766, A	905	7	1.0	146	15	US-10-424-599-242899	Sequence 242899,
833	8	1.1	967	16	US-10-437-963-118384	Sequence 118384, A	906	7	1.0	149	15	US-10-424-599-212242	Sequence 212242,
834	8	1.1	1019	14	US-10-183-992-4	Sequence 4, Appl1	907	7	1.0	151	16	US-10-437-963-147354	Sequence 147354,
835	8	1.1	1019	14	US-10-183-992-8	Sequence 8, Appl1	908	7	1.0	152	16	US-10-425-115-344973	Sequence 344973,
836	8	1.1	1019	16	US-10-638-125-4	Sequence 4, Appl1	909	7	1.0	155	13	US-10-053-200-2	Sequence 2, Appl1
837	8	1.1	1019	16	US-10-480-254-4	Sequence 4, Appl1	910	7	1.0	156	16	US-10-425-115-353363	Sequence 353363,
838	8	1.1	1019	16	US-10-480-254-8	Sequence 8, Appl1	911	7	1.0	157	15	US-10-424-599-1998827	Sequence 199887, A
839	8	1.1	1068	16	US-10-437-963-195653	Sequence 195653, A	912	7	1.0	157	15	US-10-425-114-49725	Sequence 49725, A
840	8	1.1	1083	14	US-10-183-992-6	Sequence 6, Appl1	913	7	1.0	158	16	US-10-437-963-203623	Sequence 203623,
841	8	1.1	1083	16	US-10-638-125-2	Sequence 2, Appl1	914	7	1.0	161	16	US-10-425-115-354077	Sequence 354077,
842	8	1.1	1083	16	US-10-480-254-6	Sequence 6, Appl1	915	7	1.0	164	15	US-10-259-194A-222	Sequence 222, App
843	8	1.1	1316	15	US-10-028-248A-48	Sequence 48, Appl	916	7	1.0	172	15	US-10-289-762-368	Sequence 368, App
844	8	1.1	1316	15	US-10-107-782-48	Sequence 48, Appl	917	7	1.0	172	15	US-10-282-122A-67170	Sequence 67170, A
845	8	1.1	3557	15	US-10-295-027-430	Sequence 430, App	918	7	1.0	177	16	US-10-437-963-160181	Sequence 160181,
846	8	1.1	3557	15	US-10-295-027-1297	Sequence 1297, Ap	919	7	1.0	182	16	US-10-437-963-193489	Sequence 193489,
847	8	1.1	3571	15	US-09-911-842-2	Sequence 2, Appl1	920	7	1.0	186	15	US-10-425-114-62298	Sequence 62298, A
848	8	1.1	3571	13	US-10-150-821-2	Sequence 2, Appl1	921	7	1.0	190	16	US-10-425-115-327648	Sequence 327648,
849	8	1.1	3571	16	US-10-603-283-2	Sequence 2, Appl1	922	7	1.0	192	16	US-10-437-963-104072	Sequence 104072,
850	7	1.0	11	9	US-09-192-854-170	Sequence 170, App	923	7	1.0	194	10	US-09-791-932-104	Sequence 104, App
851	7	1.0	11	9	US-09-968-561A-298	Sequence 298, App	924	7	1.0	197	16	US-10-425-115-265089	Sequence 269089,
852	7	1.0	11	10	US-09-968-744A-298	Sequence 298, App	925	7	1.0	200	9	US-09-811-284-240	Sequence 240, App
853	7	1.0	11	11	US-09-968-561A-298	Sequence 298, App	926	7	1.0	201	16	US-10-425-115-236195	Sequence 236195,
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857	7	1.0	54	9	US-09-738-626-5214	Sequence 5214, Ap	930	7	1.0	209	15	US-10-425-114-65521	Sequence 65921, A
858	7	1.0	57	16	US-10-425-115-271867	Sequence 271867, A	931	7	1.0	210	15	US-10-289-762-863	Sequence 20092, A
859	7	1.0	61	16	US-10-425-115-241375	Sequence 241375, A	932	7	1.0	210	15	US-10-289-762-863	Sequence 869, App
860	7	1.0	62	16	US-10-425-115-280568	Sequence 280568, A	933	7	1.0	210	15	US-10-282-122A-55523	Sequence 55523, A
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862	7	1.0	63	9	US-09-864-761-45299	Sequence 45299, A	935	7	1.0	212	9	US-09-815-242-10149	Sequence 10149, A
863	7	1.0	66	15	US-10-424-599-186581	Sequence 186581, A	936	7	1.0	212	15	US-10-282-122A-42990	Sequence 42990, A
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866	7	1.0	71	16	US-10-437-963-195234	Sequence 195234, A	939	7	1.0	212	15	US-10-282-122A-75987	Sequence 75987, A
867	7	1.0	72	16	US-10-425-115-226640	Sequence 226640, A	940	7	1.0	213	15	US-10-282-122A-68483	Sequence 68483, A
868	7	1.0	72	16	US-10-437-963-169418	Sequence 169418, A	941	7	1.0	214	15	US-10-425-114-71387	Sequence 71387, A
869	7	1.0	73	16	US-10-437-963-170815	Sequence 170815, A	942	7	1.0	218	15	US-10-425-114-64477	Sequence 64477, A
870	7	1.0	74	11	US-09-864-408A-8324	Sequence 8324, Ap	943	7	1.0	218	15	US-10-425-114-66377	Sequence 66377, A
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873	7	1.0	85	15	US-10-424-599-275249	Sequence 275249, A	946	7	1.0	222	15	US-10-424-599-215367	Sequence 215367, A
874	7	1.0	87	16	US-10-767-701-59878	Sequence 59878, A	947	7	1.0	223	16	US-10-437-963-178810	Sequence 178810, A
875	7	1.0	87	16	US-10-425-115-354871	Sequence 354871, A	948	7	1.0	225	16	US-10-437-963-143960	Sequence 143960, A
876	7	1.0	96	16	US-10-425-115-325970	Sequence 325970, A	949	7	1.0	227	15	US-10-282-122A-66048	Sequence 68048, A
877	7	1.0	103	16	US-10-425-115-221235	Sequence 221235, A	950	7	1.0	227	16	US-10-437-963-141632	Sequence 141632, A
878	7	1.0	104	16	US-10-425-115-230893	Sequence 230893, A	951	7	1.0	228	15	US-10-282-122A-69437	Sequence 69437, A
879	7	1.0	105	14	US-10-006-869-18	Sequence 18, Appl	952	7	1.0	230	16	US-10-437-963-178045	Sequence 178045, A
880	7	1.0	105	15	US-10-395-032-18	Sequence 18, Appl	953	7	1.0	231	15	US-10-282-122A-54986	Sequence 54986, A
881	7	1.0	105	16	US-10-654-578-18	Sequence 18, Appl	954	7	1.0	232	9	US-09-815-242-1151	Sequence 5151, Ap
882	7	1.0	107	16	US-10-425-115-293428	Sequence 293428, A	955	7	1.0	232	15	US-10-282-122A-44330	Sequence 44330, A
883	7	1.0	107	16	US-10-425-115-338738	Sequence 338738, A	956	7	1.0	239	15	US-10-282-122A-77383	Sequence 77383, A
884	7	1.0	108	9	US-09-800-095A-86	Sequence 86, Appl	957	7	1.0	244	16	US-10-437-963-155664	Sequence 155664, A
885	7	1.0	108	15	US-10-424-599-253529	Sequence 253529, A	958	7	1.0	248	15	US-10-424-599-270715	Sequence 270715, A
886	7	1.0	109	16	US-10-425-115-308576	Sequence 308576, A	959	7	1.0	250	10	US-09-898-837A-45	Sequence 45, Appl
887	7	1.0	109	16	US-10-425-115-361136	Sequence 361136, A	960	7	1.0	251	10	US-09-898-837A-41	Sequence 41, Appl
888	7	1.0	115	15	US-10-425-114-41281	Sequence 41281, A	961	7	1.0	254	16	US-10-437-963-178860	Sequence 178860, A
889	7	1.0	115	15	US-10-424-599-218597	Sequence 218597, A	962	7	1.0	257	9	US-09-815-242-13845	Sequence 13845, A
890	7	1.0	124	15	US-10-425-114-60253	Sequence 60253, A	963	7	1.0	259	11	US-09-789-210-52	Sequence 52, Appl
891	7	1.0	125	15	US-10-424-599-147558	Sequence 147558, A	964	7	1.0	259	15	US-10-165-442-2	Sequence 2, Appl1
892	7	1.0	125	16	US-10-425-115-221283	Sequence 221283, A	965	7	1.0	259	15	US-10-165-442-4	Sequence 4, Appl1
893	7	1.0	126	16	US-10-425-115-349190	Sequence 349190, A	966	7	1.0	259	16	US-10-699-393-2	Sequence 2, Appl1
894	7	1.0	127	16	US-10-425-115-322387	Sequence 322387, A	967	7	1.0	259	16	US-10-699-393-4	Sequence 4, Appl1
895	7	1.0	130	16	US-10-437-963-129837	Sequence 129837, A	968	7	1.0	259	17	US-10-872-198-5	Sequence 5, Appl1

969	7	1.0	259	17	US-10-872-197A-5	Sequence 5, Appl1	1042	7	1.0	503	9	US-09-071-035-360	Sequence 360, App
970	7	1.0	263	17	US-10-822-613-30	Sequence 30, Appl1	1043	7	1.0	503	14	US-10-206-576-360	Sequence 360, App
971	7	1.0	263	17	US-10-822-613-34	Sequence 34, Appl1	1044	7	1.0	503	17	US-10-912-362-360	Sequence 360, App
972	7	1.0	265	9	US-09-791-171-16	Sequence 16, Appl1	1045	7	1.0	509	15	US-10-114-270-94	Sequence 94, Appl1
973	7	1.0	265	10	US-09-804-980-16	Sequence 16, Appl1	1046	7	1.0	513	15	US-10-369-499-11240	Sequence 11240, A
974	7	1.0	265	16	US-10-620-246-16	Sequence 16, Appl1	1047	7	1.0	517	15	US-10-381-596A-4	Sequence 4, Appl1
975	7	1.0	267	16	US-10-437-963-10989	Sequence 10989, A	1048	7	1.0	519	15	US-10-424-599-216138	Sequence 216138, A
976	7	1.0	268	16	US-10-425-115-256594	Sequence 256594, A	1049	7	1.0	520	16	US-10-425-115-323834	Sequence 323834, A
977	7	1.0	271	16	US-10-408-765A-1200	Sequence 1200, Ap	1050	7	1.0	536	17	US-10-732-923-8530	Sequence 8530, Ap
978	7	1.0	271	16	US-10-723-860-4563	Sequence 4563, Ap	1051	7	1.0	543	15	US-10-369-493-3712	Sequence 3712, Ap
979	7	1.0	285	16	US-10-437-963-134290	Sequence 134290, A	1052	7	1.0	553	9	US-09-815-242-13391	Sequence 13391, A
980	7	1.0	285	16	US-10-767-701-35097	Sequence 35097, A	1053	7	1.0	553	15	US-10-282-122A-73854	Sequence 73854, A
981	7	1.0	292	16	US-10-437-963-1615568	Sequence 161568, A	1054	7	1.0	553	17	US-10-472-928-1116	Sequence 1116, Ap
982	7	1.0	295	15	US-10-165-442-1	Sequence 1, Appl1	1055	7	1.0	556	9	US-09-795-691-2	Sequence 2, Appl1
983	7	1.0	295	15	US-10-165-442-3	Sequence 3, Appl1	1056	7	1.0	556	14	US-10-229-662-2	Sequence 2, Appl1
984	7	1.0	295	16	US-10-699-393-1	Sequence 1, Appl1	1057	7	1.0	558	15	US-10-426-776-2	Sequence 2, Appl1
985	7	1.0	295	16	US-10-699-393-3	Sequence 3, Appl1	1058	7	1.0	558	18	US-10-617-320-4472	Sequence 4472, Ap
986	7	1.0	295	16	US-10-761-886-2	Sequence 2, Appl1	1059	7	1.0	560	16	US-10-437-963-165707	Sequence 165707, A
987	7	1.0	306	16	US-10-437-963-182869	Sequence 182869, A	1060	7	1.0	566	17	US-10-831-070-58	Sequence 58, Appl1
988	7	1.0	308	10	US-09-510-332-155	Sequence 155, App	1061	7	1.0	571	16	US-10-437-963-111762	Sequence 111762, A
989	7	1.0	308	16	US-10-770-127-155	Sequence 155, App	1062	7	1.0	573	15	US-10-282-122A-46569	Sequence 46569, A
990	7	1.0	308	17	US-10-962-365-155	Sequence 155, App	1063	7	1.0	580	17	US-10-732-923-23773	Sequence 23773, A
991	7	1.0	312	16	US-10-425-115-256595	Sequence 256595, A	1064	7	1.0	581	17	US-10-732-923-23772	Sequence 23767, A
992	7	1.0	314	15	US-10-261-845-2	Sequence 2, Appl1	1065	7	1.0	582	17	US-10-732-923-23772	Sequence 23772, A
993	7	1.0	324	15	US-10-264-049-2827	Sequence 2827, Ap	1066	7	1.0	588	15	US-10-369-493-17841	Sequence 17841, A
994	7	1.0	330	15	US-10-369-493-15829	Sequence 15829, A	1067	7	1.0	593	16	US-10-437-963-126554	Sequence 126554, A
995	7	1.0	330	15	US-10-369-493-16209	Sequence 16209, A	1068	7	1.0	600	14	US-10-156-761-8406	Sequence 8406, Ap
996	7	1.0	331	15	US-10-425-114-52205	Sequence 52205, A	1069	7	1.0	632	14	US-10-020-141-8	Sequence 8, Appl1
997	7	1.0	332	10	US-09-510-332-101	Sequence 101, App	1070	7	1.0	632	14	US-10-017-631-2	Sequence 2, Appl1
998	7	1.0	332	15	US-10-369-493-15461	Sequence 15461, A	1071	7	1.0	632	14	US-10-214-932-116	Sequence 116, App
999	7	1.0	332	16	US-10-770-127-101	Sequence 101, App	1072	7	1.0	632	14	US-10-172-712-29	Sequence 29, Appl1
1000	7	1.0	332	17	US-10-962-365-101	Sequence 101, App	1073	7	1.0	632	16	US-10-733-966A-67	Sequence 67, Appl1
1001	7	1.0	336	15	US-10-389-566-1548	Sequence 1548, Ap	1074	7	1.0	632	17	US-10-872-199-149	Sequence 149, App
1002	7	1.0	336	17	US-10-732-923-17895	Sequence 17895, A	1075	7	1.0	639	17	US-10-792-498-16	Sequence 16, Appl1
1003	7	1.0	338	15	US-10-389-566-1565	Sequence 1565, Ap	1076	7	1.0	639	17	US-10-792-498-17	Sequence 17, Appl1
1004	7	1.0	338	17	US-10-732-923-17894	Sequence 17894, A	1077	7	1.0	639	16	US-10-423-115-206708	Sequence 206708, A
1005	7	1.0	347	18	US-10-424-599-266834	Sequence 266834, A	1078	7	1.0	716	16	US-10-282-122A-50120	Sequence 50120, A
1006	7	1.0	347	18	US-10-844-096-2	Sequence 2, Appl1	1079	7	1.0	722	16	US-10-437-963-147102	Sequence 147102, A
1007	7	1.0	368	17	US-10-732-923-2972	Sequence 2972, Ap	1080	7	1.0	722	16	US-10-437-963-152918	Sequence 152918, A
1008	7	1.0	375	15	US-10-375-026A-94	Sequence 94, Appl1	1081	7	1.0	776	15	US-10-320-797-3297	Sequence 3297, Ap
1009	7	1.0	381	17	US-10-732-923-2973	Sequence 2973, Ap	1082	7	1.0	783	15	US-10-389-694-553	Sequence 553, App
1010	7	1.0	383	15	US-10-424-599-160824	Sequence 160824, A	1083	7	1.0	784	15	US-10-359-194A-178	Sequence 178, App
1011	7	1.0	386	15	US-10-425-114-50358	Sequence 50358, A	1084	7	1.0	790	14	US-10-174-677-17	Sequence 17, Appl1
1012	7	1.0	409	15	US-10-282-122A-65178	Sequence 65178, A	1085	7	1.0	799	9	US-09-738-626-4131	Sequence 4131, Ap
1013	7	1.0	416	10	US-09-976-782-114	Sequence 114, App	1086	7	1.0	799	17	US-10-494-672-142	Sequence 142, App
1014	7	1.0	427	15	US-10-425-114-38905	Sequence 38905, A	1087	7	1.0	799	17	US-10-732-923-8896	Sequence 8896, Ap
1015	7	1.0	429	16	US-10-437-963-117075	Sequence 117075, A	1088	7	1.0	839	8	US-08-945-749-1	Sequence 1, Appl1
1016	7	1.0	443	15	US-10-282-122A-62604	Sequence 62604, A	1089	7	1.0	839	16	US-10-437-963-166508	Sequence 166508, A
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1019	7	1.0	448	15	US-10-424-599-199828	Sequence 199828, A	1092	7	1.0	984	17	US-10-211-028-25	Sequence 25, Appl1
1020	7	1.0	453	15	US-10-425-114-48669	Sequence 48669, A	1093	7	1.0	986	9	US-09-850-048A-4	Sequence 4, Appl1
1021	7	1.0	456	10	US-09-932-227-64	Sequence 64, Appl1	1094	7	1.0	1074	9	US-09-071-035-358	Sequence 358, App
1022	7	1.0	456	14	US-10-183-708-6	Sequence 6, Appl1	1095	7	1.0	1074	9	US-09-071-035-394	Sequence 394, App
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1024	7	1.0	461	15	US-10-382-122A-61657	Sequence 61657, A	1097	7	1.0	1074	14	US-10-206-576-394	Sequence 394, App
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1026	7	1.0	461	15	US-10-382-122A-64914	Sequence 64914, A	1099	7	1.0	1074	17	US-10-912-362-358	Sequence 358, App
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1035	7	1.0	492	9	US-09-801-368-192	Sequence 192, App	1108	7	1.0	1346	14	US-10-201-365-5	Sequence 5, Appl1
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1119	7	1.0	2911	15	US-10-295-027-162	Sequence 162, Appl	1193	6	0.8	20	US-10-414-583-67	Sequence 67, Appl
1120	7	1.0	2911	16	US-10-408-765A-421	Sequence 421, Appl	1194	6	0.8	21	US-10-062-710-147	Sequence 47, Appl
1121	7	1.0	2911	16	US-10-723-660-1021	Sequence 1021, Appl	1195	6	0.8	21	US-10-062-710-169	Sequence 169, Appl
1122	7	1.0	3365	16	US-10-739-930-6537	Sequence 6537, Ap	1196	6	0.8	21	US-10-084-813-286	Sequence 286, Appl
1123	7	1.0	3564	15	US-10-016-248-45	Sequence 45, Appl	1197	6	0.8	21	US-10-084-813-287	Sequence 287, Appl
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1145	6	0.8	9	15	US-10-013-312-1651	Sequence 1650, Ap	1219	6	0.8	35	US-10-133-128-83	Sequence 62, Appl1
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1151	6	0.8	9	15	US-10-013-312-1922	Sequence 1922, Ap	1225	6	0.8	35	US-10-840-723-62	Sequence 62, Appl1
1152	6	0.8	10	15	US-10-013-312-178	Sequence 178, Appl	1226	6	0.8	35	US-10-871-602-62	Sequence 62, Appl1
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1159	6	0.8	10	15	US-10-013-312-2098	Sequence 2098, Appl	1233	6	0.8	37	US-10-716-379-14	Sequence 14, Appl1
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1264	6	0.8	45	9	US-09-877-665-13	Sequence 13, Appl	1337	6	0.8	56	14	US-10-080-170-237	Sequence 237, App
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1275	6	0.8	46	15	US-10-242-515-1274	Sequence 1274, App	1348	6	0.8	56	16	US-10-425-115-229357	Sequence 229357, App
1276	6	0.8	46	15	US-10-424-599-211167	Sequence 211167, A	1349	6	0.8	56	16	US-10-425-115-229359	Sequence 229359, App
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